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(54) Title: METHODS OF DIAGNOSIS OF BLADDER CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF BLADDER CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in bladder cancer. Also described are such genes whose expression is further up-regulated or down-regulated in drug-resistant bladder cancer cells. Related methods and compositions that can be used for diagnosis, prognosis, or treatment of bladder cancer are disclosed. Also described herein are methods that can be used to identify modulators of bladder cancer.



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METHODS OF DIAGNOSIS OF BLADDER CANCER, COMPOSITIONS AND
METHODS OF SCREENING FOR MODULATORS OF BLADDER CANCER

CROSS-REFERENCES TO RELATED APPLICATIONS

5 This application is related to USSN 60/302,814, filed July 3, 2001; USSN 60/310,099, filed August 3, 2001; USSN 60/343,705, filed November 8, 2001; USSN 60/350,666, filed November 13, 2001; and USSN 60/372,246, filed April 12, 2001, each of which is incorporated herein by reference.

10 FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in bladder cancer; and to the use of such expression profiles and compositions in the diagnosis, prognosis, and therapy of bladder cancer. The invention further relates to methods for identifying and using agents and/or targets that inhibit bladder cancer.

BACKGROUND OF THE INVENTION

In the United States, over 50,000 new cases of bladder cancer are diagnosed annually, and more than 10,000 deaths will be attributed to bladder cancer. Bladder cancer is now the fourth most common cancer among American men and the ninth most common cancer among American women. It occurs three times more frequently in men than in women, and it occurs roughly twice more frequently in white versus black men.

Bladder cancer rarely occurs in people younger than 40 years of age, being primarily a disease of older men. Nonetheless, bladder cancer is a significant cause of illness and death in the United States. The risk of bladder cancer increases steeply with age, with over half of all bladder cancer deaths occurring after age 70. In white men older than 65, the annual disease rate of bladder cancer is approximately 2 cases per 1,000 persons; this contrasts with a rate of 0.1 cases per 1,000 persons younger than 65.

Within the United States, bladder cancer rates are higher among people who reside in northern versus southern states, and is higher for people who live in urban versus rural areas. Although this difference suggests that environmental as well as genetic factors may contribute to the development and progression of the disease, other studies confirm that certain genes play a role in bladder cancer.. For example, expression of the tumor suppressor gene p53 has been associated with an adverse prognosis for patients with invasive bladder cancer. A retrospective study of 243 patients treated by radical cystectomy found that the presence of nuclear p53 was an independent predictor for recurrence among patients with mid to late stage tumors. Esrig, et al (1994) N.E.J. Med. 331:1259-64.

Urinary bladder cancers represent a spectrum of diseases that can be grouped into three general categories: superficial, invasive, and metastatic. The prognosis for treatment is highly dependent on the stage at which the tumor is first diagnosed. A unique aspect of bladder cancer treatment is that repeated surgical biopsy is an integral part of routine patient management. This has permitted the conduct of molecular genetic studies of tumors from specific stages of the disease. The results of these studies suggest that bladder cancers develop and progress along at least two discrete pathways, which may account for differences in invasiveness and metastatic potential. Incorporating molecular genetic factors into the current paradigm for diagnosis and treatment will optimize the probability of cure and allow the quality of life for bladder cancer patients to be maintained.

Early detection and treatment can prevent reoccurrence and progression of the disease to an incurable stage. Thus, the identification of novel diagnostic markers and therapeutic targets will improve the current treatment of bladder cancer patients. While industry and academia have identified novel sequences, there has not been an equal effort exerted to identify the function of these novel sequences in disease states. The elucidation of a role for novel proteins and compounds in disease states for identification of diagnostic markers and therapeutic targets is essential for improving the current treatment of bladder cancer patients. Accordingly, provided herein are methods that can be used in diagnosis and prognosis of bladder cancer. Additionally, provided herein are molecular targets for therapeutic intervention in bladder cancer and other related bladder diseases.. Further provided are

methods that can be used to screen candidate bioactive agents for the ability to modulate bladder cancer.

SUMMARY OF THE INVENTION

5 The present invention therefore provides nucleotide sequences of genes that are up- and down-regulated in bladder cancer cells. Such genes are useful for diagnostic purposes, and also as targets for screening for therapeutic compounds that modulate bladder cancer, such as hormones or antibodies. Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

10 In one aspect, the present invention provides a method of detecting a bladder cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-13.

15 In one embodiment, the present invention provides a method of determining the level of a bladder cancer associated transcript in a cell from a patient.

 In one embodiment, the present invention provides a method of detecting a bladder cancer-associated transcript in a cell from a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-13.

20 In one embodiment, the polynucleotide selectively hybridizes to a sequence at least 95% identical to a sequence as shown in Tables 1A-13.

 In one embodiment, the biological sample is a tissue sample. In another embodiment, the biological sample comprises isolated nucleic acids, e.g., mRNA.

 In one embodiment, the polynucleotide is labeled, e.g., with a fluorescent label.

25 In one embodiment, the polynucleotide is immobilized on a solid surface.

 In one embodiment, the patient is undergoing a therapeutic regimen to treat bladder cancer. In another embodiment, the patient is suspected of having metastatic bladder cancer.

 In one embodiment, the patient is a human.

 In one embodiment, the bladder cancer associated transcript is mRNA.

In one embodiment, the method further comprises the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide.

In another aspect, the present invention provides a method of monitoring the efficacy of a therapeutic treatment of bladder cancer, the method comprising the steps of: (i) providing
5 a biological sample from a patient undergoing the therapeutic treatment; and (ii) determining the level of a bladder cancer-associated transcript in the biological sample by contacting the biological sample with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-13, thereby monitoring the efficacy of the therapy. In a further embodiment, the patient has metastatic bladder cancer. In a further
10 embodiment, the patient has a drug resistant form of bladder cancer.

In one embodiment, the method further comprises the step of: (iii) comparing the level of the bladder cancer-associated transcript to a level of the bladder cancer-associated transcript in a biological sample from the patient prior to, or earlier in, the therapeutic treatment.

15 Additionally, provided herein is a method of evaluating the effect of a candidate bladder cancer drug comprising administering the drug to a patient and removing a cell sample from the patient. The expression profile of the cell is then determined. This method may further comprise comparing the expression profile to an expression profile of a healthy individual. In a preferred embodiment, said expression profile includes a gene of Tables 1A-
20 13.

In one aspect, the present invention provides an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1A-13.

In one embodiment, an expression vector or cell comprises the isolated nucleic acid.

In one aspect, the present invention provides an isolated polypeptide which is encoded
25 by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-13.

In another aspect, the present invention provides an antibody that specifically binds to an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1A-13.

In one embodiment, the antibody is conjugated to an effector component, e.g., a
30 fluorescent label, a radioisotope or a cytotoxic chemical.

In one embodiment, the antibody is an antibody fragment. In another embodiment, the antibody is humanized.

In one aspect, the present invention provides a method of detecting a bladder cancer cell in a biological sample from a patient, the method comprising contacting the biological
5 sample with an antibody as described herein.

In another aspect, the present invention provides a method of detecting antibodies specific to bladder cancer in a patient, the method comprising contacting a biological sample from the patient with a polypeptide encoded by a nucleic acid comprising a sequence from
Tables 1A-13.

10 In another aspect, the present invention provides a method for identifying a compound that modulates a bladder cancer-associated polypeptide, the method comprising the steps of: (i) contacting the compound with a bladder cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-13; and (ii) determining the functional effect of the
15 compound upon the polypeptide.

In one embodiment, the functional effect is a physical effect, an enzymatic effect, or a chemical effect.

In one embodiment, the polypeptide is expressed in a eukaryotic host cell or cell membrane. In another embodiment, the polypeptide is recombinant.

20 In one embodiment, the functional effect is determined by measuring ligand binding to the polypeptide.

In another aspect, the present invention provides a method of inhibiting proliferation of a bladder cancer-associated cell to treat bladder cancer in a patient, the method comprising the step of administering to the subject a therapeutically effective amount of a compound
25 identified as described herein.

In one embodiment, the compound is an antibody.

In another aspect, the present invention provides a drug screening assay comprising the steps of: (i) administering a test compound to a mammal having bladder cancer or to a cell sample isolated therefrom; (ii) comparing the level of gene expression of a
30 polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence

as shown in Tables 1A-13 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell sample or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of bladder cancer.

5 In one embodiment, the control is a mammal with bladder cancer or a cell sample therefrom that has not been treated with the test compound. In another embodiment, the control is a normal cell or mammal.

 In one embodiment, the test compound is administered in varying amounts or concentrations. In another embodiment, the test compound is administered for varying time
10 periods. In another embodiment, the comparison can occur after addition or removal of the drug candidate.

 In one embodiment, the levels of a plurality of polynucleotides that selectively hybridize to a sequence at least 80% identical to a sequence as shown in Tables 1A-13 are individually compared to their respective levels in a control cell sample or mammal. In a
15 preferred embodiment the plurality of polynucleotides is from three to ten.

 In another aspect, the present invention provides a method for treating a mammal having bladder cancer comprising administering a compound identified by the assay described herein.

 In another aspect, the present invention provides a pharmaceutical composition for
20 treating a mammal having bladder cancer, the composition comprising a compound identified by the assay described herein and a physiologically acceptable excipient.

 In one aspect, the present invention provides a method of screening drug candidates by providing a cell expressing a gene that is up- and down-regulated as in a bladder cancer. In one embodiment, a gene is selected from Tables 1A-13. The method further includes
25 adding a drug candidate to the cell and determining the effect of the drug candidate on the expression of the expression profile gene.

 In one embodiment, the method of screening drug candidates includes comparing the level of expression in the absence of the drug candidate to the level of expression in the presence of the drug candidate, wherein the concentration of the drug candidate can vary
30 when present, and wherein the comparison can occur after addition or removal of the drug

candidate. In a preferred embodiment, the cell expresses at least two expression profile genes. The profile genes may show an increase or decrease.

Also provided is a method of evaluating the effect of a candidate bladder cancer drug comprising administering the drug to a transgenic animal expressing or over-expressing the
5 bladder cancer modulatory protein, or an animal lacking the bladder cancer modulatory protein, for example as a result of a gene knockout.

Moreover, provided herein is a biochip comprising one or more nucleic acid segments of Tables 1A-13, wherein the biochip comprises fewer than 1000 nucleic acid probes. Preferably, at least two nucleic acid segments are included. More preferably, at least three
10 nucleic acid segments are included.

Furthermore, a method of diagnosing a disorder associated with bladder cancer is provided. The method comprises determining the expression of a gene of Tables 1A-13 in a first tissue type of a first individual, and comparing the distribution to the expression of the gene from a second normal tissue type from the first individual or a second unaffected
15 individual. A difference in the expression indicates that the first individual has a disorder associated with bladder cancer.

In a further embodiment, the biochip also includes a polynucleotide sequence of a gene that is not up- and down-regulated in bladder cancer.

In one embodiment a method for screening for a bioactive agent capable of interfering
20 with the binding of a bladder cancer modulating protein (bladder cancer modulatory protein) or a fragment thereof and an antibody which binds to said bladder cancer modulatory protein or fragment thereof. In a preferred embodiment, the method comprises combining a bladder cancer modulatory protein or fragment thereof, a candidate bioactive agent and an antibody which binds to said bladder cancer modulatory protein or fragment thereof. The method
25 further includes determining the binding of said bladder cancer modulatory protein or fragment thereof and said antibody. Wherein there is a change in binding, an agent is identified as an interfering agent. The interfering agent can be an agonist or an antagonist. Preferably, the agent inhibits bladder cancer.

Also provided herein are methods of eliciting an immune response in an individual.
30 In one embodiment a method provided herein comprises administering to an individual a

composition comprising a bladder cancer modulating protein, or a fragment thereof. In another embodiment, the protein is encoded by a nucleic acid selected from those of Tables 1A-13.

Further provided herein are compositions capable of eliciting an immune response in an individual. In one embodiment, a composition provided herein comprises a bladder cancer modulating protein, preferably encoded by a nucleic acid of Tables 1A-13 or a fragment thereof, and a pharmaceutically acceptable carrier. In another embodiment, said composition comprises a nucleic acid comprising a sequence encoding a bladder cancer modulating protein, preferably selected from the nucleic acids of Tables 1A-13, and a pharmaceutically acceptable carrier.

Also provided are methods of neutralizing the effect of a bladder cancer protein, or a fragment thereof, comprising contacting an agent specific for said protein with said protein in an amount sufficient to effect neutralization. In another embodiment, the protein is encoded by a nucleic acid selected from those of Tables 1A-13.

In another aspect of the invention, a method of treating an individual for bladder cancer is provided. In one embodiment, the method comprises administering to said individual an inhibitor of a bladder cancer modulating protein. In another embodiment, the method comprises administering to a patient having bladder cancer an antibody to a bladder cancer modulating protein conjugated to a therapeutic moiety. Such a therapeutic moiety can be a cytotoxic agent or a radioisotope.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and prognosis evaluation for bladder disease (BD), e.g., cancer, including metastatic bladder cancer, as well as methods for screening for compositions which modulate bladder diseases. Also provided are methods and compositions for treating bladder disease. Various related conditions where these markers may be useful also, include, e.g., carcinoma in situ, various stages of papillary carcinomas; and such conditions in different stages, layers, structural portions, etc.

Recent advances in molecular medicine, generally, have increased the interest in tumor-specific cell surface antigens that could serve as diagnostic or prognostic markers, or as targets for various immunotherapeutic or small molecule strategies. Antigens suitable for immunotherapeutic strategies should be highly expressed in cancer tissues and ideally not expressed in other, e.g., normal, adult tissues. Expression in tissues that are dispensable for life, however, may be tolerated, as a physiological consequence of such expression would be limited. Examples of such antigens in cancers other than bladder cancer include Her2/neu and the B-cell antigen CD20. Humanized monoclonal antibodies directed to Her2/neu (Herceptin®/trastuzumab) are currently in use for the treatment of metastatic breast cancer. Ross and Fletcher (1998) Stem Cells 16:413-428. Similarly, anti-CD20 monoclonal antibodies (Rituxin®/rituximab) are used to effectively treat non-Hodgkin's lymphoma. Maloney, et al. (1997) Blood 90:2188-2195; and Leget and Czuczman (1998) Curr. Opin. Oncol. 10:548-551.

Definitions

The term "bladder cancer protein" or "bladder cancer polynucleotide" or "bladder cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologues that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater nucleotide sequence identity, preferably over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a gene of Tables 1A-13; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1A-13, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1A-13 and conservatively modified variants thereof; or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater amino sequence identity, preferably over a region of at least

about 25, 50, 100, 200, 500, 1000, or more amino acid, to an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1A-13. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A
5 "bladder cancer polypeptide" and a "bladder cancer polynucleotide," include both naturally occurring or recombinant forms.

A "full length" bladder cancer protein or nucleic acid refers to a bladder cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains all of the elements normally contained in one or more naturally occurring, wild type bladder cancer
10 polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of splicing, including alternative splicing, or post-translation processing.

"Biological sample" as used herein is a sample of biological tissue or fluid, e.g., that contains nucleic acids or polypeptides of a bladder cancer protein, polynucleotide, or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g.,
15 humans, or rodents, e.g., mice and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, blood, plasma, serum, sputum, stool, urine, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most
20 preferably a mammal such as a primate, e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, or mouse; rabbit; or a bird; reptile; or fish.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g.,
25 isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same
30 or have a specified percentage of amino acid residues or nucleotides that are the same (e.g.,

about 60% identity, preferably 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters
5 described below, or by manual alignment and visual inspection (see, e.g., NCBI web site <http://www.ncbi.nlm.nih.gov/BLAST/> or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes sequences that have deletions and/or additions, substitutions, naturally occurring variants, e.g., polymorphic or allelic, and man-
10 made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to
15 which test sequences are compared. When using a sequence comparison computer algorithm, test and reference sequences, subsequence coordinates, and sequence algorithm program parameters are typically designated. Default or alternative program parameters can be selected. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

20 A "comparison window", as used herein, includes reference to a segment of one of the number of contiguous positions selected from the group consisting typically of from about 20-600, usually about 50-200, more usually about 100-150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are
25 well-known in the art. Optimal alignment of sequences for comparison can be conducted, by, e.g., the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482, the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443-453, the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l Acad. Sci. USA 85:2444-448, computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer
30

Group, 575 Science Dr., Madison, WI), or manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology Lippincott.

Preferred algorithms suitable for determining percent sequence identity and sequence
5 similarity include the BLAST and BLAST 2.0 algorithms. See Altschul, et al. (1977) Nuc.
Acids Res. 25:3389-3402; and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and
BLAST 2.0 are used, with the parameters described herein, to determine percent sequence
identity for the nucleic acids and proteins of the invention. Software for performing BLAST
analyses is publicly available through the National Center for Biotechnology Information
10 (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring
sequence pairs (HSPs) by identifying short words of length W in the query sequence, which
either match or satisfy some positive-valued threshold score T when aligned with a word of
the same length in a database sequence. T is referred to as the neighborhood word score
threshold (Altschul, et al., supra). These initial neighborhood word hits act as seeds for
15 initiating searches to find longer HSPs containing them. The word hits are extended in both
directions along each sequence for as far as the cumulative alignment score can be increased.
Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M
(reward score for a pair of matching residues; always > 0) and N (penalty score for
mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to
20 calculate the cumulative score. Extension of the word hits in each direction are halted when:
the cumulative alignment score falls off by the quantity X from its maximum achieved value;
the cumulative score goes to zero or below, due to the accumulation of one or more negative-
scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm
parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN
25 program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation
(E) of 10, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the
BLASTP program uses as defaults a wordlength of 3, expectation (E) of 10, and the
BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Nat'l Acad. Sci. USA
89:10915-919) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of
30 both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) Proc. Nat'l Acad. Sci. USA 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between
5 two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be large negative numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

10 An indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid, as described below. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another
15 indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions, as described below. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an
20 expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells in vivo, and the like. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

25 The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a
30 preparation is substantially purified. In particular, an isolated nucleic acid is separated from

some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments typically denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least 85% pure, more preferably at least 95%
5 pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing at least one contaminant from the composition to be purified. In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% pure.

The terms "polypeptide," "peptide," and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which
10 at least one amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and a non-naturally occurring amino acid polymer.

The term "amino acid" embraces naturally occurring or synthetic amino acids, amino acid analogs, and amino acid mimetics. Naturally occurring amino acids are those encoded
15 by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs include compounds that share a basic chemical structure with a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, or an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have
20 modified R groups (e.g., norleucine) or modified peptide backbones, but share some basic chemical structure with a naturally occurring amino acid. Amino acid mimetics include chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that function similarly to a naturally occurring amino acid.

Amino acids may be referred to herein by their commonly known three letter symbols
25 or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to amino acid or nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to
30 those nucleic acids which encode identical or essentially identical amino acid sequences, or

where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU all encode the amino acid alanine. Thus, at
5 each position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Each nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. One of skill will recognize that in certain contexts each
10 codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, often silent variations of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not with respect to actual probe sequences.

15 As to amino acid sequences, one of skill will recognize that individual substitutions, deletions, or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds, or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution
20 tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions for one another include: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L),
25 Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M). See, e.g., Creighton (1984) Proteins: Structure and Molecular Properties Freeman.

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. See, e.g., Alberts, et al. (eds. 2001) Molecular Biology of the
30 Cell (4th ed.) Garland; and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The

Conformation of Biological Macromolecules Freeman. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains, which are portions of a polypeptide that often form a compact unit of the polypeptide, and are typically about 25-500 amino acids long. Typical domains are made of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50 or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are polymers, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds. In some cases, nucleic acid analogs are included that may have alternate backbones, e.g., phosphoramidate (Beaucage, et al. (1993) Tetrahedron 49:1925-963 and references therein; Letsinger (1970) J. Org. Chem. 35:3800-803; Sprinzl, et al. (1977) Eur. J. Biochem. 81:579-589; Letsinger, et al. (1986) Nucl. Acids Res. 14:3487-499; Sawai, et al. (1984) Chem. Lett. 805; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-471; and Pauwels, et al. (1986) Chemica Scripta 26:141-149); phosphorothioate (Mag, et al. (1991), Nucleic Acids Res. 19:1437-441; and U.S. Patent No. 5,644,048); phosphorodithioate (Brill, et al. (1989) J. Am. Chem. Soc. 111:2321-322); O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford Univ. Press); and peptide nucleic acid backbones and linkages (see Egholm (1992) J. Am. Chem. Soc. 114:1895-897; Meier, et al. (1992) Chem. Int. Ed. Engl. 31:1008-010; Nielsen (1993) Nature 365:566-568; Carlsson, et al. (1996) Nature 380:207. Other analog nucleic acids include those with positively charged backbones (Denpcy, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:6097-101); non-ionic backbones (U.S. Patent Nos. 5,386,023; 5,637,684; 5,602,240; 5,216,141; and 4,469,863; Kiedrowshi, et al. (1991) Angew. Chem. Intl. Ed. English 30:423-426;

- Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-471; Jung, et al. (1994) Nucleoside and Nucleotide 13:1597-xxx; Chapters 2-3 of Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580; Mesmaeker, et al. (1994) Bioorganic and Medicinal Chem. Lett. 4:395-398; Jeffs, et al. (1994) J. Biomolecular NMR 34:17; Horn, et al. (1996) Tetrahedron Lett. 37:743-xxx); and non-ribose backbones (see U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6-7 of Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also contemplated. See Jenkins and Turner (1995) Chem. Soc. Rev. 24:169-176. Several nucleic acid analogs are described in Rawls (page 35, June 2, 1997) C&E News. Modifications of the ribose-phosphate backbone may be made, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.
- 15 Particularly preferred are peptide nucleic acids (PNA) which include peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. The PNA backbone typically exhibits improved hybridization kinetics, exhibiting larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs.
- 20 DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. And due to their non-ionic nature, hybridization of the polymers is relatively insensitive to salt concentration. In addition, PNAs are not as easily degraded by cellular enzymes, and can be more stable.

25 The nucleic acids may be single stranded or double stranded, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary strand; thus the sequences described herein also provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases,

30 including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine, hypoxanthine,

isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures.

5 Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A "label" or "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, chemical, or other physical means. Direct or indirect methods are contemplated. For example, useful labels include ³²P, fluorescent
10 dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide. The labels may be incorporated into the bladder cancer nucleic acids, proteins, and antibodies. Methods are well known for conjugating the antibody to the label,
15 including those methods described by Hunter, et al. (1962) Nature 144:945-946; David, et al. (1974) Biochemistry 13:1014-021; Pain, et al. (1981) J. Immunol. Meth. 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or
20 noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to a target, e.g., an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds; fluorescent compounds; an enzyme or substrate; tags such as epitope tags; a toxin; activatable moieties; a chemotherapeutic agent; a lipase; an antibiotic; a radioisotope emitting "hard", e.g., beta radiation; or an attracting moiety.

25 A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method using high affinity interactions may achieve the same results where one of a pair of binding
30 partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is defined as a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (e.g., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled as with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which streptavidin linked label may bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed, or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operable linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, e.g., using in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced

recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention. Similarly, a "recombinant protein" is a protein made using recombinant techniques, e.g., through the expression of a recombinant nucleic acid as depicted above.

5 The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a
10 coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is defined as an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid
15 sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is
20 active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

25 An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed operably linked to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

- 5 The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview
10 of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Hybridization with Nucleic Probes (Techniques in Biochemistry and Molecular Biology; vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic acid concentration) at which
15 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g.,
20 about 10-50 nucleotides) and at least about 60° C for long probes (e.g., greater than about 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is at least about two times background, preferably about 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC,
25 and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32-48° C depending on primer length. For high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50-

65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90-95° C for 30-120 sec, an annealing phase lasting 30-120 sec, and an extension phase of about 72° C for 1-2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis, et al. (1990) PCR Protocols, A Guide to Methods and Applications Academic Press NY.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is at least about twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous references, e.g., Ausubel, et al. Current Protocols in Molecular Biology Lippincott.

The phrase "functional effects" in the context of assays for testing compounds that modulate activity of a bladder cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the bladder cancer protein or nucleic acid, e.g., a functional, physical, or chemical effect, such as the ability to decrease bladder cancer. It includes ligand binding activity; cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cell viability, cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis, and other characteristics of bladder cancer cells. "Functional effects" include in vitro, in vivo, and ex vivo activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a bladder cancer protein sequence, e.g., functional, enzymatic, physical and chemical effects.

Such functional effects can be measured by many means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the bladder cancer protein;

5 measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring cellular proliferation or metabolism. Determination of the functional effect of a compound on bladder cancer can also be performed using bladder cancer assays, such as, in vitro assays, e.g., cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or

10 serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis, and other characteristics of bladder cancer cells. Functional effects can be evaluated by many means, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for bladder

15 cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators", and "modulators" of bladder cancer polynucleotide and

20 polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using in vitro and in vivo assays of bladder cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of bladder cancer proteins, e.g., antagonists. Antisense nucleic acids

25 may seem to inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate bladder cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of bladder cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small

30 chemical molecules and the like. Such assays for inhibitors and activators include, e.g.,

expressing the bladder cancer protein in vitro, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of bladder cancer can also be identified by incubating bladder cancer cells with the test compound and determining increases or decreases in the expression of 1 or more bladder cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50 or more bladder cancer proteins, such as bladder cancer proteins encoded by the sequences set out in Tables 1A-13.

Samples or assays comprising bladder cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably about 50%, more preferably about 25-0%. Activation of a bladder cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is about 110%, more preferably about 150%, more preferably about 200-500% (e.g., two to five fold higher relative to the control), more preferably about 1000-3000% higher.

The phrase "changes in cell growth" refers to a change in cell growth and proliferation characteristics in vitro or in vivo, such as cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., pp. 231-241 of Freshney (1994) Culture of Animal Cells: A Manual of Basic Technique (3d ed.).

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene.

Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy. See, Freshney (2000) Culture of Animal Cells: A Manual of Basic Technique (4th ed.) Wiley-Liss.

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself is a light chain joined to V_H - C_H1 by a disulfide bond. The $F(ab)'_2$ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab)'_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region. See Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven. While various antibody fragments are defined in terms of the digestion of an intact antibody, such fragments may be synthesized de novo either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized de novo using

recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries. See, e.g., McCafferty, et al. (1990) Nature 348:552-554.

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many techniques can be used. See, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. pp. 77-96 in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; Coligan (1991) Current Protocols in Immunology Lippincott; Harlow and Lane (1988) Antibodies: A Laboratory Manual CSH Press; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.) Academic Press. Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens. See, e.g., McCafferty, et al. (1990) Nature 348:552-554; and Marks, et al. (1992) Biotechnology 10:779-783.

A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a portion thereof, is altered, replaced, or exchanged with a variable region having a different or altered antigen specificity.

Identification of bladder cancer-associated sequences

In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue (e.g., normal bladder or other

tissue) may be distinguished from cancerous or metastatic cancerous tissue of the bladder, or bladder cancer tissue or metastatic bladder cancerous tissue can be compared with tissue samples of bladder and other tissues from surviving cancer patients. By comparing expression profiles of tissue in known different bladder cancer states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained.

The identification of sequences that are differentially expressed in bladder cancer versus non-bladder cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate bladder cancer, and thus tumor growth or recurrence, in a particular patient; or does chemotherapy or radiation therapy induce expression of particular targets. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Metastatic tissue can also be analyzed to determine the stage of bladder cancer in the tissue or origin of a primary tumor. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the bladder cancer expression profile. This may be done by making biochips comprising sets of important bladder cancer genes, which can then be used in these screens. These methods can also be applied on the protein basis; that is, protein expression levels of the bladder cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the bladder cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense or inhibitory nucleic acids, or the bladder cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in bladder disease or cancer relative to normal tissues and/or non-malignant bladder tissue, herein termed "bladder cancer sequences." As outlined below, bladder cancer sequences include those that are up-regulated (e.g., expressed at a higher level) in bladder cancer, as well as those that are down-regulated (e.g., expressed at a lower level). In a preferred embodiment, the bladder cancer sequences are from humans; however,

as will be appreciated by those in the art, bladder cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other bladder cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets, e.g., (dogs, cats, etc.). Bladder cancer sequences from other organisms may be obtained using the techniques outlined below.

Bladder cancer sequences can include both nucleic acid and amino acid sequences. Bladder cancer nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications. Biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the bladder cancer sequences can be generated.

A bladder cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the bladder cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

For identifying bladder cancer-associated sequences, the bladder cancer screen typically includes comparing genes identified in different tissues, e.g., normal, non-malignant, or cancerous tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing bladder cancer samples with metastatic cancer samples from other cancers, such as lung, bladder, gastrointestinal cancers, ovarian, etc. Samples of different stages of bladder cancer, e.g., survivor tissue, drug resistant states, and tissue undergoing metastasis, are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated for the preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, preferably normal bladder, but also including, and not limited to lung, heart, brain, liver, bladder, kidney,

muscle, colon, small intestine, large intestine, spleen, bone, and placenta. In a preferred embodiment, those genes identified during the bladder cancer screen that are expressed in a significant amount in other tissues are removed from the profile, although in some embodiments, this is not necessary. That is, when screening for drugs, it is usually preferable that the target be disease specific, e.g., not be expressed on critical organs.

In a preferred embodiment, bladder cancer sequences are those that are up-regulated in bladder cancer; that is, the expression of these genes is higher in the bladder cancer tissue as compared to non-cancerous tissue. "Up-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. Unigene cluster identification numbers and accession numbers herein are for the GenBank sequence database and sequences of accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, e.g., Benson, et al. (1998) *Nuc. Acids Res.* 26:1-7 and <http://www.ncbi.nlm.nih.gov/>. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ).

In another preferred embodiment, bladder cancer sequences are those that are down-regulated in the bladder cancer; that is, the expression of these genes is lower in bladder cancer tissue as compared to non-cancerous tissue (see, e.g., Tables 1A-13). "Down-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred.

Informatics

The ability to identify genes that are over or under expressed in bladder cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with bladder cancer. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation. See Anderson (June 11-12, 1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference,

Coronado, CA. Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, 5 saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic 10 database of the invention can be maintained on an electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent that similar databases can be assembled for 15 assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample undergoing bladder cancer, e.g., the identification of bladder cancer-associated sequences described herein, provide an abundance of information, which can be correlated 20 with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, prior data processing using high-speed computers is utilized.

25 An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing 30 information in a format that allows a collection of partial-length DNA sequences to be

catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity
5 between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis
10 described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as
15 the merger of two or more such tree structures.

See also Mount, et al. (2001) Bioinformatics CSH Press, NY; Durbin, et al. (eds. 1999) Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids Cambridge Univ. Press; Baxevanis and Ouellette (eds. 1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins (2d. ed.) Wiley-Liss; Rashidi and Buehler
20 (1999) Bioinformatics: Basic Applications in Biological Science and Medicine CRC Press; Setubal, et al. (eds 1997) Introduction to Computational Molecular Biology Brooks/Cole; Misener and Krawetz (eds. 2000) Bioinformatics: Methods and Protocols Oxford Univ. Press; Higgins and Taylor (eds. 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical Approach Oxford Univ. Press; Brown (2001) Bioinformatics: A Biologist's Guide to
25 Biocomputing and the Internet Eaton Pub.; Han and Kamber (2000) Data Mining: Concepts and Techniques Kaufmann Pub.; and Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes Chap and Hall.

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g.,

with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for bladder cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention
5 in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at
10 least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem,
15 ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result
20 obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data
25 file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of
30 the query target and results are output via an I/O device. For example, a central processor

can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

Characteristics of bladder cancer-associated proteins

Bladder cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In one embodiment, the bladder cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or dysregulated cellular processes (see, e.g., Alberts, et al. (1994) Molecular Biology of the Cell (3d ed.) Garland. For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In

addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden. See, e.g., Bateman, et al. (2000) Nuc. Acids Res. 28:263-266; Sonnhammer, et al. (1997) Proteins 28:405-420; Bateman, et al. (1999) Nuc. Acids Res. 27:260-262; and Sonnhammer, et al. (1998) Nuc. Acids Res. 26:320-322.

In another embodiment, the bladder cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases

and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain
5 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site <http://psort.nibb.ac.jp/>). Important transmembrane protein receptors
10 include, but are not limited to the insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, and interleukin receptors, e.g., IL-1 receptor, IL-2 receptor, etc.

The extracellular domains of transmembrane proteins are diverse; however, conserved
15 motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example,
20 growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or
25 may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Bladder cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful
30 in imaging modalities. Antibodies may be used to label such readily accessible proteins in

situ. Alternatively, antibodies can also label intracellular proteins, in which case samples are typically permeabilized to provide access to intracellular proteins.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods.

5 Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the bladder cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted
10 proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion into the blood stream), or exocrine (secretion, e.g., through a
15 duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, wax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or altering numerous aspects of physiology. Bladder cancer proteins that are secreted or released proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, e.g., for blood, plasma, serum,
20 or urine tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms.

Use of bladder cancer nucleic acids

As described above, bladder cancer sequence is initially identified by substantial
25 nucleic acid and/or amino acid sequence homology or linkage to the bladder cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

The bladder cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1A-13, can be fragments of larger genes, e.g., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the bladder cancer genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, et al., supra. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, <http://www.ncbi.nlm.nih.gov/UniGene/>).

Once a bladder cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire bladder cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant bladder cancer nucleic acid can be further-used as a probe to identify and isolate other bladder cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant bladder cancer nucleic acids and proteins.

The bladder cancer nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the bladder cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, vaccine, and/or antisense/inhibition applications. Alternatively, the bladder cancer nucleic acids that include coding regions of bladder cancer proteins can be put into expression vectors for the expression of bladder cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to bladder cancer nucleic acids (both the nucleic acid sequences outlined in the tables and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the bladder cancer nucleic acids, e.g., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that

hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be a number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

10 A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally whole
15 genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a particular target. The probes can be overlapping (e.g., have some sequence in common), or
20 separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of
25 the biotinylated probe to the streptavidin. By "covalent binding" and grammatical
30

equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified to contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. See WO 00/55627.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being

particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers as are known in the art; e.g., homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized as is known in the art, and then attached to the surface of the solid support. As will be appreciated by those skilled in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using well known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affimetrix GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of bladder cancer-associated sequences. These assays are typically performed in conjunction with reverse transcription. In such assays, a bladder cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of bladder cancer-associated RNA. Methods of quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative

PCR are provided, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications Academic Press.

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification. See, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com.

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) Genomics 4:560-569; Landegren, et al. (1988) Science 241:1077-1080; and Barringer, et al. (1990) Gene 89:117-122), transcription amplification (Kwoh, et al. (1989) Proc. Nat'l Acad. Sci. USA 86:1173-1177), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Nat'l Acad. Sci. USA 87:1874-1878), dot PCR, and linker adapter PCR, etc.

Expression of bladder cancer proteins from nucleic acids

In a preferred embodiment, bladder cancer nucleic acids, e.g., encoding bladder cancer proteins, are used to make a variety of expression vectors to express bladder cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known to those of skill in the art (see, e.g., Ausubel, supra, and Fernandez and Hoeffler (eds. 1999) Gene Expression Systems Academic Press) and are used to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the bladder cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a

promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation; two sequences may be operably linked if they are physically linked on a single polynucleotide. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the bladder cancer protein. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences encode either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are useful in the present invention.

In addition, an expression vector may comprise additional elements. The expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a procaryotic host for cloning and replication. For integrating expression vectors, the expression vector may contain at least one sequence homologous to the host cell genome, and preferably two homologous sequences

which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known (e.g., Fernandez and Hoeffler, supra).

- 5 In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

 The bladder cancer proteins of the present invention may be produced by culturing a host cell transformed with an expression vector under the appropriate conditions to induce or
10 cause expression of the bladder cancer protein. Conditions appropriate for bladder cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will typically require optimizing the growth and proliferation of the host cell, while the use of an
15 inducible promoter typically requires identifying the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and harvest time selection can be crucial for product yield.

 Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, insect, and
20 animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

 In a preferred embodiment, the bladder cancer proteins are expressed in mammalian
25 cells. Mammalian expression systems include retroviral and adenoviral systems. Retroviral vector systems are described in PCT/US97/01019 and PCT/US97/01048. Of particular use are promoters from mammalian viral genes, since viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the
30 CMV promoter (see, e.g., Fernandez and Hoeffler, supra). Typically, transcription

termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

5 Methods of introducing exogenous nucleic acid into mammalian and other hosts are well known, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

10 In another embodiment, bladder cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used. Synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. A bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. Often an efficient
15 ribosome binding site is desirable. The expression vector may include a signal peptide sequence that provides for secretion of the bladder cancer protein. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may include a selectable marker gene to allow for the selection of bacterial
20 strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs, e.g., ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin, and tetracycline, or biosynthetic genes, e.g., those in the histidine, tryptophan, and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus*
25 cremoris, and *Streptococcus lividans*, among others (e.g., Fernandez and Hoeffler, supra). The bacterial expression vectors are transformed into bacterial host cells using, e.g., calcium chloride treatment, electroporation, and other methods.

 Bladder cancer proteins can also be produced in insect cells. See, e.g., Miller, et al. (1997) Baculovirus Expression Vectors: A Laboratory Manual Oxford Books; ISBN: 0716770172; and Makrides (1999) Prot. Expr. Purif. 17:183-202.

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Bladder cancer protein may be produced in yeast cells. Yeast expression systems exist with expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guilliermondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*. See, e.g., Jones, et al. (eds. 5 1993) The Molecular and Cellular Biology of the Yeast Saccharomyces: Gene Expression CSH Press; ISBN: 0879693657.

The bladder cancer protein may also be made as a fusion protein, using techniques well known in the art. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the bladder cancer protein may be fused to a carrier protein to form an 10 immunogen. Alternatively, the bladder cancer protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the bladder cancer protein is a bladder cancer peptide, the nucleic acid encoding the peptide may be linked to other nucleic acid for expression or purification purposes.

The bladder cancer protein is typically purified or isolated after expression. Bladder 15 cancer proteins may be isolated or purified in a variety of ways, depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological, and chromatographic techniques, including ion exchange, hydrophobic, affinity, reverse-phase HPLC chromatography, and chromatofocusing. The bladder cancer protein may be purified using a standard anti-bladder cancer protein antibody 20 affinity column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For general guidance in suitable purification techniques, see, e.g., Scopes (1982) Protein Purification Springer-Verlag. The degree of purification necessary will vary depending on the use of the bladder cancer protein. In some instances no purification will be necessary, which may depend on the intended use.

25 Once expressed and purified, if necessary, the bladder cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, etc.

Variants of bladder cancer proteins

In one embodiment, the bladder cancer proteins are derivative or variant bladder cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative bladder cancer peptide will often contain at least one amino acid substitution, deletion, or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion, or deletion may occur at most residues within the bladder cancer peptide.

Certain embodiments of bladder cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes: substitutional, insertional, or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the bladder cancer protein, using cassette or PCR, mutagenesis, or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant bladder cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are often characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the bladder cancer protein amino acid sequence. The variants typically exhibit the same qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. To optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed bladder cancer variants screened for the optimal combination of desired activities. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is performed using assays of bladder cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be

tolerated. Deletions range from about 1-20 residues, although in some cases deletions may be much larger.

Substitutions, deletions, insertions, or combinations thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the bladder cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution relationships provided in the definition section.

The variants typically exhibit the same qualitative biological activity and elicit the same immune response as the naturally-occurring analog, although variants also are selected to modify the characteristics of the bladder cancer proteins as needed. Alternatively, the variant may be designed such that the biological activity of the bladder cancer protein is altered. For example, glycosylation sites may be altered or removed.

Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those described above. Substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, e.g., the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. Substitutions which are expected to produce the greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, e.g., serine or threonine is substituted for (or by) a hydrophobic residue, e.g., leucine, isoleucine, phenylalanine, valine, or alanine; (b) a cysteine or proline is substituted for (or by) another residue; (c) a residue having an electropositive side chain, e.g., lysine, arginine, or histidine, is substituted for (or by) an electronegative residue, e.g., glutamic acid or aspartic acid; or (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine.

Covalent modifications of bladder cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a bladder cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a bladder cancer polypeptide. Derivatization with bifunctional agents is useful, e.g., for crosslinking bladder

cancer polypeptides to a water-insoluble support matrix or surface for use in the method for purifying anti-bladder cancer polypeptide antibodies or screening assays. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimide.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamic and aspartic residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serine, threonine or tyrosine residues, methylation of the amino groups of the lysine, arginine, and histidine side chains (pp. 79-86, Creighton (1984) Proteins: Structure and Molecular Properties Freeman), acetylation of the N-terminal amine, and amidation of a C-terminal carboxyl group.

Another type of covalent modification of the bladder cancer polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence bladder cancer polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence bladder cancer polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express bladder cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to bladder cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence bladder cancer polypeptide (for O-linked glycosylation sites). The bladder cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the bladder cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the bladder cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide.

Such methods are described in the art, e.g., in WO 87/05330, and pp. 259-306 in Aplin and Wriston (1981) CRC Crit. Rev. Biochem.

Removal of carbohydrate moieties present on the bladder cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art. See, e.g., Hakimuddin, et al. (1987) Arch. Biochem. Biophys. 259:52-57; and Edge, et al. (1981) Anal. Biochem. 118:131-137. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases. See, e.g., Thotakura, et al. (1987) Meth. Enzymol. 138:350-359.

Another type of covalent modification of bladder cancer comprises linking the bladder cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192; or 4,179,337.

Bladder cancer polypeptides of the present invention may also be modified to form chimeric molecules comprising a bladder cancer polypeptide fused to a heterologous polypeptide or amino acid sequence. In one embodiment, a chimeric molecule comprises a fusion of a bladder cancer polypeptide with an epitope tag. The epitope tag is generally placed at the amino-or carboxyl-terminus of the bladder cancer polypeptide. The presence of such epitope-tagged forms of a bladder cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the bladder cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a bladder cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7, and 9E10 antibodies thereto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616);

and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3:547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) Proc. Nat'l Acad. Sci. USA 87:6393-6397).

Also included are other bladder cancer proteins of the bladder cancer family, and bladder cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related bladder cancer proteins from humans or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include the unique areas of the bladder cancer nucleic acid sequence. Preferred PCR primers are from about 15-35 nucleotides in length, with from about 20-30 being preferred, and may contain inosine as needed. The conditions for the PCR reaction are well known. See, e.g., Innis (1990) PCR Protocols, supra.

Antibodies to bladder cancer proteins

In a preferred embodiment, when the bladder cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the bladder cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller bladder cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity.

Methods of preparing polyclonal antibodies are known (see, e.g., Coligan, supra; and Harlow and Lane, supra). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a

nucleic acid of the tables or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor.

- 5 Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected as appropriate.

- The antibodies may be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495-497. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of Tables 1A-13 or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (pp. 59-103, Goding (1986) Monoclonal Antibodies: Principles and Practice Academic Press). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.
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- In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are typically monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two
- 30

epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid Tables 1A-13 or a fragment thereof, the other one is for another antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to bladder cancer protein are capable of reducing or eliminating a biological function of a bladder cancer protein, as is described below. That is, the addition of anti-bladder cancer protein antibodies (either polyclonal or preferably monoclonal) to bladder cancer tissue (or cells containing bladder cancer) may reduce or eliminate the bladder cancer. Generally, at least about 25% decrease in activity, growth, size, or the like is preferred, with at least about 50% being particularly preferred, and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the bladder cancer proteins are humanized antibodies (e.g., Xenerex Biosciences; Medarex, Inc.; Abgenix, Inc.; Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat, or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human

immunoglobulin. See Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; and Presta (1992) Curr. Op. Struct. Biol. 2:593-596. Humanization can be performed, e.g., following the method of Winter and co-workers (see Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-327; Verhoeyen, et al. (1988) Science 239:1534-1536), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries (Hoogenboom and Winter (1991) J. Mol. Biol. 227:381-388; Marks, et al. (1991) J. Mol. Biol. 222:581-597) or of human monoclonal antibodies (e.g., p. 77, Cole, et al. in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; and Boerner, et al. (1991) J. Immunol. 147:86-95). Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Neuberger (1996) Nature Biotechnology 14:826 commenting on Fishwild, et al. (1996) Nature Biotechnology 14:845-51; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

By immunotherapy is meant treatment of bladder cancer with an antibody raised against bladder cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient), which may be used to target a label or toxin. Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. As

appreciated by one of ordinary skill in the art, the antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

- 5 In a preferred embodiment the bladder cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted bladder cancer protein.

- 10 In another preferred embodiment, the bladder cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment, bind the extracellular domain of the bladder cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane bladder cancer protein. As will be appreciated by one of ordinary skill in the art, the antibody may be a competitive, non-
15 competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the bladder cancer protein. The antibody is also an antagonist of the bladder cancer protein. Further, the antibody prevents activation of the transmembrane bladder cancer protein. In one aspect, when the antibody prevents the binding of other molecules to the bladder cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or
20 sensitize the cell to cytotoxic agents, including, but not limited to $\text{TNF-}\alpha$, $\text{TNF-}\beta$, IL-1, INF- γ and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, bladder cancer is
25 treated by administering to a patient antibodies directed against the transmembrane bladder cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

- In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be a number of molecules, including labelling moieties such as
30 radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the

therapeutic moiety is a small molecule that modulates the activity of the bladder cancer protein. In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the bladder cancer protein. The therapeutic moiety may inhibit enzymatic activity such as protease or collagenase or protein kinase activity associated with bladder cancer.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to bladder cancer tissue or cells, results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with bladder cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin, and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against bladder cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane bladder cancer proteins not only serves to increase the local concentration of therapeutic moiety in the bladder cancer afflicted area, but also serves to reduce deleterious side effects that may be associated with the therapeutic moiety.

In another preferred embodiment, the bladder cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the bladder cancer protein can be targeted within a cell, e.g., the nucleus, an antibody thereto contains a signal for that target localization, e.g., a nuclear localization signal.

The bladder cancer antibodies of the invention specifically bind to bladder cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_D of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding is also important.

Detection of bladder cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the bladder cancer phenotype. Expression levels of genes in normal tissue (e.g., not experiencing bladder cancer) and in bladder cancer tissue (and in some cases, for varying severities of bladder cancer that relate to prognosis, as outlined below), or in non-malignant disease, are evaluated to provide expression profiles. An expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state. While two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus bladder cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; e.g., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays. See Lockhart (1996) Nature Biotechnology 14:1675-1680. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR,

northern analysis and RNase protection. As outlined above, preferably the change in expression (e.g., upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from about 300-1000% being especially preferred.

5 Evaluation may be at the gene transcript, or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the bladder cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass
10 spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to bladder cancer genes, e.g., those identified as being important in a bladder cancer or disease phenotype, can be evaluated in a bladder cancer diagnostic test.

 In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes. Multiple protein expression monitoring can be performed as well.
15 Similarly, these assays may be performed on an individual basis as well.

 In this embodiment, the bladder cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of bladder cancer sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity.

20 In a preferred embodiment nucleic acids encoding the bladder cancer protein are detected. Although DNA or RNA encoding the bladder cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a bladder cancer protein is detected. Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to,
25 oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method detection of the mRNA is performed in situ. In this method
30 permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid

probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example, a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a bladder cancer protein is detected by binding the digoxigenin with an anti-digoxigenin
5 secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The bladder cancer proteins, antibodies, nucleic acids, modified proteins and cells
10 containing bladder cancer sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, bladder cancer proteins, including intracellular, transmembrane or secreted proteins, find use as diagnostic or prognostic markers of bladder cancer, or to assist in selecting therapy based on expression profile and archival data. Detection of these proteins in putative bladder cancer tissue allows for detection or diagnosis of bladder cancer. In one embodiment, antibodies are used to detect bladder cancer proteins.
20 A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the bladder cancer protein is detected, e.g., by immunoblotting with antibodies raised against the bladder cancer protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the bladder cancer protein find use in in situ imaging techniques, e.g., in histology (e.g., Asai (ed. 1993) "Antibodies in Cell Biology" Methods in Cell Biology (vol. 37). In this method cells are contacted with from one to many antibodies to the bladder cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment
30 the antibody is detected by incubating with a secondary antibody that contains a detectable

label. In another method the primary antibody to the bladder cancer protein(s) contains a detectable label, e.g. an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of bladder cancer proteins. As will be appreciated by one of ordinary skill in the art, many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing bladder cancer from blood, serum, plasma, stool, urine, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of bladder cancer proteins. Antibodies can be used to detect a bladder cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous bladder cancer protein.

In a preferred embodiment, in situ hybridization of labeled bladder cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including bladder cancer tissue and/or normal tissue, are made. In situ hybridization (see, e.g., Ausubel, supra) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the bladder cancer proteins, antibodies, nucleic acids, modified proteins and cells containing bladder cancer sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to bladder cancer, clinical, pathological, or other information, e.g., in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple genes may be useful in various combinations. As above, bladder cancer probes may

be attached to biochips for the detection and quantification of bladder cancer sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR methods may provide more sensitive and accurate quantification.

5 Assays for therapeutic compounds

In a preferred embodiment members of the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The bladder cancer proteins, antibodies, nucleic acids, modified proteins and cells containing bladder cancer sequences are used in drug screening assays or by evaluating the effect of drug candidates on a "gene expression
10 profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent. See, e.g., Zlokarnik, et al. (1998) Science 279:84-88; and Heid (1996) Genome Res. 6:986-94.

In a preferred embodiment, the bladder cancer proteins, antibodies, nucleic acids,
15 modified proteins and cells containing the native or modified bladder cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the bladder cancer phenotype or an identified physiological function of a bladder cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred
20 embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, supra.

Having identified the differentially expressed genes herein, a variety of assays may be executed. In a preferred embodiment, assays may be run on an individual gene or protein
25 level. That is, having identified a particular gene as up regulated in bladder cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the bladder cancer protein. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing bladder cancer, with changes of at least
30 about 10%, preferably about 50%, more preferably about 100-300%, and in some

embodiments about 300-1000% or greater. Thus, if a gene exhibits about 4-fold increase in bladder cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, about 10-fold decrease in bladder cancer tissue compared to normal tissue often provides a target value of about 10-fold increase in expression to be induced by the test
5 compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the bladder cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of
10 expression.

In a preferred embodiment, gene expression or protein monitoring of a number of entities, e.g., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein..

In this embodiment, the bladder cancer nucleic acid probes are attached to biochips as
15 outlined herein for the detection and quantification of bladder cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring can be performed to identify compounds that modify the
20 expression of one or more bladder cancer-associated sequences, e.g., a polynucleotide sequence set out in Tables 1A-13. Generally, in a preferred embodiment, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate bladder cancer, modulate bladder cancer proteins, bind to a bladder cancer protein, or interfere with the binding of a bladder cancer protein and an antibody or other
25 binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the bladder cancer phenotype or the expression of a bladder cancer sequence,
30 e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter

expression profiles, or expression profile nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses a bladder cancer phenotype, e.g., to a normal tissue or non-malignant fingerprint. In another embodiment, a modulator induced a bladder cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, e.g., at zero concentration or below the level of detection.

Drug candidates encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than about 100 and less than about 2,500 daltons. Preferred small molecules are less than about 2000, or less than about 1500 or less than about 1000 or less than about 500 D.

Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl, or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups.

Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof. Particularly preferred are peptides.

In one aspect, a modulator will neutralize the effect of a bladder cancer protein. By "neutralize" is meant that activity of a protein is inhibited or blocked and the consequent effect on the cell.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a bladder cancer polypeptide or to modulate activity.

Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (e.g., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks. See, e.g., Gallop, et al. (1994) J. Med. Chem. 37:1233-1251.

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka (1991) Pept. Prot. Res. 37:487-493, Houghton, et al. (1991) Nature 354:84-88); peptoids (PCT Publication No WO 91/19735); encoded peptides (PCT Publication WO 93/20242); random bio-oligomers (PCT Publication WO 92/00091); benzodiazepines (U.S. Pat. No. 5,288,514); diversomers such as hydantoins, benzodiazepines, and dipeptides (Hobbs, et al. (1993) Proc. Nat'l Acad. Sci. USA 90:6909-6913); vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568-6570); nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et al. (1992) J. Amer. Chem. Soc. 114:9217-9218); analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661-2662); oligocarbamates (Cho, et al. (1993) Science 261:1303-1305); and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658-xxx). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385-1401, nucleic acid libraries (see, e.g., Strategene, Corp.); peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083); antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14:309-314, and PCT/US96/10287);

carbohydrate libraries (Liang, et al. (1996) Science 274:1520-1522, and U.S. Patent No. 5,593,853); and small organic molecule libraries (see, e.g., benzodiazepines, Baum (p. 33, Jan 18, 1993) C&E News); isoprenoid (U.S. Patent No. 5,569,588); thiazolidinones and metathiazanones (U.S. Patent No. 5,549,974); pyrrolidines (U.S. Patent Nos. 5,525,735 and 5,519,134); morpholino compounds (U.S. Patent No. 5,506,337); benzodiazepines (U.S. Patent No. 5,288,514); and the like.

Devices for the preparation of combinatorial libraries are commercially available. See, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY; Symphony, Rainin, Woburn, MA; 433A Applied Biosystems, Foster City, CA; and 9050 Plus, Millipore, Bedford, MA.

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, MA; Orca, Hewlett-Packard, Palo Alto, CA), which mimic the manual synthetic operations performed by a chemist. The above devices are suitable for use with the present invention. The nature and implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent to persons skilled in the relevant art. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, NJ; Asinex, Moscow, Ru; Tripos, Inc., St. Louis, MO; ChemStar, Ltd, Moscow, RU; 3D Pharmaceuticals, Exton, PA; Martek Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect enhancement or inhibition of bladder cancer gene transcription, inhibition or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

High throughput assays for the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (e.g., in

arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g., Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA; etc.). These systems typically automate entire procedures, including all sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5-30 amino acids, with from about 5-20 amino acids being preferred, and from about 7-15 being particularly preferred. The peptides may be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate nucleotide or amino acid substitutions. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the

length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc., or to purines, etc.

Modulators of bladder cancer can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. Digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an in vitro transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag

or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

As will be appreciated by those in the art, these assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc., which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the bladder cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind and/or modulate the biological activity of the gene product.

In addition screens can be done for genes that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress a bladder cancer expression pattern leading to a normal expression pattern, or to modulate a single bladder cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated bladder cancer tissue reveals genes that are not expressed in normal tissue or bladder cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for bladder cancer genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated bladder cancer tissue sample.

Thus, in one embodiment, a test compound is administered to a population of bladder cancer cells, that have an associated bladder cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (e.g., a peptide) may be put into a viral construct such as an adenoviral or

retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

Once the test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some
5 period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, e.g., bladder cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress the bladder cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on
10 bladder cancer activity. By defining such a signature for the bladder cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

In a preferred embodiment, as outlined above, screens may be done on individual
15 genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "bladder cancer proteins" or a "bladder cancer modulatory protein". The bladder cancer modulatory protein may be a
20 fragment, or alternatively, be the full length protein to the fragment encoded by the nucleic acids of the Tables 1A-13. Preferably, the bladder cancer modulatory protein is a fragment. In a preferred embodiment, the bladder cancer amino acid sequence which is used to determine sequence identity or similarity is encoded by a nucleic acid of Tables 1A-13. In another embodiment, the sequences are naturally occurring allelic variants of a protein
25 encoded by a nucleic acid of Tables 1A-13. In another embodiment, the sequences are sequence variants as further described herein.

Preferably, the bladder cancer modulatory protein is a fragment of approximately 14 to 24 amino acids long. More preferably the fragment is a soluble fragment. Preferably, the fragment includes a non-transmembrane region. In a preferred embodiment, the fragment has

an N-terminal Cys to aid in solubility. In one embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in coupling, e.g., to cysteine.

In one embodiment the bladder cancer proteins are conjugated to an immunogenic agent as discussed herein. In one embodiment the bladder cancer protein is conjugated to
5 BSA.

Measurements of bladder cancer polypeptide activity, or of bladder cancer or the bladder cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the bladder cancer polypeptides can be measured by examining parameters described above. A suitable physiological change that
10 affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of bladder cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g.,
15 northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian bladder cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed in vitro. For example, a bladder cancer polypeptide is first contacted with a potential modulator and
20 incubated for a suitable amount of time, e.g., from 0.5-48 hours. In one embodiment, the bladder cancer polypeptide levels are determined in vitro by measuring the level of protein or mRNA. The level of protein is measured using immunoassays such as western blotting, ELISA and the like with an antibody that selectively binds to the bladder cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or
25 hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using the bladder cancer protein
30 promoter operably linked to a reporter gene such as luciferase, green fluorescent protein,

CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual
5 genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "bladder cancer proteins." The bladder cancer protein may be a fragment, or alternatively, be the full length protein to a fragment shown
10 herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate
15 differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products,
20 and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the bladder cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a bladder cancer protein and a candidate compound, and determining the binding of the compound to the bladder cancer protein. Preferred embodiments utilize the human bladder cancer protein,
25 although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative bladder cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the bladder cancer protein or the candidate agent is non-diffusably bound to an insoluble support having isolated
30 sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be

made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition and is nondiffusible. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the bladder cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the bladder cancer protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the bladder cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the bladder cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ^{125}I for the proteins and a fluorophore for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor is a binding moiety known to bind to the target molecule (e.g., a bladder cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between 4 and 40°C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by the test compound. Displacement of the competitor is an indication that the test compound is binding to the bladder cancer protein and thus is capable of binding to, and potentially modulating, the activity of the bladder cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the bladder cancer protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the bladder cancer protein.

In a preferred embodiment, the methods comprise differential screening to identify agents that are capable of modulating the activity of the bladder cancer proteins. In this embodiment, the methods comprise combining a bladder cancer protein and a competitor in a first sample. A second sample comprises a test compound, a bladder cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the bladder cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the bladder cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native bladder cancer protein, but cannot bind to modified bladder cancer proteins. The structure of the bladder cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a bladder cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc. which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a bladder cancer protein. The methods

comprise adding a test compound, as defined above, to a cell comprising bladder cancer proteins. Many different cell types may be transfected to contain a recombinant nucleic acid that encodes a bladder cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

5 In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, and pharmacological agents including, e.g., chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In one example, the determinations are determined at different stages of the cell cycle process.

10 In this way, compounds that modulate bladder cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the bladder cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

 In one embodiment, a method of inhibiting bladder cancer cell division is provided.

15 The method comprises administration of a bladder cancer inhibitor. In another embodiment, a method of inhibiting bladder cancer is provided. The method comprises administration of a bladder cancer inhibitor. In a further embodiment, methods of treating cells or individuals with bladder cancer are provided. The method comprises administration of a bladder cancer inhibitor. In one embodiment, a bladder cancer inhibitor is an antibody as discussed above.

20 In another embodiment, the bladder cancer inhibitor is an antisense molecule.

 A variety of cell growth, proliferation, and metastasis assays are known to those of skill in the art, as described below.

Soft agar growth or colony formation in suspension

 Normal cells require a solid substrate to attach and grow. When the cells are

25 transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify

30 modulators of bladder cancer sequences, which when expressed in host cells, inhibit

abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described in Freshney (1994) Culture of Animal Cells: A Manual of Basic Technique (3d ed.) Wiley-Liss, herein incorporated by reference. See also, the methods section of Garkavtsev, et al. (1996), *supra*, herein incorporated by reference.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (³H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (1994), *supra*. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (³H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a bladder cancer-associated sequence and are grown for 24 hours at saturation density in non-limiting medium conditions. The percentage of cells labeling with (³H)-thymidine is determined autoradiographically. See, Freshney (1994), *supra*.

Growth factor or serum dependence

Transformed cells have a lower serum dependence than their normal counterparts (see, e.g., Temin (1966) J. Nat'l Cancer Inst. 37:167-175; Eagle, et al. (1970) J. Exp. Med. 131:836-879; Freshney (1994), *supra*). This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells. See, e.g., "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer Plenum. Similarly, tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) Sem Cancer Biol. 3:89-96.

Various techniques which measure the release of these factors are described in Freshney (1994), supra. See also, Unkeless, et al. (1974) J. Biol. Chem. 249:4295-4305; Strickland and Beers (1976) J. Biol. Chem. 251:5694-5702; Whur, et al. (1980) Br. J. Cancer 42:305-312; Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer, Plenum; and Freshney (1985) Anticancer Res. 5:111-130.

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate bladder cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1984), supra, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved, or by prelabeling the cells with ^{125}I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (2000), supra.

Tumor growth in vivo

Effects of bladder cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the bladder cancer gene is disrupted or in which a bladder cancer gene is inserted. Knock-out

transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous bladder cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous bladder cancer gene with a mutated version of the bladder cancer gene, or by mutating the endogenous bladder cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. By breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion. See, e.g., Capecchi, et al. (1989) Science 244:1288-1292. Chimeric targeted mice can be made. See Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual, CSH Press; and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) J. Nat'l Cancer Inst. 52:921-930), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) Br. J. Cancer 38:263-272; Selby, et al. (1980) Br. J. Cancer 41:52-61) can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a bladder cancer-associated sequences are injected subcutaneously. After a suitable length of time, preferably about 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

Polynucleotide modulators of bladder cancer

Antisense and RNAi Polynucleotides

In certain embodiments, the activity of a bladder cancer-associated protein is down-regulated, or entirely inhibited, by the use of antisense polynucleotide, e.g., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a bladder cancer protein mRNA, or a subsequence thereof.

- 5 Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-
10 sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the bladder cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means,
15 or can be synthesized in vitro. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known.

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, e.g., be employed to block transcription by binding to the anti-
20 sense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for bladder cancer molecules. A preferred antisense molecule is for a bladder cancer sequences in Tables 1A-13, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at
25 least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, e.g., Stein and Cohen (1988) Cancer Res. 48:2659-2668; and van der Krol, et al. (1988) BioTechniques 6:958-976.

RNA interference is a mechanism to suppress gene expression in a sequence specific
30 manner. See, e.g., Brumelkamp, et al. (2002) Scienceexpress (21March2002); Sharp (1999)

Genes Dev. 13:139-141; and Cathew (2001) Curr. Op. Cell Biol. 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) Nature 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g.,
5 treatment of or validation of relevance to disease

Ribozymes

In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of bladder cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have
10 been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes. See, e.g., Castanotto, et al. (1994) Adv. in Pharmacology 25: 289-317 for a general review of the properties of different ribozymes.

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No.
15 5,254,678. Methods of preparing them are well known. See, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Nat'l Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Human Gene Therapy 1:39-45; Leavitt, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:699-703; Leavitt, et al. (1994) Human Gene Therapy 5:1151-120; and Yamada, et al. (1994) Virology 205: 121-126.

Polynucleotide modulators of bladder cancer may be introduced into a cell containing
20 the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its
25 corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of bladder cancer may be introduced into a cell containing the target nucleic acid sequence, e.g., by formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be
30 used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating bladder cancer in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-bladder cancer antibody that reduces or eliminates the biological activity of an endogenous bladder cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding a bladder cancer protein. This may be accomplished in many ways. In a preferred embodiment, e.g., when the bladder cancer sequence is down-regulated in bladder cancer, such state may be reversed by increasing the amount of bladder cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous bladder cancer gene or administering a gene encoding the bladder cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, e.g., when the bladder cancer sequence is up-regulated in bladder cancer, the activity of the endogenous bladder cancer gene is decreased, e.g., by the administration of a bladder cancer antisense nucleic acid.

In one embodiment, the bladder cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to bladder cancer proteins. Similarly, the bladder cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify bladder cancer antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a bladder cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The bladder cancer antibodies may be coupled to standard affinity chromatography columns and used to purify bladder cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the bladder cancer protein.

Methods of identifying variant bladder cancer-associated sequences

Without being bound by theory, expression of various bladder cancer sequences is correlated with bladder cancer. Accordingly, disorders based on mutant or variant bladder cancer genes may be determined. In one embodiment, the invention provides methods for

identifying cells containing variant bladder cancer genes, e.g., determining all or part of the sequence of at least one endogenous bladder cancer genes in a cell. This may be accomplished using many sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the bladder cancer genotype of an individual, e.g.,
5 determining all or part of the sequence of at least one bladder cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced bladder cancer gene to a known bladder cancer gene, e.g., a wild-type gene.

10 The sequence of all or part of the bladder cancer gene can then be compared to the sequence of a known bladder cancer gene to determine if differences exist. This can be done using many known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the bladder cancer gene of the patient and the known bladder cancer gene correlates with a disease state or a propensity for a disease
15 state, as outlined herein.

In a preferred embodiment, the bladder cancer genes are used as probes to determine the number of copies of the bladder cancer gene in the genome.

In another preferred embodiment, the bladder cancer genes are used as probes to determine the chromosomal localization of the bladder cancer genes. Information such as
20 chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the bladder cancer gene locus.

Administration of pharmaceutical and vaccine compositions

25 In one embodiment, a therapeutically effective dose of a bladder cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques. See, e.g., Ansel, et al. (1999) Pharmaceutical Dosage Forms and Drug
30 Delivery Lippincott; Lieberman (1992) Pharmaceutical Dosage Forms (vols. 1-3) Dekker,

ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding Amer. Pharma. Assn.; and Pickar (1999) Dosage Calculations Thomson. As is known in the art, adjustments for bladder cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art. USSN 09/687,576, further discloses the use of compositions and methods of diagnosis and treatment in bladder cancer and is hereby expressly incorporated by reference.

10 A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the bladder cancer proteins and modulators thereof of the present invention can be done in a variety of ways as discussed above, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the bladder cancer proteins and modulators may be directly applied as a solution or spray.

20 The pharmaceutical compositions of the present invention comprise a bladder cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like.

"Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that bladder cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are well known in the art.

The compositions for administration will commonly comprise a bladder cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary

widely, and will be selected primarily based on fluid volumes, viscosities, body weight and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., Remington's Pharmaceutical Science (15th ed., 1980) and Hardman and Limbird (eds. 2001) Goodman and Gilman: The Pharmacological Basis of Therapeutics McGraw-Hill.

5 Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1-10 mg per patient per day. Dosages from about 0.1-100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally
10 administrable compositions will be known or apparent to those skilled in the art, e.g., Remington's Pharmaceutical Science and Goodman and Gilman: The Pharmacological Basis of Therapeutics, supra.

 The compositions containing modulators of bladder cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications,
15 compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered
20 depending on the dosage and frequency as required and tolerated by the patient. The composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition
25 and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, at least in part, upon gene expression profiles. Vaccine strategies
30 may be used, in either a DNA vaccine form, or protein vaccine.

It will be appreciated that the present bladder cancer protein-modulating compounds can be administered alone or in combination with additional bladder cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in Tables 1A-13, such as antisense polynucleotides or ribozymes, will be introduced into cells, in vitro or in vivo. The present invention provides methods, reagents, vectors, and cells useful for expression of bladder cancer-associated polypeptides and nucleic acids using in vitro (cell-free), ex vivo, or in vivo (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors, and other methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell. See, e.g., Berger and Kimmel (1987) Guide to Molecular Cloning Techniques from Methods in Enzymology (vol. 152) Academic Press; Ausubel, et al. (eds. 1999 and supplements) Current Protocols in Molecular Biology Lippincott; and Sambrook, et al. (1989) Molecular Cloning: A Laboratory Manual (2d ed., Vol. 1-3) CSH Press.

In a preferred embodiment, bladder cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, bladder cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the bladder cancer coding regions) can be administered in a gene therapy application. These bladder cancer genes can include antisense applications, either as gene therapy (e.g., for incorporation into the genome) or as antisense compositions, as will be appreciated by those in the art.

Bladder cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses.. Such vaccine compositions can include, e.g., lipidated peptides (Vitiello, et al. (1995) J. Clin. Invest. 95:341-349); peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres

(Eldridge, et al. (1991) Molec. Immunol. 28:287-294; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681); peptide compositions contained in immune stimulating complexes (ISCOMS) (Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin. Exp. Immunol. 113:235-243); multiple antigen peptide systems (MAPs) (Tam
5 (1988) Proc. Nat'l Acad. Sci. USA 85:5409-5413; Tam (1996) J. Immunol. Methods 196:17-32); peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al. in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Chakrabarti, et al. (1986) Nature 320:535-537; Hu, et al. (1986) Nature 320:537-547; Kieny, et al. (1986) AIDS
10 Bio/Technology 4:790; Top, et al. (1971) J. Infect. Dis. 124:148-154; Chanda, et al. (1990) Virology 175:535-547), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25-35; Eldridge, et al. (1993) Sem. Hematol. 30:16-24; Falo, et al. (1995) Nature Med. 7:649-653), adjuvants (Warren, et al. (1986) Annu. Rev. Immunol. 4:369-388; Gupta, et al. (1993) Vaccine 11:293-306), liposomes (Reddy, et al. (1992) J.
15 Immunol. 148:1585-1589; Rock (1996) Immunol. Today 17:131-137), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745-1749; Robinson, et al. (1993) Vaccine 11:957-960; Shiver, et al. in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Cease and Berzofsky (1994) Annu. Rev. Immunol. 12:923-989; and Eldridge, et al. (1993) Sem. Hematol. 30:16-24). Toxin-targeted delivery technologies,
20 also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc., Needham, MA, may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, Bortadella pertussis or
25 Mycobacterium tuberculosis derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated
30 tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides;

polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A.

Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA
5 encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff, et al. (1990) Science 247:1465-1468 as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery,
10 cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of
15 vaccinia virus, e.g., as a vector to express nucleotide sequences that encode bladder cancer polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are
20 described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors useful for therapeutic administration or immunization, e.g., adeno and adeno-associated virus vectors, retroviral vectors, Salmonella typhi vectors, detoxified anthrax toxin vectors, and the like. See, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85.

25 Methods for the use of genes as DNA vaccines are well known, and include placing a bladder cancer gene or portion of a bladder cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a bladder cancer patient. The bladder cancer gene used for DNA vaccines can encode full-length bladder cancer proteins, but more preferably encodes portions of the bladder cancer proteins including peptides
30 derived from the bladder cancer protein. In one embodiment, a patient is immunized with a

DNA vaccine comprising a plurality of nucleotide sequences derived from a bladder cancer gene. For example, bladder cancer-associated genes or sequence encoding subfragments of a bladder cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the bladder cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment bladder cancer genes find use in generating animal models of bladder cancer. When the bladder cancer gene identified is repressed or diminished in cancer tissue, gene therapy technology, e.g., wherein antisense RNA directed to the bladder cancer gene will also diminish or repress expression of the gene. Animal models of bladder cancer find use in screening for modulators of a bladder cancer-associated sequence or modulators of bladder cancer. Similarly, transgenic animal technology including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the bladder cancer protein. When desired, tissue-specific expression or knockout of the bladder cancer protein may be necessary.

It is also possible that the bladder cancer protein is overexpressed in bladder cancer. As such, transgenic animals can be generated that overexpress the bladder cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods find use as animal models of bladder cancer and are additionally useful in screening for modulators to treat bladder cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In the diagnostic and research applications such kits may include one or more of the following: assay reagents, buffers, bladder cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense or inhibitory

5 polynucleotides, ribozymes, dominant negative bladder cancer polypeptides or polynucleotides, small molecules inhibitors of bladder cancer-associated sequences etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing directions (e.g.,
10 protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. A medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such
15 media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of bladder cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a bladder cancer-associated polypeptide or polynucleotide, control positive or negative
20 samples, reaction tubes, and instructions for testing bladder cancer-associated activity. Optionally, the kit contains biologically active bladder cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will be selected based on
25 correlations with important parameters in disease which may be identified in historical or outcome data.

EXAMPLES

Example 1: Gene Chip Analysis

Molecular profiles of various normal and cancerous tissues were determined and analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described
 5 (Glynne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).

TABLE DESCRIPTIONS

Table 1A shows about 3413 that exhibit increased or decreased expression in bladder cancer
 10 samples. See USSN 60/302,814.

Table 2A shows about 485 genes overexpressed in bladder tumors relative to normal tissues as analyzed using the Affymetrix/Eos Hu03 GeneChip array. See USSN 60/343,705.

15 Table 3A shows about 414 genes upregulated in bladder cancer relative to normal body tissues and preferred for utility as small molecule, antibody, DNA vaccine targets for the therapy of bladder cancer. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the
 20 relative level of mRNA expression.

Table 4A shows about 129 genes upregulated in bladder cancer relative to normal body tissues and preferred for utility as diagnostics of bladder cancer. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for
 25 each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 5A shows about 149 genes upregulated in bladder cancer relative to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03
 30 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 6A shows about 199 genes upregulated in bladder cancer relative to normal bladder
 35 tissue. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

40 Table 7A shows about 63 genes downregulated in bladder tumors relative to normal bladder. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip

array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5 Table 8A shows about 1440 genes upregulated in Ta or T1 bladder tumors from patients who later presented with muscle-invasive bladder tumors (stage T2-T4). Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

10 Table 9A shows about 1200 genes upregulated in Ta or T1 tumors of patients who later presented with either more Ta tumors or no tumors at all. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

15 Table 10A shows about 65 genes upregulated in non-invasive exophytic Ta bladder tumors relative to T2-T4 muscle-invasive tumors. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

20 Table 11A shows about 106 genes upregulated in muscle-invasive T2-T4 bladder tumors relative to non-invasive exophytic Ta bladder tumors. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

25 Table 12A shows the Pkey, ExAccn, UnigeneID, and Unigene Title for all of the sequences in Table 13. Seq ID No. is used to link Table 12A to table 13.

30 Tables 1B-12B show the accession numbers for those Pkey's lacking UnigeneID's for tables 1A-12A, respectively. For each probeset is listed a gene cluster number from which oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

35 Tables 1C-12C show genomic positioning for Pkey's lacking Unigene ID's and accession numbers for tables 1A-12A, respectively. For each predicted exon, is listed genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

40 **TABLE 1A:**

45 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: please refer to original application
 R2: please refer to original application
 Target Type: downregulate stage if target is downregulated in bladder tumors relative to normal bladder or

early stage if target is an earl stage (Ta) bladder tumor marker or
late stage if target is a late stage (T2-T4) bladder tumor marker or
T2-T4 grade 3 papilloma marker or T2-T4 grade 3 solid tumor marker or Upregulate stage

	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2	Target Type
5	400440	X83957	Hs.83870	nebulin	0.17	2.05	downregulate stage
	400888				0.24	1.97	downregulate stage
	401566				0.19	4.05	downregulate stage
	401669				0.2	2.05	downregulate stage
10	401691				0.04	10.13	downregulate stage
	401905				0.3	1.87	downregulate stage
	402076				0.06	6.51	downregulate stage
	402110				0.43	2.35	downregulate stage
	402271	NM_002197	Hs.154721	aconitase 1, soluble	0.21	2.16	downregulate stage
15	403362				0.18	4.44	downregulate stage
	403687				0.32	1.91	downregulate stage
	403959				0.14	2.27	downregulate stage
	404015				0.2	2.48	downregulate stage
20	404059				0.36	1.84	downregulate stage
	404152				0.32	1.85	downregulate stage
	404498				0.14	2.18	downregulate stage
	404819				0.19	5.25	downregulate stage
	405001	U58196	Hs.296281	Interleukin enhancer binding factor 1	0.16	2.92	downregulate stage
	405349				0.18	3.8	downregulate stage
25	405390				0.3	2.64	downregulate stage
	405735				0.13	2.44	downregulate stage
	405968				0.26	1.85	downregulate stage
	406017				0.32	2.28	downregulate stage
	406305	BE261320	Hs.297096	transcriptional adaptor 3 (ADA3, yeast h	0.42	1.93	downregulate stage
30	406320				0.37	2.01	downregulate stage
	406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac mus	0.3	2.84	downregulate stage
	406706	X03740	Hs.231581	myosin, heavy polypeptide 1, skeletal mu	0.14	7.4	downregulate stage
	406707	S73840	Hs.931	myosin, heavy polypeptide 2, skeletal mu	0.05	12.51	downregulate stage
	407013	U35637		gb:Human nebulin mRNA, partial cds	0.14	2.17	downregulate stage
35	407245	X90568	Hs.172004	titin	0.02	15.21	downregulate stage
	407330	AA582607		gb:mn51b05.s1 NCL_CGAP_Kid6 Homo sapiens	0.42	1.87	downregulate stage
	407571	AA46183	Hs.9572	ESTs	0.38	2.13	downregulate stage
	407682	AL035858	Hs.3807	FXD domain-containing ion transport reg	0.34	2.56	downregulate stage
	407815	AW373860	Hs.301716	ESTs	0.31	2.44	downregulate stage
40	407834	AW084991	Hs.26100	ESTs	0.15	2.98	downregulate stage
	407891	AA486620	Hs.41135	endomucin-2	0.15	3.33	downregulate stage
	407906	AA369665	Hs.41185	Homo sapiens mRNA; cDNA DKFZp564O1262 (f	0.12	8.05	downregulate stage
	407938	AA905097	Hs.85050	phospholamban	0.08	8.77	downregulate stage
	407965	W21483	Hs.41707	heat shock 27kD protein 3	0.26	2.29	downregulate stage
45	408009	AF020498	Hs.41735	purinergic receptor P2X, ligand-gated io	0.49	1.91	downregulate stage
	408139	AA451966	Hs.43005	RAB9-like protein	0.41	1.88	downregulate stage
	408221	AA912183	Hs.47447	ESTs	0.04	24.1	downregulate stage
	408374	AW025430	Hs.155591	forkhead box F1	0.35	2.85	downregulate stage
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	0.09	9.04	downregulate stage
50	408508	AI805109	Hs.135736	KIAA1580 protein	0.45	2.2	downregulate stage
	408614	AL137698	Hs.46531	Homo sapiens mRNA; cDNA DKFZp434C1915 (f	0.13	5.48	downregulate stage
	408652	R43409	Hs.6829	ESTs	0.33	2.5	downregulate stage
	408753	AI337192	Hs.47438	SH3 domain binding glutamic acid-rich pr	0.05	6.94	downregulate stage
	408896	AI610447	Hs.48778	niban protein	0.39	2.01	downregulate stage
55	409277	T05558	Hs.155880	ESTs	0.18	2.75	downregulate stage
	410023	AB017169	Hs.57929	slit (Drosophila) homolog 3	0.07	2.7	downregulate stage
	410036	R57171	Hs.57975	caldesmon 2, cardiac muscle	0.09	5.23	downregulate stage
	410132	NM_003480	Hs.58882	Microfibril-associated glycoprotein-2	0.24	2.34	downregulate stage
	410168	AW834050	Hs.9973	tensin	0.39	2.17	downregulate stage
60	410243	D83402	Hs.289006	ESTs, Weakly similar to alternatively sp	0.11	2.82	downregulate stage
	410339	AI916499	Hs.298258	ESTs	0.15	2.16	downregulate stage
	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	0.32	2.65	downregulate stage
	410688	T06529	Hs.98518	Homo sapiens cDNA FLJ11490 fis, clone HE	0.2	2.74	downregulate stage
	411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522	0.2	1.92	downregulate stage
65	411067	AI681006	Hs.301543	ESTs	0.11	3.41	downregulate stage
	411069	AL133092	Hs.68055	hypothetical protein DKFZp434I0428	0.17	5.8	downregulate stage
	411644	H92064	Hs.301543	ESTs	0.06	13.8	downregulate stage
	411741	AW859650		gb:RC0-CT0358-071299-011-d03 CT0358 Homo	0.36	2.5	downregulate stage
	412047	AA934589	Hs.49696	ESTs	0.18	3.57	downregulate stage
70	412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	0.32	1.89	downregulate stage
	412389	AW947655		gb:RC0-MT0003-140300-031-b07 MT0003 Homo	0.38	2.6	downregulate stage
	412442	AI983730	Hs.26530	serum deprivation response (phosphatidyl	0.12	3.67	downregulate stage
	412519	AA196241	Hs.73980	troponin T1, skeletal, slow	0.24	1.86	downregulate stage
	412622	AW664708	Hs.171959	ESTs	0.06	5.45	downregulate stage
75	412649	NM_002206	Hs.74369	integrin, alpha 7	0.29	2.95	downregulate stage
	412659	AW753865	Hs.74376	olfactomedin related ER localized protei	0.18	2.06	downregulate stage
	412758	Y07818	Hs.74566	dihydropyrimidinase-like 3	0.3	2.23	downregulate stage

	412802	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr	0.11	2.71	downregulate stage
	412975	T70956	Hs.75106	clusterin (complement lysis inhibitor, S	0.44	2.03	downregulate stage
	413074	A1871368	Hs.8417	ESTs	0.47	1.91	downregulate stage
5	413272	AA127923	Hs.293256	ESTs	0.09	4.44	downregulate stage
	413276	Z24725	Hs.75260	mitogen inducible 2	0.23	2.48	downregulate stage
	413508	BE145364		gb3L0-HT0198-151099-125-e05 HT0198 Homo	0.31	2.53	downregulate stage
	413624	BE177019	Hs.75445	SPARC-like 1 (masi9, hevin)	0.33	2.17	downregulate stage
	413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory,	0.33	2.63	downregulate stage
10	414063	H26904	Hs.75736	apoptoprotein D	0.42	1.85	downregulate stage
	414241	AA425085	Hs.4007	Sarcolemmal-associated protein	0.16	2.22	downregulate stage
	414280	AI568801	Hs.71721	ESTs	0.02	10	downregulate stage
	414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/macrophage	0.13	4.14	downregulate stage
	414657	AA424074	Hs.76780	protein phosphatase 1, regulatory (inhib	0.33	2.14	downregulate stage
	414712	N88858	Hs.77039	ribosomal protein S3A	0.4	2.5	downregulate stage
15	414903	AA451700	Hs.85835	Homo sapiens cDNA: FLJ22841 fis, clone K	0.3	3.3	downregulate stage
	415165	AW887604	Hs.78065	complement component 7	0.04	3.41	downregulate stage
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	0.2	3.29	downregulate stage
	415447	Z97171	Hs.78454	myoclin, trabecular meshwork inducible	0.15	6.55	downregulate stage
	415672	N53097	Hs.193579	ESTs	0.28	3.55	downregulate stage
20	415934	NM_000928	Hs.992	phospholipase A2, group 1B (pancreas)	0.34	2.64	downregulate stage
	416127	N49843	Hs.79022	GTP-binding protein overexpressed in ske	0.3	1.98	downregulate stage
	416349	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	0.41	1.95	downregulate stage
	416585	X54162	Hs.79386	leiomodlin 1 (smooth muscle)	0.02	49.3	downregulate stage
	416854	H40164	Hs.80296	Purkinje cell protein 4	0.02	7.55	downregulate stage
25	416941	BE000150	Hs.48778	niban protein	0.27	2.16	downregulate stage
	416982	J05401	Hs.80691	creatine kinase, mitochondrial 2 (sarcom	0.29	2.43	downregulate stage
	417011	F08212	Hs.234898	ESTs	0.41	2.06	downregulate stage
	417298	AW665639	Hs.37958	ESTs	0.27	3.7	downregulate stage
30	417501	AL041219	Hs.82222	sama domain, immunoglobulin domain (Ig),	0.39	2.08	downregulate stage
	417553	L09190	Hs.82276	trichohyalin	0.29	2.59	downregulate stage
	417987	AA210872	Hs.50133	ESTs	0.22	2.09	downregulate stage
	418297	R91254		gb:yp94e12a1 Soares fetal liver spleen	0.28	1.9	downregulate stage
	418332	R34976	Hs.78293	ESTs	0.2	3.9	downregulate stage
35	418391	NM_003281	Hs.84673	tropontin 1, skeletal, slow	0.35	2.02	downregulate stage
	418409	AA219332	Hs.120869	ESTs, Weakly similar to AF092922 1 retin	0.21	3.8	downregulate stage
	418421	R58620	Hs.85050	phospholamban	0.2	2.08	downregulate stage
	418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	0.05	21.55	downregulate stage
	418533	NM_004533	Hs.85937	myosin-binding protein C, fast-type	0.42	1.95	downregulate stage
40	418787	AW286134	Hs.86999	ESTs	0.48	1.87	downregulate stage
	418793	AW382987	Hs.88474	prostaglandin-endoperoxide synthase 1 (p	0.26	2.43	downregulate stage
	418947	W52990	Hs.22860	ESTs	0.13	7.18	downregulate stage
	419037	R39895	Hs.7864	ESTs	0.27	2	downregulate stage
	419441	AW023731	Hs.274368	Homo sapiens mRNA; cDNA DKFZp5861524 (f	0.19	5.25	downregulate stage
45	419535	AW139550	Hs.115173	ESTs	0.31	2.59	downregulate stage
	419682	H13139	Hs.92282	paired-like homeodomain transcription fa	0.28	2.38	downregulate stage
	419685	W76083	Hs.173077	ESTs	0.4	2.21	downregulate stage
	419703	AI793257	Hs.128151	ESTs	0.09	3.52	downregulate stage
	419942	U25138	Hs.93841	potassium large conductance calcium-acti	0.28	2.96	downregulate stage
50	420058	AK001423	Hs.94694	Homo sapiens cDNA FLJ10561 fis, clone NT	0.3	2.09	downregulate stage
	420195	N44348	Hs.300794	ESTs	0.22	2.79	downregulate stage
	420261	AW206093	Hs.748	fibroblast growth factor receptor 1 (fms	0.35	1.98	downregulate stage
	420674	NM_000055	Hs.1327	butyrylcholinesterase	0.29	3.5	downregulate stage
	421296	NM_002666	Hs.103253	perilipin	0.36	2.11	downregulate stage
55	421639	NM_012082	Hs.297921	Homo sapiens mRNA full length insert cDN	0.13	4.3	downregulate stage
	421763	AW163500	Hs.108080	cysteine and glycine-rich protein 1	0.26	3.49	downregulate stage
	421853	AL117472	Hs.108924	DKFZP586P1422 protein	0.14	5	downregulate stage
	422103	AA984330	Hs.111676	protein kinase H11; small stress protein	0.2	2.29	downregulate stage
	422287	F16365	Hs.114346	cytochrome c oxidase subunit VIIa polype	0.27	2.58	downregulate stage
60	422320	AI745249	Hs.23650	ESTs, Weakly similar to AAB47496 NG5 (H.	0.24	2.95	downregulate stage
	422633	X56832	Hs.118804	enolase 3, (beta, muscle)	0.23	3.57	downregulate stage
	422639	AI929377	Hs.173724	creatine kinase, brain	0.39	1.97	downregulate stage
	423334	AK000906	Hs.127273	hypothetical protein FLJ10044	0.37	2.29	downregulate stage
	423587	AA328074	Hs.284256	hypothetical protein FLJ14033 similar to	0.37	2.47	downregulate stage
65	423889	AL035447	Hs.134594	hypothetical protein LOC57158	0.24	2.43	downregulate stage
	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	0.27	2.28	downregulate stage
	424206	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc	0.3	2.59	downregulate stage
	424479	AF064238	Hs.149098	smoothelin	0.26	3.29	downregulate stage
	424580	AA446539	Hs.35092	ESTs	0.15	2.57	downregulate stage
70	424846	AU077324	Hs.1832	neuropeptide Y	0.4	2.04	downregulate stage
	424938	AW102607	Hs.245233	ESTs	0.29	2.16	downregulate stage
	424982	U94777	Hs.154084	phosphorylase, glycogen; muscle (McArdle	0.42	1.89	downregulate stage
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	0.14	1.86	downregulate stage
	425545	N98529	Hs.158295	Human mRNA for myosin light chain 3 (MLC	0.03	13.25	downregulate stage
75	425622	AW360847	Hs.16578	ESTs	0.3	2.19	downregulate stage
	425751	T19239	Hs.1940	crystallin, alpha B	0.47	1.92	downregulate stage
	425869	AA524547	Hs.160318	FXYD domain-containing ion transport reg	0.45	1.85	downregulate stage
	425887	AL049443	Hs.161283	Homo sapiens mRNA; cDNA DKFZp586N2020 (f	0.19	2.85	downregulate stage

5	425932	MB1650	Hs.1968	semenogelin I	0.02	16.3	downregulate stage
	426354	NM_004010	Hs.169470	dystrophin (muscular dystrophy, Duchenne	0.27	2.52	downregulate stage
	426429	X73114	Hs.169849	myosin-binding protein C, slow-type	0.1	10.3	downregulate stage
	426752	X69490	Hs.172004	titin	0.03	31.3	downregulate stage
	426809	BE313114	Hs.29706	ESTs	0.34	2.95	downregulate stage
10	427078	AI676062	Hs.111902	ESTs	0.22	2.11	downregulate stage
	427136	AL117415	Hs.173716	Homo sapiens mRNA; cDNA DKFZp434K0521 (f	0.37	2.33	downregulate stage
	427164	AB037721	Hs.173871	KJAA1300 protein	0.12	5.47	downregulate stage
	427185	AA398930	Hs.186674	ESTs	0.22	4.65	downregulate stage
	427373	AB007972	Hs.177533	Homo sapiens mRNA; cDNA DKFZp586N0318 (f	0.22	3.18	downregulate stage
15	427393	AB029018	Hs.177635	KJAA1095 protein	0.27	2.13	downregulate stage
	427665	AF134803	Hs.180141	cofilin 2 (muscle)	0.05	4	downregulate stage
	427676	AA394062	Hs.180266	tropomyosin 2 (beta)	0.45	1.87	downregulate stage
	427888	AA417088	Hs.137598	ESTs	0.36	2.04	downregulate stage
	427980	AA418305		gb:zv96g05.s1 Soares_NhMPu_S1 Homo sapi	0.32	2.39	downregulate stage
20	428087	AA100573	Hs.182421	tropoin C2, fast	0.17	4.37	downregulate stage
	428138	AA773842	Hs.293799	ESTs	0.45	2.2	downregulate stage
	428221	U96781	Hs.183075	ESTs, Highly similar to Ca2+ ATPase of f	0.23	3.36	downregulate stage
	428329	AA426091	Hs.98453	ESTs	0.21	2.09	downregulate stage
	428409	AW117207	Hs.98523	ESTs	0.1	7.63	downregulate stage
25	428411	AW291464	Hs.10338	ESTs	0.32	1.98	downregulate stage
	428648	AF052728	Hs.188021	potassium voltage-gated channel, subfam	0.08	2.99	downregulate stage
	428649	AL045716	Hs.188228	Homo sapiens cDNA FLJ11003 fis, clone PL	0.11	2.07	downregulate stage
	428899	AA744610	Hs.194431	palladin	0.42	1.84	downregulate stage
	429350	AI754634	Hs.131987	ESTs	0.06	4.73	downregulate stage
30	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	0.18	2.31	downregulate stage
	429545	AI824164	Hs.17667	lymphocyte antigen 6 complex, locus E	0.31	2.07	downregulate stage
	429655	U48959	Hs.211582	myosin, light polypeptide kinase	0.33	2.18	downregulate stage
	429892	NM_003803	Hs.2504	myomesin 1 (skelemin) (185kD)	0.36	2.17	downregulate stage
	429930	AI580809	Hs.99569	ESTs	0.18	5.6	downregulate stage
35	429956	AI374651	Hs.22542	ESTs	0.22	4.45	downregulate stage
	430013	AA463833	Hs.151275	ESTs	0.21	3.03	downregulate stage
	430271	T06199	Hs.237506	heat shock cognate 40	0.47	1.85	downregulate stage
	430310	U60115	Hs.239069	four and a half LIM domains 1	0.18	3.44	downregulate stage
	430418	R98852	Hs.36029	heart and neural crest derivatives expre	0.38	2.26	downregulate stage
40	430699	AW969847	Hs.292718	ESTs, Weakly similar to RET2_HUMAN RETIN	0.16	2.52	downregulate stage
	430712	AW044647	Hs.196284	ESTs	0.29	1.94	downregulate stage
	430778	D90337	Hs.247916	atriuretic peptide precursor C	0.14	4.48	downregulate stage
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	0.35	1.87	downregulate stage
	432247	AA531287	Hs.105805	ESTs	0.21	3.99	downregulate stage
45	432689	AB018320	Hs.278626	Arg/Abi-interacting protein ArgBP2	0.11	1.98	downregulate stage
	432792	AA448114	Hs.278950	protocadherin beta 1	0.22	2.93	downregulate stage
	433142	AL120697	Hs.110640	ESTs	0.21	2.18	downregulate stage
	433633	AI880516	Hs.84630	ESTs	0.34	2.67	downregulate stage
	433688	AA628467	Hs.112572	Homo sapiens cDNA FLJ14130 fis, clone MA	0.35	2.27	downregulate stage
50	433826	AA609938	Hs.144492	ESTs	0.24	1.91	downregulate stage
	434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mRNA	0.07	3.46	downregulate stage
	434160	BE551196	Hs.114275	ESTs	0.5	2	downregulate stage
	434352	AF129505	Hs.86492	small muscle protein, X-linked	0.34	2.13	downregulate stage
	434361	AF129755	Hs.117772	ESTs	0.03	31.3	downregulate stage
55	435731	AA699581	Hs.186811	ESTs	0.31	3.25	downregulate stage
	435869	AF255910	Hs.54650	vascular endothelial junction-associated	0.21	3.73	downregulate stage
	435978	AF272899	Hs.135118	Homo sapiens PR-domain zinc finger prote	0.35	2.25	downregulate stage
	436359	Z83806		gb:HL.sapiens mRNA for axonemal dynein he	0.24	3.28	downregulate stage
	436638	AI271945	Hs.134984	ESTs	0.36	1.87	downregulate stage
60	436953	AW959074	Hs.23648	Homo sapiens cDNA FLJ13097 fis, clone NT	0.14	6.95	downregulate stage
	437176	AW176909	Hs.42346	calcineurin-binding protein calcisarcin-1	0.32	2.19	downregulate stage
	437233	D81448	Hs.153961	ARP1 (actin-related protein 1, yeast) ho	0.27	2.38	downregulate stage
	438619	AB032773	Hs.6341	TU12B1-TY protein	0.19	2.69	downregulate stage
	438666	AW014493	Hs.128727	ESTs	0.16	1.98	downregulate stage
65	439231	AW581935	Hs.141480	ESTs	0.1	3.9	downregulate stage
	439973	AI733308	Hs.124663	ESTs	0.16	6.2	downregulate stage
	440172	AA868584	Hs.126154	ESTs	0.24	2.34	downregulate stage
	440274	R24595	Hs.7122	scrapie responsive protein 1	0.11	3.02	downregulate stage
	440687	AL080222	Hs.7358	hypothetical protein FLJ13110	0.19	2.95	downregulate stage
70	440700	AW952281	Hs.296184	ESTs, Highly similar to GB01_HUMAN GUANI	0.13	2.69	downregulate stage
	440737	AI375167	Hs.132221	Homo sapiens cDNA FLJ12401 fis, clone MA	0.5	2	downregulate stage
	441805	AA285136	Hs.7974	neuronal specific transcription factor D	0.07	13.55	downregulate stage
	441969	AI733386	Hs.129194	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.38	1.86	downregulate stage
	442109	BE218975	Hs.212395	ESTs	0.24	2.86	downregulate stage
75	442985	AI025984	Hs.55467	ESTs	0.19	2	downregulate stage
	443060	D78874	Hs.8944	procollagen C-endopeptidase enhancer 2	0.09	3.66	downregulate stage
	443164	AI038503	Hs.55780	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.2	1.86	downregulate stage
	443476	AW068594	Hs.133878	ESTs, Weakly similar to AF151889 1 CGI-1	0.11	2.79	downregulate stage
	443604	C03577	Hs.5615	myosin regulatory light chain 2, smooth	0.24	3.41	downregulate stage
	443790	NM_003500	Hs.9795	acyl-Coenzyme A oxidase 2, branched chai	0.28	3.6	downregulate stage
	443932	AW888222	Hs.9973	tensin	0.32	2.57	downregulate stage

	444195	AB002351	Hs.10587	KIAA0353 protein	0.19	4.04	downregulate stage
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	0.38	2.04	downregulate stage
	444684	AW044070	Hs.147037	ESTs	0.36	2.25	downregulate stage
5	444793	U89281	Hs.11958	oxidative 3 alpha hydroxysteroid dehydro	0.29	2.19	downregulate stage
	444938	AW470690	Hs.148814	ESTs	0.43	2.3	downregulate stage
	445230	U97018	Hs.12451	echinoderm microtubule-associated protel	0.13	2.64	downregulate stage
	445235	AI564022	Hs.138207	ESTs	0.13	2.4	downregulate stage
	445621	AI733818	Hs.145549	ESTs	0.25	1.91	downregulate stage
10	445687	W80382	Hs.149297	ESTs	0.2	3.5	downregulate stage
	445850	AI262049	Hs.145560	ESTs	0.53	1.9	downregulate stage
	446406	AI553681	Hs.25248	ESTs	0.07	3.25	downregulate stage
	446500	U78093	Hs.15154	sushi-repeat-containing protein, X chrom	0.33	1.9	downregulate stage
	447595	AW379130	Hs.18953	phosphodiesterase 9A	0.28	1.85	downregulate stage
	447918	AI129320	Hs.16930	ESTs	0.29	2.46	downregulate stage
15	448076	AJ133123	Hs.20196	adenylate cyclase 9	0.2	2.27	downregulate stage
	448283	AJ340462	Hs.182979	ribosomal protein L12	0.53	1.9	downregulate stage
	448303	BE622468	Hs.11924	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.39	1.84	downregulate stage
	448425	AI500359	Hs.233401	ESTs	0.16	1.97	downregulate stage
20	448429	D17408	Hs.21223	calponin 1, basic, smooth muscle	0.12	5.43	downregulate stage
	448555	AI536697	Hs.159863	ESTs	0.32	2.86	downregulate stage
	448901	AK001021	Hs.22505	hypothetical protein FLJ10159	0.17	2.66	downregulate stage
	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	0.24	1.86	downregulate stage
	449226	AB002365	Hs.23311	KIAA0367 protein	0.1	4.96	downregulate stage
25	449238	AA428229	Hs.85524	muscle-specific RING-finger protein homo	0.14	2.53	downregulate stage
	449422	AA001373	Hs.59821	ESTs	0.43	2.3	downregulate stage
	449690	AA002140	Hs.33024	ESTs	0.5	2	downregulate stage
	449874	AA135688	Hs.10083	ESTs	0.33	2.7	downregulate stage
	449925	AI342493	Hs.24192	Homo sapiens cDNA FLJ20767 fis, clone CO	0.11	5.57	downregulate stage
30	450300	AL041440	Hs.58210	ESTs	0.41	2.13	downregulate stage
	450578	AI971773	Hs.232268	ESTs	0.44	2.25	downregulate stage
	450810	BE207588	Hs.25511	transforming growth factor beta 1 induce	0.51	1.86	downregulate stage
	450831	R37974	Hs.25255	ESTs	0.23	1.96	downregulate stage
	451331	AK002039	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	0.37	2.18	downregulate stage
35	451533	NM_004657	Hs.26530	serum deprivation response (phosphatidyl	0.1	9.36	downregulate stage
	451782	AF233588	Hs.27018	Ris	0.35	2.43	downregulate stage
	451948	AW452473	Hs.211125	ESTs	0.43	1.88	downregulate stage
	452422	AA521416	Hs.22701	ESTs	0.41	1.85	downregulate stage
	452463	R36452	Hs.300817	ESTs	0.09	4.05	downregulate stage
40	452776	AA194540	Hs.13522	ESTs	0.36	2.16	downregulate stage
	452814	AI092790	Hs.55016	hypothetical protein FLJ21935	0.06	4.7	downregulate stage
	453064	R40334	Hs.301395	Homo sapiens cDNA: FLJ21204 fis, clone C	0.07	4.47	downregulate stage
	453351	AI625721	Hs.61814	Homo sapiens cDNA: FLJ22750 fis, clone K	0.33	3.05	downregulate stage
	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	0.03	7.14	downregulate stage
45	453359	AA448787	Hs.24872	ESTs, Weakly similar to sortic carboxype	0.4	1.92	downregulate stage
	453464	AI884911	Hs.32989	receptor (calcatonin) activity modifying	0.24	3.29	downregulate stage
	453500	AI478427	Hs.43125	ESTs	0.02	11.41	downregulate stage
	453582	AW854339	Hs.33476	hypothetical protein FLJ11937	0.39	2.04	downregulate stage
	453586	AA248089	Hs.50841	ESTs, Weakly similar to tuftelin [M.musc	0.43	1.86	downregulate stage
50	453666	AW015681	Hs.135229	ESTs, Moderately similar to AF107203 1 a	0.28	2.42	downregulate stage
	453698	AA037615	Hs.42746	ESTs	0.2	1.88	downregulate stage
	453702	AA037637	Hs.42128	ESTs	0.32	2.42	downregulate stage
	453725	W28543		gb:48c5 Human retina cDNA randomly prime	0.2	2.06	downregulate stage
	453950	AA156998	Hs.211568	eukaryotic translation Initiation factor	0.07	7.86	downregulate stage
55	454078	AA601518	Hs.22209	secreted modular calcium-binding protein	0.16	2.49	downregulate stage
	454471	AW902125		gb:QV0-NN1022-120500-220-h12 NN1022 Homo	0.41	2.45	downregulate stage
	454637	AW811613		gb:CM3-ST0157-300999-017-f05 ST0157 Homo	0.18	2.2	downregulate stage
	454750	AW866285		gb:QV4-SN0024-080400-167-a09 SN0024 Homo	0.49	2.05	downregulate stage
	455073	AW854829		gb:QV2-CT0261-201099-011-f01 CT0261 Homo	0.27	2.09	downregulate stage
60	455485	AA102287	Hs.26756	Homo sapiens cDNA: FLJ20896 fis, clone A	0.32	2.07	downregulate stage
	455611	L06419	Hs.75093	procollagen-lysine, 2-oxoglutarate 5-dio	0.15	2.87	downregulate stage
	456100	AI983981	Hs.189114	ESTs	0.4	2.5	downregulate stage
	456841	AA875863	Hs.152345	poliiovirus receptor-related 1 (herpesvir	0.35	1.9	downregulate stage
	457064	AA776743	Hs.191589	ESTs	0.17	2.34	downregulate stage
65	457108	N74724	Hs.108479	ESTs	0.48	2.1	downregulate stage
	457506	AF131757	Hs.274533	Homo sapiens clone 24926 mRNA sequence	0.29	2.59	downregulate stage
	457625	T10073		gb:seq1293 b4HB3MA Col8-HAP-Fl Homo sapi	0.29	3.45	downregulate stage
	458482	AV648858	Hs.29488	ESTs	0.26	2.17	downregulate stage
	458622	AA972412	Hs.13755	f-box and WD-40 domain protein 2	0.51	1.95	downregulate stage
70	458841	W28965		gb:54d10 Human retina cDNA randomly prim	0.32	3.1	downregulate stage
	459037	AW439497	Hs.290656	EST	0.43	2.35	downregulate stage
	400762				0.71	0.4	early stage
	400937				1.2	0.26	early stage
	400977				0.63	0.48	early stage
75	401024				0.8	0.3	early stage
	401048				1.9	0.22	early stage
	401537				1.3	0.2	early stage
	401619				3.5	0.19	early stage

	402089			0.39	0.55	early stage
	402176			0.35	0.91	early stage
	402407			1	0.15	early stage
5	402430			0.28	1.25	early stage
	402435			2.15	0.21	early stage
	402522			1.8	0.14	early stage
	402546			0.17	1.66	early stage
	402604			0.41	0.66	early stage
10	402716			0.14	0.86	early stage
	402846			0.61	0.52	early stage
	402922			0.14	0.83	early stage
	403567			0.44	0.49	early stage
	403590			1	0.34	early stage
15	404336			0.49	0.44	early stage
	404345	AA730407	Hs.159156	0.38	0.4	early stage
	404501	AW247252	Hs.75514	0.32	0.8	early stage
	404594			0.37	0.91	early stage
	404874			1.87	0.26	early stage
	404881			0.36	0.5	early stage
20	404896	NM_000429	Hs.106845	1	0.36	early stage
	404999	U58196	Hs.296281	0.19	1.06	early stage
	405071			0.19	0.77	early stage
	405308			0.4	0.55	early stage
	405463			0.41	1	early stage
25	405580			1.89	0.19	early stage
	405600			0.22	0.63	early stage
	405720			0.37	0.61	early stage
	405863			0.53	0.26	early stage
	405867			0.24	1.1	early stage
30	405920			0.39	1.15	early stage
	406036			2.15	0.17	early stage
	406243			0.32	1.23	early stage
	406367			0.38	0.76	early stage
35	406834	AI318680		0.4	0.67	early stage
	406881	D16154		0.14	1.55	early stage
	407411	AF060170		0.39	0.69	early stage
	407639	AW205369	Hs.252936	0.61	0.34	early stage
	408112	AW451982	Hs.248613	0.2	0.54	early stage
	408732	AL117490	Hs.47225	1	0.32	early stage
40	409103	AF251237	Hs.112208	0.33	1.03	early stage
	409840	AW502122		0.56	0.28	early stage
	410128	AW904599		1.26	0.37	early stage
	411474	AW848427		1	0.14	early stage
45	412564	X83703	Hs.74019	0.36	0.44	early stage
	413266	BE300352		1.46	0.25	early stage
	413341	H78472	Hs.191325	0.41	0.48	early stage
	414055	AW818687	Hs.5366	0.33	0.67	early stage
	414170	AA335996	Hs.3743	1.15	0.21	early stage
50	414220	BE298094		0.16	0.52	early stage
	414276	BE297852		1.75	0.2	early stage
	414327	BE408145	Hs.185254	0.1	0.99	early stage
	414366	BE549143		1	0.31	early stage
	414376	BE393856	Hs.66915	0.18	0.96	early stage
55	414555	N98569	Hs.76422	0.48	0.67	early stage
	415199	AA161125	Hs.57893	0.75	0.72	early stage
	417304	H15635		0.6	0.58	early stage
	417371	N74613	Hs.269149	0.3	0.58	early stage
	418133	R43504	Hs.6181	1.28	0.29	early stage
60	419273	BE271180	Hs.293490	0.54	0.28	early stage
	419716	AA953770		0.45	0.66	early stage
	420390	AA330047	Hs.191187	1.45	0.12	early stage
	421745	AF205849	Hs.107740	0.33	0.71	early stage
	421813	BE048255		0.52	0.67	early stage
65	422669	H12402	Hs.119122	1	0.26	early stage
	422743	BE304678	Hs.119598	0.2	0.57	early stage
	422760	BE409561		0.41	0.64	early stage
	422880	AF228704	Hs.121524	3.75	0.1	early stage
	423457	F08208	Hs.155606	0.55	0.54	early stage
70	425349	AA425234	Hs.79886	1	0.21	early stage
	425360	BE547704		0.28	0.85	early stage
	426356	BE536836		0.31	0.69	early stage
	426521	AF161445	Hs.170219	0.11	0.69	early stage
	426670	AA383047	Hs.193718	1	0.55	early stage
	426699	AA383337	Hs.121269	0.33	0.71	early stage
75	427827	AA416577	Hs.189105	1.16	0.41	early stage
	428651	AF186478	Hs.188401	1.85	0.24	early stage
	430727	X75917	Hs.2654	0.78	0.46	early stage

	430750	AI650360	Hs.100256	ESTs	2.15	0.17	early stage
	430795	AW971398		gb:EST383487 MAGE resequences, MAGL Homo	1.95	0.21	early stage
	431900	AW972048	Hs.192534	ESTs	0.36	0.73	early stage
5	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	1.8	0.17	early stage
	432791	NM_014554	Hs.278949	sentrin/SUMO-specific protease	2.8	0.15	early stage
	433404	T32982	Hs.102720	ESTs	2.2	0.13	early stage
	433782	AF090945		gb:Homo sapiens clone HQ0670	3.3	0.15	early stage
	433877	BE146567	Hs.257475	ESTs	0.65	0.7	early stage
10	434483	AA223646	Hs.57222	nurim (nuclear envelope membrane protein	0.38	0.49	early stage
	435752	AF230801	Hs.125180	growth hormone receptor	0.52	0.4	early stage
	436178	BE152396	Hs.21590	Homo sapiens HSPC304 mRNA, partial cds	1.65	0.14	early stage
	436391	AJ227892	Hs.146274	ESTs	1.35	0.16	early stage
	436602	AI793222	Hs.166817	ESTs	0.17	1.46	early stage
	436777	AA731199	Hs.293130	ESTs	1	0.2	early stage
15	436813	AW975714	Hs.129004	ESTs	0.19	1.45	early stage
	436869	NM_014867	Hs.297661	Homo sapiens YAC clone 377A1 unknown mRN	0.96	0.2	early stage
	437169	AA309612	Hs.118797	ubiquitin-conjugating enzyme E2D 3 (homo	0.07	1.8	early stage
	438649	AA813136	Hs.143014	ESTs	1.38	0.19	early stage
20	438681	AW384815	Hs.149208	KIAA1555 protein	0.25	0.54	early stage
	438802	AA825976	Hs.136954	ESTs	1.8	0.14	early stage
	438887	R68857	Hs.265499	ESTs	1.05	0.32	early stage
	440128	AA952623	Hs.189144	ESTs, Weakly similar to NPT2_HUMAN RENAL	1	0.19	early stage
	440397	AA884448	Hs.157239	ESTs	0.59	0.38	early stage
25	440509	BE410132	Hs.134202	ESTs, Weakly similar to B41182 collagen	0.26	0.9	early stage
	440605	Z40094	Hs.185698	ESTs	0.51	0.43	early stage
	442238	AW135374	Hs.270949	ESTs	1	0.18	early stage
	443258	AF169301	Hs.9098	sulfate transporter 1	0.85	0.49	early stage
	445739	AW136354	Hs.145303	ESTs	0.88	0.4	early stage
30	447306	AI373163	Hs.170333	ESTs	0.15	0.8	early stage
	447346	AI525135	Hs.210507	ESTs	1.35	0.27	early stage
	448265	N46272	Hs.26812	ESTs	0.47	0.26	early stage
	448678	AI560776	Hs.199854	ESTs	0.19	0.68	early stage
	448778	AF074913		gb:Homo sapiens transcription factor Pax	0.57	0.53	early stage
35	448871	BE616709		gb:601279937F1 NIH_MGC_39 Homo sapiens c	0.26	0.94	early stage
	449180	AI633836	Hs.195649	ESTs	0.46	0.45	early stage
	449213	BE616861		gb:601279056F1 NIH_MGC_39 Homo sapiens c	0.73	0.56	early stage
	449231	BE410360		gb:601302340F1 NIH_MGC_21 Homo sapiens c	0.27	0.76	early stage
	449450	AL039852	Hs.256990	ESTs, Moderately similar to ALU7_HUMAN A	1	0.26	early stage
40	449815	AI671000	Hs.199739	ESTs	1.2	0.15	early stage
	450972	AW967906	Hs.194617	ESTs	0.28	0.83	early stage
	451236	AI767406	Hs.207026	ESTs, Weakly similar to B56205 transcrip	0.35	0.77	early stage
	451283	H83979		gb:ys93d11.1.r1 Soares retina N2b5HR Homo	1	0.23	early stage
	451375	AI792066	Hs.283902	Homo sapiens BAC clone RP11-481J13 from	0.16	1.37	early stage
45	452530	AI905518		gb:RC-BT091-210199-098 BT091 Homo sapien	1.35	0.21	early stage
	452550	AA026735		gb:ze93d05.r1 Soares_fetal_heart_NbHH19W	0.44	0.6	early stage
	454121	AW090524	Hs.244967	ESTs	2.85	0.17	early stage
	454554	AW847505		gb:RCO-CT0210-280999-021-c10 CT0210 Homo	0.36	0.5	early stage
	454697	AW813728	Hs.15036	ESTs, Highly similar to AF161358 1 HSPC0	0.43	0.6	early stage
50	454851	AW835127		gb:RC4-LT0011-100100-012-c07 LT0011 Homo	0.77	0.32	early stage
	455040	AW852286		gb:QV0-CT0225-100400-187-d08 CT0225 Homo	0.26	0.52	early stage
	455225	AW996689		gb:QV3-BN0046-150400-151-g09 BN0046 Homo	1.7	0.18	early stage
	455970	AI733857	Hs.71483	ESTs	0.66	0.45	early stage
	456235	AA203637		gb:zx58b12.r1 Soares_fetal_liver_spleen_	0.64	0.43	early stage
55	456450	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	0.38	0.76	early stage
	456526	AA782222	Hs.192008	ESTs	0.63	0.43	early stage
	456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Dr	0.49	0.46	early stage
	456983	AI081687	Hs.170225	thymopoietin	0.27	0.75	early stage
	457089	AA416556	Hs.98234	ESTs	0.34	0.48	early stage
60	458198	AI286100	Hs.192739	ESTs	0.47	0.48	early stage
	458425	AI084057	Hs.301149	ESTs	0.4	0.37	early stage
	458660	AI299739	Hs.99601	Homo sapiens cDNA FLJ12553 fis, clone NT	0.79	0.68	early stage
	458703	AW749121	Hs.282901	ESTs	1	0.23	early stage
	458767	T97083	Hs.148355	ESTs	1	0.17	early stage
65	459399	BE407712		gb:601299745F1 NIH_MGC_21 Homo sapiens c	0.68	0.56	early stage
	400860				4.9	0.08	late stage
	408190	AB032963	Hs.43577	ATPase, Class I, type 8B, member 2	0.58	0.84	late stage
	408558	AW015759	Hs.235709	ESTs	1.26	0.45	late stage
	410077	AF097645	Hs.58570	deleted in cancer 1; RNA helicase HDB/DI	6.2	0.12	late stage
70	410295	AA741357	Hs.62041	nidogen (enactin)	0.77	0.86	late stage
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	1.45	0.27	late stage
	410614	AI091195	Hs.65029	growth arrest-specific 1	0.4	1.12	late stage
	410867	X63556	Hs.750	fibrillin 1 (Marfan syndrome)	0.71	1.07	late stage
	411573	AB029000	Hs.70823	KIAA1077 protein	3.64	0.19	late stage
	412116	AW402166	Hs.784	Epstein-Barr virus induced gene 2 (lymph	5.18	0.13	late stage
75	412178	AW898526		gb:RC6-NN0072-040500-011-E05 NN0072 Homo	7.55	0.08	late stage
	412429	AV650262	Hs.75765	GRO2 oncogene	3.37	0.15	late stage
	412652	AI801777	Hs.6774	ESTs	0.49	1.24	late stage

5	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob	3.6	0.11	late stage
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	4.62	0.14	late stage
	414183	AW957446	Hs.301711	ESTs	3.18	0.16	late stage
	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	0.81	0.73	late stage
	414476	AA301867	Hs.76224	EGF-containing fibulin-like extracellular	0.37	0.99	late stage
10	414504	AW069181	Hs.293523	ESTs, Weakly similar to transformalion-r	0.97	0.65	late stage
	414812	X72755	Hs.73767	monokine induced by gamma interferon	3.84	0.1	late stage
	415116	AA160363	Hs.269956	ESTs	7.45	0.07	late stage
	415714	NM_002290	Hs.78672	laminin, alpha 4	0.49	1.39	late stage
	415822	D59243		gb:HUM526E07B Clontech human placenta po	8.15	0.09	late stage
15	415994	NM_002923	Hs.78944	regulator of G-protein signalling 2, 24k	0.48	1.46	late stage
	417059	AL037672	Hs.81071	extracellular matrix protein 1	1.52	0.44	late stage
	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	2	0.39	late stage
	417733	AL048678	Hs.82503	syntrophin	0.2	2.67	late stage
	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	4.56	0.12	late stage
20	417849	AW291587	Hs.82733	nidogen 2	1.81	0.38	late stage
	418005	AI185220	Hs.83164	collagen, type XV, alpha 1	0.97	0.74	late stage
	418283	S79895	Hs.83942	cathepsin K (pseudosclerosis)	1.21	0.56	late stage
	418875	W19971	Hs.233459	ESTs	2.63	0.33	late stage
	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	7.65	0.07	late stage
25	419925	AA159850	Hs.93765	lipoma HMGIC fusion partner	0.91	0.82	late stage
	420411	AI581085	Hs.24678	ESTs	7.3	0.1	late stage
	420943	AI718702	Hs.105341	ESTs	7.05	0.07	late stage
	421116	T19132	Hs.101850	retinol-binding protein 1, cellular	0.99	0.42	late stage
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	8.1	0.08	late stage
30	421786	AI188653	Hs.21351	ESTs	8.15	0.08	late stage
	422414	AW875237	Hs.13701	ESTs	1.05	0.59	late stage
	422550	BE297626	Hs.296049	microfibrillar-associated protein 4	0.28	1.53	late stage
	422790	AA809875	Hs.25933	ESTs	2.69	0.28	late stage
	423057	AW961597	Hs.130816	ESTs	7.55	0.08	late stage
35	423720	AL044191	Hs.23388	Homo sapiens cDNA: FLJ21310 fis, clone C	1.24	0.61	late stage
	423905	AW579950	Hs.135150	lung type-I cell membrane-associated gly	2.12	0.24	late stage
	423915	AF039018	Hs.135281	alpha-actinin-2-associated LIM protein	0.29	2.45	late stage
	423961	D13666	Hs.136348	osteoblast specific factor 2 (fascilin	4.47	0.17	late stage
	424247	X14008	Hs.234734	lysosome (renal amyloidosis)	2.44	0.26	late stage
40	424839	AA740632	Hs.120850	ESTs	2.74	0.23	late stage
	426780	BE242284	Hs.172199	adenylate cyclase 7	8.55	0.09	late stage
	426974	AB002298	Hs.173035	KIAA0300 protein	1.56	0.36	late stage
	427055	AI301740	Hs.173381	dihydropyrimidinase-like 2	0.72	1	late stage
	427882	AA540987	Hs.193767	ESTs	2.25	0.29	late stage
45	428065	AI634046	Hs.157313	ESTs	6.19	0.1	late stage
	428147	AW629965	Hs.234983	ESTs	8.42	0.08	late stage
	428585	AB007863	Hs.185140	KIAA0403 protein	6.85	0.08	late stage
	428825	AI084336	Hs.128783	ESTs	0.9	0.8	late stage
	429490	AI971131	Hs.293684	ESTs, Weakly similar to alternatively sp	1.59	0.39	late stage
50	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxicin)	0.77	0.49	late stage
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	0.92	0.3	late stage
	431319	AA873350		gb:oh64h02.s1 NCI_CGAP_Kid5 Homo sapiens	1.36	0.44	late stage
	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	4.69	0.17	late stage
	432314	AA533447	Hs.285173	ESTs	1.75	0.31	late stage
55	432331	W37862	Hs.274368	Homo sapiens mRNA; cDNA DKFZp586i1524 (f	0.35	1.58	late stage
	432559	AW452948	Hs.257631	ESTs	1.37	0.49	late stage
	433470	AW960564	Hs.3337	transmembrane 4 superfamily member 1	2.58	0.24	late stage
	433586	T85301		gb:yd78d06.s1 Soares fetal liver spleen	5.06	0.11	late stage
	436428	AW246900	Hs.283712	hypothetical protein	8.25	0.09	late stage
60	436729	BE621807	Hs.3337	transmembrane 4 superfamily member 1	1.6	0.26	late stage
	438873	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	8.15	0.08	late stage
	439584	AA838114	Hs.221612	ESTs	8.6	0.09	late stage
	439653	AW021103	Hs.6631	hypothetical protein FLJ20373	2.21	0.27	late stage
	440524	R71264	Hs.16798	ESTs	3.44	0.21	late stage
65	440624	AF017987	Hs.7306	secreted frizzled-related protein 1	0.42	0.63	late stage
	441976	AA428403	Hs.106131	ESTs	8.5	0.09	late stage
	442739	NM_007274	Hs.8679	cytosolic acyl coenzyme A thioester hydr	7.95	0.06	late stage
	443852	AI679966	Hs.150603	ESTs	6.84	0.12	late stage
	443896	AI680242	Hs.271687	Homo sapiens cDNA FLJ13527 fis, clone PL	7.95	0.08	late stage
70	444212	AW503976	Hs.10649	basement membrane-induced gene	2.31	0.28	late stage
	444331	AW193342	Hs.24144	ESTs	0.32	1.64	late stage
	445142	AW978484	Hs.93842	Homo sapiens cDNA: FLJ22554 fis, clone H	2.52	0.24	late stage
	445701	AF055581	Hs.13131	lymphocyte adaptor protein	1.43	0.47	late stage
	446584	U53445	Hs.15432	downregulated in ovarian cancer 1	0.54	1.39	late stage
75	447526	AL048753	Hs.340	small inducible cytokine A2 (monocyte ch	1.43	0.43	late stage
	447744	AA313230	Hs.19413	S100 calcium-binding protein A12 (calgr	1.35	0.26	late stage
	447818	W79940	Hs.21905	ESTs	6.63	0.13	late stage
	449567	AI990790	Hs.188614	ESTs	4.7	0.13	late stage
	450455	AL117424	Hs.25035	chloride intracellular channel 4	0.64	1.31	late stage
	452239	AW379378	Hs.170121	protein tyrosine phosphatase, receptor t	0.59	1.18	late stage
	452698	NM_001295	Hs.301921	ESTs	2.31	0.26	late stage

	453212	H15416	Hs.21865	ESTs	2.51	0.26	late stage
	455510	AA422029	Hs.143640	ESTs, Weakly similar to hyperpolarization	8.6	0.06	late stage
	400775	R58624	Hs.2186	eukaryotic translation elongation factor	1	1	T2-T4 grade 3 papilloma marker
5	401508				1	1	T2-T4 grade 3 papilloma marker
	403092				1	1	T2-T4 grade 3 papilloma marker
	404232				1	1	T2-T4 grade 3 papilloma marker
	407020	U49973		gb:Human Tigger1 transposable element, c	1	1	T2-T4 grade 3 papilloma marker
	407345	AJ053836	Hs.169365	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	1	T2-T4 grade 3 papilloma marker
10	407420	AF084362		gb:Homo sapiens lipote-protein ligase B	1	1	T2-T4 grade 3 papilloma marker
	407577	AW131324	Hs.246759	ESTs, Weakly similar to KIAA1074 protein	1	1	T2-T4 grade 3 papilloma marker
	407666	AF071107	Hs.37501	MAD (mothers against decapentaplegic, Dr	1	1	T2-T4 grade 3 papilloma marker
	407916	L09234	Hs.603	ATPase, H+ transporting, lysosomal (vacu	1	1	T2-T4 grade 3 papilloma marker
	407936	AW118147	Hs.270935	ESTs	1	1	T2-T4 grade 3 papilloma marker
	408186	AW168847	Hs.250156	ESTs	1	1	T2-T4 grade 3 papilloma marker
15	408950	AA707814	Hs.7396	ESTs	1	1	T2-T4 grade 3 papilloma marker
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	1.2	0.12	T2-T4 grade 3 papilloma marker
	409045	AA635062	Hs.50094	Homo sapiens mRNA: cDNA DKFZp434O0515 (f	1	1	T2-T4 grade 3 papilloma marker
	409196	NM_001874	Hs.169765	carboxypeptidase M	1	1	T2-T4 grade 3 papilloma marker
20	409281	AA069998		gb:zrn67b03.r1 Stratagene neuroepithelium	1	1	T2-T4 grade 3 papilloma marker
	410010	AW572853	Hs.257683	ESTs, Weakly similar to ALU3_HUMAN ALU S	1	0.5	T2-T4 grade 3 papilloma marker
	410157	AW593277	Hs.225056	ESTs	1	0.69	T2-T4 grade 3 papilloma marker
	411112	AW818158		gb:CM1-ST0277-161299-070-g07 ST0277 Homo	1	1	T2-T4 grade 3 papilloma marker
	411336	AW837675		gb:QV2-LT0039-260300-107-b04 LT0039 Homo	1	1	T2-T4 grade 3 papilloma marker
25	412051	T15872	Hs.268713	ESTs, Weakly similar to hypothetical pro	1	1	T2-T4 grade 3 papilloma marker
	413485	N52628		gb:yv37g11.s1 Soares fetal liver spleen	1	1	T2-T4 grade 3 papilloma marker
	413574	BE149158	Hs.129998	Homo sapiens cDNA FLJ14267 fis, clone PL	1	1	T2-T4 grade 3 papilloma marker
	413782	BE546104		gb:601072642F1 NIH_MGC_12 Homo sapiens c	1	1	T2-T4 grade 3 papilloma marker
	414749	H94622	Hs.193358	ESTs, Moderately similar to diabetes mel	1	1	T2-T4 grade 3 papilloma marker
30	415293	R49462	Hs.106541	ESTs	1	1	T2-T4 grade 3 papilloma marker
	415442	F12963	Hs.7045	GL004 protein	1	1	T2-T4 grade 3 papilloma marker
	416255	T87587	Hs.272082	ESTs	1	1	T2-T4 grade 3 papilloma marker
	417047	AA192640	Hs.1526	ATPase, Ca++ transporting, cardiac muscl	1	1	T2-T4 grade 3 papilloma marker
	417181	L10123	Hs.1071	surfactant protein A binding protein	1	1	T2-T4 grade 3 papilloma marker
35	417367	N73877	Hs.171815	ESTs	1	1	T2-T4 grade 3 papilloma marker
	419721	NM_001650	Hs.288650	aquaporin 4	1	1	T2-T4 grade 3 papilloma marker
	420294	AA808259	Hs.196716	ESTs	1	0.65	T2-T4 grade 3 papilloma marker
	423589	AA328082	Hs.209569	ESTs, Weakly similar to thrombospondin t	1	1	T2-T4 grade 3 papilloma marker
	424549	AJ873205	Hs.183114	Homo sapiens cDNA FLJ14236 fis, clone NT	1	1	T2-T4 grade 3 papilloma marker
40	425458	H89317	Hs.182889	ESTs	1	1	T2-T4 grade 3 papilloma marker
	426475	AL134728		gb:DKFZp547A1890_r1 547 (synonym: hfr1)	1	1	T2-T4 grade 3 papilloma marker
	429453	AA453196	Hs.124222	ESTs	1	1	T2-T4 grade 3 papilloma marker
	431200	AF044823	Hs.250752	hook1 protein	1	1	T2-T4 grade 3 papilloma marker
	431938	AA938471	Hs.115242	developmentally regulated GTP-binding pr	1	1	T2-T4 grade 3 papilloma marker
45	431944	AJ360891	Hs.143619	ESTs	1	1	T2-T4 grade 3 papilloma marker
	432021	AA524470	Hs.58753	ESTs	1	1	T2-T4 grade 3 papilloma marker
	432205	AJ806583	Hs.125291	ESTs	1	0.31	T2-T4 grade 3 papilloma marker
	432527	AW975028	Hs.102754	ESTs	1	1	T2-T4 grade 3 papilloma marker
	434069	AF116651	Hs.283058	hypothetical protein PRO0800	1	0.41	T2-T4 grade 3 papilloma marker
50	435278	AW994242	Hs.173495	ESTs	1	1	T2-T4 grade 3 papilloma marker
	435965	AJ034368	Hs.132650	ESTs	1	0.36	T2-T4 grade 3 papilloma marker
	436227	AA706937	Hs.120802	ESTs, Moderately similar to A26541 Na+/K	1	1	T2-T4 grade 3 papilloma marker
	436635	AW104325	Hs.272093	ESTs, Weakly similar to STK2_HUMAN SERIN	1	0.74	T2-T4 grade 3 papilloma marker
	436640	AA724411	Hs.156065	ESTs	1	1	T2-T4 grade 3 papilloma marker
55	436884	BE046657		gb:h42e02.x1 NCL_CGAP_RDF2 Homo sapiens	1	1	T2-T4 grade 3 papilloma marker
	437251	AW976082		gb:EST388191 MAGE resequences, MAGN Homo	1	1	T2-T4 grade 3 papilloma marker
	437348	AA749149	Hs.163114	ESTs	1	1	T2-T4 grade 3 papilloma marker
	437769	AA767853	Hs.122895	ESTs	1	1	T2-T4 grade 3 papilloma marker
	437771	AA811071	Hs.123349	ESTs	1	1	T2-T4 grade 3 papilloma marker
60	438347	AA909686	Hs.293397	ESTs	1	1	T2-T4 grade 3 papilloma marker
	439171	AA831133	Hs.294128	ESTs	1	0.95	T2-T4 grade 3 papilloma marker
	439914	AA854066	Hs.145394	ESTs	1	1	T2-T4 grade 3 papilloma marker
	440399	AJ215527	Hs.125589	ESTs	1	1	T2-T4 grade 3 papilloma marker
	440972	BE044588	Hs.276158	ESTs	1	1	T2-T4 grade 3 papilloma marker
65	442004	AA973568	Hs.128317	ESTs	1	1	T2-T4 grade 3 papilloma marker
	442270	BE565699	Hs.62005	ESTs	1	1	T2-T4 grade 3 papilloma marker
	443413	AJ056457	Hs.221642	ESTs	1	1	T2-T4 grade 3 papilloma marker
	443927	AW016726	Hs.134860	ESTs	1	1	T2-T4 grade 3 papilloma marker
	445442	N20392	Hs.42846	ESTs	1	1	T2-T4 grade 3 papilloma marker
70	445611	AW418497	Hs.145583	ESTs	1	0.49	T2-T4 grade 3 papilloma marker
	445888	AF070564	Hs.13415	Homo sapiens clone 24571 mRNA sequence	1	1	T2-T4 grade 3 papilloma marker
	446552	AW470827	Hs.156241	ESTs	1	1	T2-T4 grade 3 papilloma marker
	447399	AJ815401	Hs.251967	Homo sapiens clone 785627 unknown mRNA	2.9	0.14	T2-T4 grade 3 papilloma marker
	449111	T83109	Hs.196180	ESTs	1	1	T2-T4 grade 3 papilloma marker
75	449232	AW192780	Hs.196080	ESTs	1	0.8	T2-T4 grade 3 papilloma marker
	451373	AJ792030		gb:os03e11.y5 NCL_CGAP_Lu5 Homo sapiens	1	1	T2-T4 grade 3 papilloma marker
	452453	AJ902519		gb:QV-BT009-101198-051 BT009 Homo sapien	1	1	T2-T4 grade 3 papilloma marker
	452534	AW083022	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	1	0.67	T2-T4 grade 3 papilloma marker

5	452536	BE063380		gb:PM0-BT0275-291099-002-g10 BT0275 Homo	1.65	0.26	T2-T4 grade 3 papilloma marker
	452640	AA027115	Hs.100206	ESTs, Weakly similar to AAAAD_HUMAN ARYL	1	1	T2-T4 grade 3 papilloma marker
	452645	AI911325	Hs.212049	EST	1	1	T2-T4 grade 3 papilloma marker
	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	1	1	T2-T4 grade 3 papilloma marker
	453472	AL037925		gb:DKFZp564M037_r1 564 (synonym: h1br2)	1	0.8	T2-T4 grade 3 papilloma marker
	453609	AL045301	Hs.13427	ESTs	1	1	T2-T4 grade 3 papilloma marker
	453677	AL079389		gb:DKFZp434E2116_r1 434 (synonym: h1es3)	1	0.77	T2-T4 grade 3 papilloma marker
	453704	R41806	Hs.100884	ESTs	1	1	T2-T4 grade 3 papilloma marker
10	455267	AW880861		gb:QV0-OT0033-070300-152-c12 OT0033 Homo	1	1	T2-T4 grade 3 papilloma marker
	455880	BE153208		gb:PM0-HT0335-050400-007-F10 HT0335 Homo	1	1	T2-T4 grade 3 papilloma marker
	456520	AW835416	Hs.29417	HCF-binding transcription factor Zhangfe	1	1	T2-T4 grade 3 papilloma marker
	456763	AJ271351	Hs.128180	B-cell translocation gene 4	1	0.71	T2-T4 grade 3 papilloma marker
	456912	AI458843	Hs.158112	protein tyrosine phosphatase, receptor I	1	1	T2-T4 grade 3 papilloma marker
15	457018	AA761820	Hs.250965	ESTs	1	1	T2-T4 grade 3 papilloma marker
	457323	AW867813	Hs.201064	ESTs	1	1	T2-T4 grade 3 papilloma marker
	457339	AW971949	Hs.291252	ESTs	1	1	T2-T4 grade 3 papilloma marker
	457340	AA492071		gb:ne97b04.s1 NCI_CGAP_Kid1 Homo sapiens	1	1	T2-T4 grade 3 papilloma marker
	457507	AW300248	Hs.181693	ESTs	1	1	T2-T4 grade 3 papilloma marker
20	458106	AF086561	Hs.37	acetyl-Coenzyme A acetyltransferase 1 (a	1	1	T2-T4 grade 3 papilloma marker
	458624	AI362790	Hs.181801	ESTs	1	0.34	T2-T4 grade 3 papilloma marker
	459396	AI907536	Hs.103869	ESTs	1	1	T2-T4 grade 3 papilloma marker
	401002				1	1	T2-T4 grade 3 solid tumor marker
	401866				1.35	0.14	T2-T4 grade 3 solid tumor marker
25	403615				1	1	T2-T4 grade 3 solid tumor marker
	403776				1	1	T2-T4 grade 3 solid tumor marker
	404113				1	0.43	T2-T4 grade 3 solid tumor marker
	404488				1	0.17	T2-T4 grade 3 solid tumor marker
	404653				1	1	T2-T4 grade 3 solid tumor marker
30	406076	AL390179	Hs.137011	Homo sapiens mRNA; cDNA DKFZp547P134 (tr	1	0.24	T2-T4 grade 3 solid tumor marker
	406471				1	0.42	T2-T4 grade 3 solid tumor marker
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	2.75	0.05	T2-T4 grade 3 solid tumor marker
	407624	AW157431	Hs.248941	ESTs	3.05	0.15	T2-T4 grade 3 solid tumor marker
	409153	W03754	Hs.50813	hypothetical protein FLJ20022	3.85	0.03	T2-T4 grade 3 solid tumor marker
35	409464	X69115	Hs.54488	zinc finger protein 37a (KOX 21)	1.15	0.29	T2-T4 grade 3 solid tumor marker
	409731	AA125985	Hs.55145	thymosin, beta, identified in neuroblast	1	0.24	T2-T4 grade 3 solid tumor marker
	410025	BE220489	Hs.113592	ESTs	1	0.3	T2-T4 grade 3 solid tumor marker
	410589	AW770768	Hs.266717	ESTs	1	0.28	T2-T4 grade 3 solid tumor marker
	411840	AW866330		gb:QV4-SN0024-080400-167-e01 SN0024 Homo	1.05	0.15	T2-T4 grade 3 solid tumor marker
40	412198	AA937111	Hs.69165	ESTs	1	0.26	T2-T4 grade 3 solid tumor marker
	412305	AW936369		gb:QV4-DT0021-301299-071-d07 DT0021 Homo	1	0.53	T2-T4 grade 3 solid tumor marker
	412753	AI065016	Hs.6390	ESTs	1	0.33	T2-T4 grade 3 solid tumor marker
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	1	0.69	T2-T4 grade 3 solid tumor marker
	413530	AA130158	Hs.19977	ESTs, Moderately similar to ALU8_HUMAN A	1	0.29	T2-T4 grade 3 solid tumor marker
45	415027	D31010		gb:HUM12147 Human fetal lung Homo sapie	1	1	T2-T4 grade 3 solid tumor marker
	416099	H18626	Hs.22634	ESTs	1	0.74	T2-T4 grade 3 solid tumor marker
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	3.8	0.12	T2-T4 grade 3 solid tumor marker
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	2.85	0.08	T2-T4 grade 3 solid tumor marker
	420347	AL033539	Hs.97124	Human DNA sequence from clone RP1-309H15	1	0.2	T2-T4 grade 3 solid tumor marker
50	421243	AW873803	Hs.102876	pancreatic lipase	1	0.38	T2-T4 grade 3 solid tumor marker
	422660	AW297582	Hs.237062	ESTs	1.05	0.32	T2-T4 grade 3 solid tumor marker
	422834	AA318334		gb:EST20402 Retina II Homo sapiens cDNA	1	0.38	T2-T4 grade 3 solid tumor marker
	422972	N59319	Hs.145404	ESTs	1	0.61	T2-T4 grade 3 solid tumor marker
	423104	AJ005273	Hs.123647	antigenic determinant of recA protein (m	2.95	0.12	T2-T4 grade 3 solid tumor marker
55	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	1	0.05	T2-T4 grade 3 solid tumor marker
	424268	AA397653	Hs.144339	Human DNA sequence from clone 495010 on	1	0.35	T2-T4 grade 3 solid tumor marker
	425196	AL037915	Hs.155097	carbonic anhydrase II	2.75	0.05	T2-T4 grade 3 solid tumor marker
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	1	0.09	T2-T4 grade 3 solid tumor marker
	430300	U60805	Hs.238648	oncostatin M receptor	1	0.25	T2-T4 grade 3 solid tumor marker
60	431098	AW501465	Hs.249230	ribonuclease L (2',5'-oligoadenylate	1	0.28	T2-T4 grade 3 solid tumor marker
	431277	AA501806	Hs.249965	ESTs	1	0.22	T2-T4 grade 3 solid tumor marker
	431750	AA514986	Hs.283705	ESTs	1	1	T2-T4 grade 3 solid tumor marker
	434273	AA913143	Hs.26303	ESTs	1	0.41	T2-T4 grade 3 solid tumor marker
	435505	AF200492	Hs.211238	Interleukin-1 homolog 1	1.8	0.19	T2-T4 grade 3 solid tumor marker
65	436281	AW411194	Hs.120051	ESTs	2.05	0.14	T2-T4 grade 3 solid tumor marker
	437010	AA741368	Hs.291434	ESTs	2.4	0.17	T2-T4 grade 3 solid tumor marker
	437814	AI088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	1.8	0.13	T2-T4 grade 3 solid tumor marker
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	1	0.3	T2-T4 grade 3 solid tumor marker
	438376	BE541211	Hs.34804	Homo sapiens cDNA FLJ11472 fis, clone HE	1	0.57	T2-T4 grade 3 solid tumor marker
70	439370	AW274369	Hs.158853	ESTs	1	0.17	T2-T4 grade 3 solid tumor marker
	440021	AW025498	Hs.270842	ESTs, Weakly similar to ALU8_HUMAN ALU S	1	0.65	T2-T4 grade 3 solid tumor marker
	440404	AI015881	Hs.125616	ESTs	1	0.26	T2-T4 grade 3 solid tumor marker
	441523	AW514263	Hs.168872	ESTs, Weakly similar to ALUF_HUMAN !!!!	1	1	T2-T4 grade 3 solid tumor marker
	442277	AW448914	Hs.202391	ESTs	2.4	0.15	T2-T4 grade 3 solid tumor marker
	442738	AW002370	Hs.131055	ESTs	1	0.29	T2-T4 grade 3 solid tumor marker
75	443297	AI049864	Hs.133029	ESTs	1	1	T2-T4 grade 3 solid tumor marker
	444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	1	0.61	T2-T4 grade 3 solid tumor marker
	445550	AI242754	Hs.137306	ESTs	1	0.5	T2-T4 grade 3 solid tumor marker

	446149	BE242980	Hs.203181	ESTs	1	0.25	T2-T4 grade 3 solid tumor marker
	446163	AA026880	Hs.25252	Homo sapiens cDNA FLJ13603 fis, clone PL	1	0.21	T2-T4 grade 3 solid tumor marker
	446434	AI823410	Hs.169149	karyopherin alpha 1 (importin alpha 5)	1	1	T2-T4 grade 3 solid tumor marker
5	446928	AI694493	Hs.246916	ESTs	1	0.31	T2-T4 grade 3 solid tumor marker
	448591	AI540111	Hs.171261	ESTs	1	1	T2-T4 grade 3 solid tumor marker
	449121	AI915858	Hs.194980	ESTs	1	1	T2-T4 grade 3 solid tumor marker
	449539	W80363	Hs.58446	ESTs	1	0.33	T2-T4 grade 3 solid tumor marker
	450451	AW591528	Hs.202072	ESTs	1	0.59	T2-T4 grade 3 solid tumor marker
10	450469	AI955049	Hs.281326	ESTs	1	0.43	T2-T4 grade 3 solid tumor marker
	450684	AA872605	Hs.25333	interleukin 1 receptor, type II	1	0.05	T2-T4 grade 3 solid tumor marker
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	1.55	0.11	T2-T4 grade 3 solid tumor marker
	451106	BE382701	Hs.25960	v-myc avian myelocytomatosis viral relat	1	0.95	T2-T4 grade 3 solid tumor marker
	451130	AI762250	Hs.211347	ESTs	3.65	0.15	T2-T4 grade 3 solid tumor marker
15	451412	AW136378	Hs.208060	ESTs	1	1	T2-T4 grade 3 solid tumor marker
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	1.35	0.22	T2-T4 grade 3 solid tumor marker
	452114	N22687	Hs.8236	ESTs	1	0.19	T2-T4 grade 3 solid tumor marker
	452743	AW965082	Hs.61455	ESTs	1	0.44	T2-T4 grade 3 solid tumor marker
	454622	U70071		gb:HSU70071 Human Homo sapiens cDNA clon	1	1	T2-T4 grade 3 solid tumor marker
20	455235	AW875951		gb:CM1-PT0013-131299-067-109 PT0013 Homo	1	0.31	T2-T4 grade 3 solid tumor marker
	457792	AL046988	Hs.268677	ESTs, Moderately similar to ALU7_HUMAN A	1	0.24	T2-T4 grade 3 solid tumor marker
	100147	D13666	Hs.136348	osteoblast specific factor 2 (fascin)	20.531	0.036	upregulate stage
	101193	L20861	Hs.152213	*wingless-type MMTV integration site fam	1	0.526	upregulate stage
	101724	M69225	Hs.620	bulbous pemphigoid antigen 1 (230/240kD)	20.67	0.037	upregulate stage
25	101809	M86849	*Hs.323733	*gap junction protein, beta 2, 26kD (con	20.78	0.019	upregulate stage
	102154	U17760	Hs.75517	*laminin, beta 3 (nicein (125kD), kalini	18.848	0.042	upregulate stage
	102211	U23070	Hs.78776	putative transmembrane protein	2.092	0.28	upregulate stage
	102623	U66083	Hs.37110	*melanoma antigen, family A, 9"	1	0.306	upregulate stage
	102915	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	3.27	0.041	upregulate stage
30	103036	X54925	*Hs.83169	matrix metalloproteinase 1 (interstitial	13.63	0.034	upregulate stage
	103119	X63629	Hs.2877	*cadherin 3, type 1, P-cadherin (placent	7.296	0.054	upregulate stage
	103312	X82693	Hs.3185	*lymphocyte antigen 6 complex, locus D"	0.908	0.485	upregulate stage
	103478	Y07755	Hs.38991	S100 calcium-binding protein A2	2.928	0.219	upregulate stage
	103587	Z29083	Hs.82128	5T4 oncofetal trophoblast glycoprotein	3.156	0.16	upregulate stage
35	106632	AA459897	Hs.11950	GPI-anchored metastasis-associated prote	1.642	0.516	upregulate stage
	107151	AA621169	Hs.8687	ESTs	2.421	0.174	upregulate stage
	107901	AA026418	*Hs.111758	keratin 6A	1.259	0.343	upregulate stage
	107922	AA028028	Hs.61460	*Homo sapiens Ig superfamily receptor LN	14.22	0.049	upregulate stage
	109166	AA179845	Hs.73625	*RAB6 interacting, kinesin-like (rabkine	11.13	0.039	upregulate stage
40	109424	AA227919	*Hs.85962	hyaluronan synthase 3	1.737	0.518	upregulate stage
	110906	N39584	Hs.17404	ESTs	20.93	0.021	upregulate stage
	112244	R51309	Hs.70823	KAA1077 protein	3.941	0.181	upregulate stage
	115060	AA253214	Hs.198249	*gap junction protein, beta 5 (connexin	1.932	0.502	upregulate stage
	115697	AA411502	Hs.63325	*transmembrane protease, serine 4"	7.394	0.101	upregulate stage
45	115978	AA447522	*Hs.69517	*Homo sapiens, clone MGC:5257, mRNA, com	1.667	0.445	upregulate stage
	116335	AA495830	Hs.41690	desmoolin 3	4.899	0.154	upregulate stage
	118314	N63402	Hs.46692	ESTs	9.75	0.069	upregulate stage
	118336	N63604	Hs.47166	HT021	4.601	0.197	upregulate stage
	119845	W79920	Hs.58561	G protein-coupled receptor 87	1.95	0.123	upregulate stage
50	120486	AA253400	Hs.137569	tumor protein 63 kDa with strong homolog	4.191	0.211	upregulate stage
	121027	AA398470	Hs.99785	*Homo sapiens cDNA: FLJ21245 fis, clone	14.25	0.058	upregulate stage
	124059	F13673	Hs.283713	*ESTs, Weakly similar to ORF YGL050w [S.	4.99	0.168	upregulate stage
	128595	U31875	*Hs.152677	*Homo sapiens cDNA FLJ20338 fis, clone H	2.433	0.306	upregulate stage
	128610	L38608	Hs.10247	activated leucocyte cell adhesion molecu	4.34	0.14	upregulate stage
55	129041	H58873	*Hs.169902	*solute carrier family 2 (facilitated gl	2.003	0.455	upregulate stage
	129466	L42583	*Hs.111758	keratin 6A	11.584	0.042	upregulate stage
	130627	L23808	Hs.1695	matrix metalloproteinase 12 (macrophage	2.376	0.233	upregulate stage
	132349	Y00705	*Hs.181286	*serine protease inhibitor, Kazal type 1	5.4	0.132	upregulate stage
	132710	W93726	Hs.55279	*serine (or cysteine) proteinase inhibit	3.888	0.187	upregulate stage
60	133391	X57579	Hs.727	*inhibin, beta A (activin A, activin AB	1.517	0.334	upregulate stage
	134110	AA242758	*Hs.79136	*LIV-1 protein, estrogen regulated"	2.221	0.387	upregulate stage
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	4.85	0.03	upregulate stage
	400297	AI127076	Hs.285381	hypothetical protein DKFZp564O1278	3.54	0.13	upregulate stage
	400346	AB041269	Hs.272263	Homo sapiens mRNA for keratin 19, parlia	8.95	0.07	upregulate stage
65	400419	AF084545	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	10.7	0.06	upregulate stage
	400495				1	0.56	upregulate stage
	400509	M97639	Hs.155585	receptor tyrosine kinase-like orphan rec	1.52	0.51	upregulate stage
	400528				3.47	0.23	upregulate stage
	400577				1	0.29	upregulate stage
70	400608				7.2	0.08	upregulate stage
	400644				1	1	upregulate stage
	400666				1.42	0.43	upregulate stage
	400750				8.7	0.1	upregulate stage
	400773				1.11	0.51	upregulate stage
75	400844				9.65	0.04	upregulate stage
	400845				2.3	0.28	upregulate stage
	400846				1.34	0.5	upregulate stage
	400880				9.4	0.06	upregulate stage

				1	1	upregulate stage
				1	0.51	upregulate stage
				7	0.08	upregulate stage
				1	0.17	upregulate stage
5				5.18	0.14	upregulate stage
				1	1	upregulate stage
				1	1	upregulate stage
				9.1	0.06	upregulate stage
				1.42	0.5	upregulate stage
10	M83738	Hs.147663	protein tyrosine phosphatase, non-recept	1	0.33	upregulate stage
				6.5	0.11	upregulate stage
				1	0.31	upregulate stage
				1	1	upregulate stage
				2.65	0.17	upregulate stage
15				12	0.05	upregulate stage
	BE247275	Hs.151787	U5 snRNP-specific protein, 116 kD	9.15	0.08	upregulate stage
	BE247275	Hs.151787	U5 snRNP-specific protein, 116 kD	8.75	0.09	upregulate stage
				1	1	upregulate stage
				29.75	0.02	upregulate stage
20				11.35	0.06	upregulate stage
				6.15	0.07	upregulate stage
	AC005261	Hs.98338	serine/threonine kinase 13 (aurora/PL1-	1	0.69	upregulate stage
				3.15	0.15	upregulate stage
25				4.4	0.14	upregulate stage
				8.75	0.06	upregulate stage
				1	0.36	upregulate stage
				5.15	0.1	upregulate stage
				9.05	0.08	upregulate stage
30				1	1	upregulate stage
				9.6	0.07	upregulate stage
				9.85	0.09	upregulate stage
				9.4	0.09	upregulate stage
				1.07	0.65	upregulate stage
35				1	1	upregulate stage
				9.6	0.06	upregulate stage
				1.5	0.21	upregulate stage
				5.15	0.12	upregulate stage
	R58624	Hs.2186	eukaryotic translation elongation factor	1	1	upregulate stage
40	R58624	Hs.2186	eukaryotic translation elongation factor	1.5	0.28	upregulate stage
				1	0.37	upregulate stage
				1	0.43	upregulate stage
				1.12	0.57	upregulate stage
	AA576664	Hs.37078	v-crk avian sarcoma virus CT10 oncogene	0.86	1.08	upregulate stage
45				7.7	0.09	upregulate stage
				1.18	0.62	upregulate stage
				6.05	0.1	upregulate stage
				4.5	0.11	upregulate stage
				3.2	0.13	upregulate stage
				10.7	0.05	upregulate stage
50				10.35	0.08	upregulate stage
				1	1	upregulate stage
				2.45	0.34	upregulate stage
				1	1	upregulate stage
				4.45	0.14	upregulate stage
55				1.39	0.58	upregulate stage
	W28077	Hs.79389	nel (chicken)-like 2	1	1	upregulate stage
				9.15	0.08	upregulate stage
				1	1	upregulate stage
60				1	1	upregulate stage
				1.3	0.2	upregulate stage
				1	0.39	upregulate stage
				1	0.28	upregulate stage
				7.05	0.06	upregulate stage
65				1	0.33	upregulate stage
				1	1	upregulate stage
				1	1	upregulate stage
				0.89	0.9	upregulate stage
				2.74	0.26	upregulate stage
70				9.35	0.08	upregulate stage
				1	0.24	upregulate stage
				3.65	0.15	upregulate stage
				2.05	0.16	upregulate stage
				1	1	upregulate stage
75	AL035754	Hs.2474	tol-like receptor 1	1	0.18	upregulate stage
				1	0.56	upregulate stage
				1	0.22	upregulate stage
				9.65	0.08	upregulate stage

	405167			1	0.67	upregulate stage
	405170			1	0.48	upregulate stage
	405177			1	0.22	upregulate stage
5	405186			3.75	0.1	upregulate stage
	405258			8.85	0.09	upregulate stage
	405281			1	1	upregulate stage
	405379			1	0.87	upregulate stage
	405494			5	0.13	upregulate stage
10	405520			1	0.95	upregulate stage
	405526			8.96	0.08	upregulate stage
	405725			3.3	0.12	upregulate stage
	405738			0.86	0.69	upregulate stage
	405809			2.4	0.18	upregulate stage
15	405838			1	0.22	upregulate stage
	405906			2.6	0.12	upregulate stage
	406137			1.54	0.52	upregulate stage
	406187			3.2	0.14	upregulate stage
	406322			3.95	0.12	upregulate stage
20	406360			4.1	0.1	upregulate stage
	406397			1	0.24	upregulate stage
	406434			7.4	0.07	upregulate stage
	406467			9.1	0.07	upregulate stage
	406511			1	1	upregulate stage
25	406517	W28077	Hs.79389	1	1	upregulate stage
	406588			0.93	0.91	upregulate stage
	406651	Al559224	Hs.277477	10.1	0.07	upregulate stage
	406665	U22961	Hs.75442	1.08	0.81	upregulate stage
	406671	AA129547	Hs.285754	5.7	0.12	upregulate stage
30	406687	M31126	Hs.272620	1.95	0.3	upregulate stage
	406732	AA487229	Hs.2064	1	0.77	upregulate stage
	406747	Al925153	Hs.217493	3.6	0.14	upregulate stage
	406753	AA505665	Hs.217493	5.45	0.13	upregulate stage
	406815	AA833930	Hs.288036	3.65	0.09	upregulate stage
35	406850	Al624300	Hs.172928	1.29	0.62	upregulate stage
	406892	D55643		1	1	upregulate stage
	406944	J04742	Hs.247945	1	1	upregulate stage
	406950	L17325	Hs.278	1	0.36	upregulate stage
	406961	L77563		1	1	upregulate stage
40	406964	M21305	Hs.247946	42.25	0.01	upregulate stage
	406993	S83249		1	1	upregulate stage
	407017	U48697		1	1	upregulate stage
	407073	Y10510		1	0.53	upregulate stage
	407105	S64699	Hs.663	1	1	upregulate stage
45	407128	R83312	Hs.237260	1	1	upregulate stage
	407132	T02871	Hs.228523	1	0.45	upregulate stage
	407137	T97307	Hs.199067	14.3	0.05	upregulate stage
	407158	N49639		1	0.57	upregulate stage
	407175	T86603		1	0.31	upregulate stage
50	407186	AA435610		1	1	upregulate stage
	407189	AA598927		1	1	upregulate stage
	407192	AA609200		6.05	0.12	upregulate stage
	407195	C21124		1	1	upregulate stage
	407202	N58172	Hs.109370	3.7	0.16	upregulate stage
55	407204	R41933	Hs.140237	10.2	0.06	upregulate stage
	407205	R78910	Hs.272620	1.9	0.22	upregulate stage
	407211	T95828	Hs.230070	1	0.59	upregulate stage
	407346	Al090210	Hs.264106	1	1	upregulate stage
	407422	AF116633		1	0.22	upregulate stage
60	407494	U10072		4.1	0.13	upregulate stage
	407547	Y10259		2.45	0.19	upregulate stage
	407564	AA042860	Hs.103005	1	1	upregulate stage
	407603	AW955705	Hs.62604	1.18	0.73	upregulate stage
	407634	AW016569	Hs.301280	9.6	0.06	upregulate stage
65	407668	BE161086	Hs.279817	1	0.39	upregulate stage
	407709	AA456135	Hs.23023	6.8	0.12	upregulate stage
	407710	AW022727	Hs.23616	3.9	0.14	upregulate stage
	407725	BE388094	Hs.21857	9.97	0.07	upregulate stage
	407729	T40707	Hs.270862	9.2	0.09	upregulate stage
70	407774	AA084958		2.65	0.22	upregulate stage
	407788	BE514982	Hs.38991	2.1	0.34	upregulate stage
	407811	AW190902	Hs.40098	8.45	0.06	upregulate stage
	407813	AL120247	Hs.40109	9.1	0.08	upregulate stage
	407833	AW955632	Hs.66666	9.2	0.07	upregulate stage
75	407839	AA045144	Hs.161566	2.11	0.25	upregulate stage
	407853	AA336797	Hs.40499	1	0.34	upregulate stage
	407881	AW072003	Hs.40968	3.52	0.18	upregulate stage
	407882	Al241264	Hs.62772	1	0.26	upregulate stage

5	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	13.6	0.05	upregulate stage
	407911	AF104922	Hs.41565	growth differentiation factor 8	1	1	upregulate stage
	407912	AW104401	Hs.243489	ESTs, Weakly similar to AF151881.1 CGI-1	10.35	0.07	upregulate stage
	407935	U31986	Hs.41683	cartilage paired-class homeoprotein 1	4.25	0.12	upregulate stage
	407939	W05608		gb:za85e07.r1 Soares_fetal_lung_NbHL19W	8.75	0.09	upregulate stage
10	407944	R34008	Hs.239727	desmocollin 2	9.2	0.06	upregulate stage
	407945	X69208	Hs.606	ATPase, Cu+++ transporting, alpha polypep	1.45	0.25	upregulate stage
	407946	AA226495	Hs.154292	ESTs	9.4	0.07	upregulate stage
	407949	W21874	Hs.247057	ESTs	3.32	0.2	upregulate stage
	407974	AW968123	Hs.146401	small inducible cytokine subfamily E, ma	3.55	0.14	upregulate stage
15	407983	U40371	Hs.41718	phosphodiesterase 1C, calmodulin-depende	8.95	0.07	upregulate stage
	407994	AW135309	Hs.244331	ESTs	4.5	0.12	upregulate stage
	408000	L11690	Hs.820	bullous pemphigoid antigen 1 (230/240kD)	2.89	0.19	upregulate stage
	408014	AA723782	Hs.41749	protein kinase, cGMP-dependent, type II	1.31	0.53	upregulate stage
	408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone NT	3.6	0.17	upregulate stage
20	408046	AW139121	Hs.183643	ESTs	1	0.36	upregulate stage
	408053	BE086548	Hs.42346	calcineurin-binding protein calcisarcin-1	10.75	0.05	upregulate stage
	408092	NM_007057	Hs.42650	ZW10 interactor	4.7	0.13	upregulate stage
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	4.5	0.14	upregulate stage
	408141	U69205	Hs.45152	ESTs, Moderately similar to neurogenic b	4.4	0.13	upregulate stage
25	408170	AW204516	Hs.31835	ESTs	5.65	0.13	upregulate stage
	408184	AW168741	Hs.22249	ESTs	1	1	upregulate stage
	408224	AW175997		gb:QV0-BT0078-190899-005-E02 BT0078 Homo	1	0.44	upregulate stage
	408239	AA053401	Hs.271827	ESTs, Moderately similar to ALU7_HUMAN A	9.95	0.04	upregulate stage
	408241	AW176546		gb:MR0-CT0063-200899-001-a01 CT0063 Homo	2.8	0.17	upregulate stage
30	408268	AL138247		gb:DKFZp547D237_r1 547 (synonym: hfr1)	1	0.61	upregulate stage
	408277	AW177959		gb:IL3-HT0060-200899-008-D03 HT0060 Homo	1	1	upregulate stage
	408306	BE141991		gb:PM2-HT0134-220999-002-d10 HT0134 Homo	1	1	upregulate stage
	408352	AA053875	Hs.95310	ESTs	1	1	upregulate stage
	408360	AI806090	Hs.44344	hypothetical protein FLJ20534	9.15	0.08	upregulate stage
35	408393	AW015318	Hs.23165	ESTs	9.35	0.07	upregulate stage
	408396	AA330496	Hs.40840	ESTs	1	0.61	upregulate stage
	408442	R59608	Hs.21435	ESTs	1	1	upregulate stage
	408514	AW206559	Hs.255903	ESTs	1	0.34	upregulate stage
	408572	AA055611	Hs.226568	ESTs, Moderately similar to ALU4_HUMAN A	1	0.33	upregulate stage
40	408617	R61736	Hs.124128	ESTs	2.75	0.14	upregulate stage
	408633	AW963372	Hs.46677	PRO2000 protein	3.14	0.25	upregulate stage
	408706	AW438503	Hs.256935	ESTs	8.45	0.09	upregulate stage
	408713	NM_001248	Hs.47042	ectonucleoside triphosphate diphosphohyd	2.81	0.21	upregulate stage
	408725	AA131539	Hs.15669	ESTs	9.1	0.08	upregulate stage
45	408728	AL137379	Hs.47125	hypothetical protein FLJ13912	3.1	0.11	upregulate stage
	408738	NM_014785	Hs.47313	KIAA0258 gene product	4.4	0.13	upregulate stage
	408739	W01556	Hs.238797	ESTs	5.65	0.11	upregulate stage
	408754	N31256	Hs.161623	ESTs	1	1	upregulate stage
	408765	AA057268	Hs.146013	ESTs	8.75	0.09	upregulate stage
50	408805	H69912	Hs.48269	vaccinia related kinase 1	4.95	0.12	upregulate stage
	408813	AI580090	Hs.48295	RNA helicase family	3.65	0.17	upregulate stage
	408817	AA524525	Hs.279864	PRO1995 protein	6.15	0.12	upregulate stage
	408849	BE219451	Hs.254919	ESTs	1	0.32	upregulate stage
	408902	AW014869	Hs.5510	ESTs	3.3	0.15	upregulate stage
55	408908	BE296227	Hs.48915	serine/threonine kinase 15	5.65	0.1	upregulate stage
	408916	AW295232	Hs.22893	ESTs	10	0.08	upregulate stage
	408933	AA058979	Hs.182133	ESTs, Highly similar to ADP-ribosylation	1	0.91	upregulate stage
	408943	NM_007070	Hs.49105	FKBP-associated protein	3.45	0.16	upregulate stage
	408950	BE158389	Hs.300976	ESTs	6.3	0.1	upregulate stage
60	409032	AW301807	Hs.297260	ESTs	8.4	0.08	upregulate stage
	409093	BE243834	Hs.50441	CGI-04 protein	1.71	0.49	upregulate stage
	409099	AK000725	Hs.50579	hypothetical protein FLJ20718	10.1	0.07	upregulate stage
	409142	AL136877	Hs.50758	chromosome-associated polypeptide C	11.85	0.05	upregulate stage
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	2.83	0.24	upregulate stage
65	409231	AA446644	Hs.692	tumor-associated calcium signal transduc	9.34	0.08	upregulate stage
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	8.7	0.09	upregulate stage
	409357	M73628	Hs.54415	casein, kappa	1.6	0.2	upregulate stage
	409402	AF208234	Hs.695	cystatin B (stefin B)	1.57	0.56	upregulate stage
	409405	AA075869	Hs.126400	ESTs, Highly similar to RL39_HUMAN 60S R	2.6	0.12	upregulate stage
70	409408	AW387837		gb:MR4-ST0118-021299-021-r08 ST0118 Homo	4.3	0.15	upregulate stage
	409420	Z15008	Hs.54451	laminin, gamma 2 (niclin (100kD), kalini	8.28	0.06	upregulate stage
	409509	AL036923	Hs.127006	ESTs	10.2	0.06	upregulate stage
	409566	AA078899		gb:zms94b01.r1 Stratagene colon HT29 (937	1	0.56	upregulate stage
	409575	AW419225	Hs.256247	ESTs	2.15	0.14	upregulate stage
75	409582	R27430	Hs.271565	ESTs	7.3	0.07	upregulate stage
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	3.78	0.19	upregulate stage
	409642	AW450809	Hs.257347	ESTs	9.55	0.07	upregulate stage
	409674	AI935146	Hs.278611	UDP-N-acetyl-alpha-D-galactosamine:polyp	1	0.29	upregulate stage
	409691	T89983	Hs.246042	ESTs	1	1	upregulate stage
	409703	NM_006187	Hs.56009	Z'-oligoadenylate synthetase 3	2.22	0.36	upregulate stage
	409727	N63786	Hs.94149	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.57	upregulate stage

5	409760	AA302840		gb:EST10534 Adipose tissue, white l Homo	9.95	0.05	upregulate stage
	409789	BE256027	Hs.180946	ribosomal protein L5	1	0.83	upregulate stage
	409794	AW885691		gb:RC4-OT0071-240300-013-b04 OT0071 Homo	1	1	upregulate stage
	409977	AW805510	Hs.97056	hypothetical protein FLJ21634	9.65	0.07	upregulate stage
	409985	AW291944	Hs.122139	ESTs	4.35	0.14	upregulate stage
10	409989	R37868	Hs.13333	ESTs	1	0.21	upregulate stage
	409995	AW960597	Hs.30164	ESTs	5.05	0.12	upregulate stage
	410013	AF067173	Hs.57904	mago-nashi (Drosophila) homolog, prolife	3.05	0.25	upregulate stage
	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	3.15	0.09	upregulate stage
	410071	AW582568		gb:RC1-ST0278-080100-011-h04 ST0278 Homo	2.5	0.18	upregulate stage
15	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	8	0.06	upregulate stage
	410114	AW590540	Hs.271280	ESTs	5.1	0.14	upregulate stage
	410117	AK001586	Hs.58650	hypothetical protein FLJ10724	1	1	upregulate stage
	410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone NT	4.7	0.11	upregulate stage
	410181	AI468210	Hs.261285	pleiotropic regulator 1 (PRL1, Arabidops	1	0.23	upregulate stage
20	410196	AI936442	Hs.59838	hypothetical protein FLJ10808	6.05	0.09	upregulate stage
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	5.55	0.12	upregulate stage
	410259	AK000337	Hs.61485	hypothetical protein	10.1	0.07	upregulate stage
	410276	AI554545	Hs.68301	ESTs	2.98	0.25	upregulate stage
	410278	AW614396	Hs.282230	ESTs	1	0.28	upregulate stage
25	410325	AB023154	Hs.62264	KIAA0937 protein	6.85	0.13	upregulate stage
	410356	BE244568	Hs.62643	dual adaptor of phosphotyrosine and 3-ph	1	1	upregulate stage
	410388	AA831460	Hs.22039	hepatocyte nuclear factor 3, alpha	1	0.33	upregulate stage
	410399	BE068889	Hs.63236	synuclein, gamma (breast cancer-specific	1.07	0.78	upregulate stage
	410420	AA224053	Hs.172405	ESTs, Moderately similar to I52835 H-NUC	1	0.14	upregulate stage
30	410429	AA310500	Hs.63657	hypothetical protein FLJ11005	11.25	0.07	upregulate stage
	410442	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	9.6	0.08	upregulate stage
	410475	AW749927		gb:QV0-BT0537-231299-049-f03 BT0537 Homo	9.8	0.08	upregulate stage
	410495	N95428		gb:zb80d09.s1 Soares_senescent_fibroblas	11.3	0.06	upregulate stage
	410501	AI675688	Hs.83286	ESTs	4.75	0.1	upregulate stage
35	410503	AW975746	Hs.188662	Homo sapiens cDNA: FLJ23421 fis, clone H	6.5	0.1	upregulate stage
	410520	AW752710		gb:IL3-CT0219-281099-024-A03 CT0219 Homo	1	1	upregulate stage
	410534	AW905138		gb:QV0-NN1071-280400-207-g07 NN1071 Homo	3.1	0.16	upregulate stage
	410537	AW753108		gb:PM1-CT0247-080100-008-e10 CT0247 Homo	10.35	0.08	upregulate stage
	410553	AW016824	Hs.68784	ESTs	1.67	0.41	upregulate stage
40	410560	N29220		gb:yx43b05.r1 Soares melanocyte 2NbHM Ho	9	0.07	upregulate stage
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	6.2	0.11	upregulate stage
	410562	AW858528		gb:CM3-CT0341-150300-119-h11 CT0341 Homo	1	1	upregulate stage
	410579	AK001828	Hs.64691	KIAA0483 protein	11.1	0.06	upregulate stage
	410634	AW888653	Hs.268859	ESTs	1	1	upregulate stage
45	410664	NM_006033	Hs.65370	lipase, endothelial	3.95	0.1	upregulate stage
	410668	BE379794	Hs.65403	hypothetical protein	1.82	0.41	upregulate stage
	410730	AW368860	Hs.293950	ESTs	9.25	0.07	upregulate stage
	410751	AA357918		gb:EST66726 Fetal lung III Homo sapiens	1	1	upregulate stage
	410754	T63840		gb:yc16b10.s1 Stratagene lung (937210) H	3.1	0.14	upregulate stage
50	410762	AF226053	Hs.66170	HSKM-B protein	5.55	0.1	upregulate stage
	410764	AW978159	Hs.250164	ESTs, Weakly similar to coded for by C.	1	0.2	upregulate stage
	410782	AW504860	Hs.288836	Homo sapiens cDNA FLJ12673 fis, clone NT	1.75	0.25	upregulate stage
	410794	AA248010	Hs.154669	ESTs	1	0.67	upregulate stage
	410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar	3.2	0.17	upregulate stage
55	410844	AW807073		gb:MR4-ST0062-031199-018-d06 ST0062 Homo	1	0.8	upregulate stage
	410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	6.5	0.12	upregulate stage
	410910	AW810204		gb:MR4-ST0125-021199-017-d08 ST0125 Homo	9.35	0.08	upregulate stage
	410973	AW812278		gb:RC0-ST0174-211099-011-h12 ST0174 Homo	1	1	upregulate stage
	410976	R36207	Hs.25092	ESTs	8.35	0.1	upregulate stage
60	410997	AW812877		gb:RC3-ST0186-300100-017-e04 ST0186 Homo	1	1	upregulate stage
	410998	W28247	Hs.82007	KIAA0094 protein	2.45	0.18	upregulate stage
	411036	AA857218	Hs.297007	ESTs	4.05	0.14	upregulate stage
	411110	H93000		gb:yyv07f01.s1 Soares fetal liver spleen	1	0.36	upregulate stage
	411132	AW819191		gb:CM1-ST0283-071299-061-d08 ST0283 Homo	1	1	upregulate stage
65	411137	AW819455		gb:RC5-ST0293-021299-031-A04 ST0293 Homo	3.65	0.18	upregulate stage
	411157	AW819867		gb:QV0-ST0294-070300-151-f02 ST0294 Homo	3.2	0.2	upregulate stage
	411159	AW820178		gb:QV0-ST0294-100400-185-e07 ST0294 Homo	1	0.27	upregulate stage
	411170	AW820503		gb:QV2-ST0298-140200-042-b05 ST0298 Homo	1	1	upregulate stage
	411193	AW821484		gb:IL2-ST0311-211299-028-F12 ST0311 Homo	1	0.24	upregulate stage
70	411242	BE146808		gb:QV4-HT0222-181099-013-g03 HT0222 Homo	2.55	0.26	upregulate stage
	411245	AW833441		gb:QV4-TT0008-271099-020-g01 TT0008 Homo	9.62	0.09	upregulate stage
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	2.4	0.32	upregulate stage
	411282	AW995011		gb:QV0-BN0040-170300-161-d07 BN0040 Homo	1	1	upregulate stage
	411284	N28519	Hs.135191	ESTs, Weakly similar to unnamed protein	3.25	0.12	upregulate stage
75	411294	AW859729	Hs.42680	ESTs	1	1	upregulate stage
	411327	AW836922		gb:QV1-LT0036-150200-074-h06 LT0036 Homo	1	0.37	upregulate stage
	411338	AW731782	Hs.116122	ESTs, Weakly similar to unnamed protein	5	0.13	upregulate stage
	411339	BE164598		gb:RC3-HT0470-120200-013-b10 HT0470 Homo	1	0.25	upregulate stage
	411383	AA001394	Hs.69749	KIAA0087 gene product	3.6	0.18	upregulate stage
	411387	AW842339	Hs.130815	hypothetical protein FLJ21870	8.75	0.09	upregulate stage
	411400	AA311919	Hs.69851	GAR1 protein	12.1	0.07	upregulate stage

5	411425	AW846012		gb:RC2-CT0163-230999-003-E01 CT0163 Homo	1	0.74	upregulate stage
	411461	AW847937		gb:IL3-CT0213-210200-042-002 CT0213 Homo	1	1	upregulate stage
	411526	AW850327		gb:IL3-CT0219-221199-029-008 CT0219 Homo	1	1	upregulate stage
	411560	AW851186		gb:IL3-CT0220-150200-071-H05 CT0220 Homo	2.8	0.17	upregulate stage
	411568	BE144593		gb:MR0-HT0167-141199-002-004 HT0167 Homo	1	1	upregulate stage
10	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	3.55	0.14	upregulate stage
	411605	AW006831	Hs.20479	ESTs	9.6	0.08	upregulate stage
	411626	AW793453	Hs.71109	KIAA1229 protein	1	1	upregulate stage
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppressor	4.1	0.11	upregulate stage
	411643	AI924519	Hs.192570	Homo sapiens cDNA: FLJ22028 fis, clone H	1	0.28	upregulate stage
15	411653	AF070578	Hs.71168	Homo sapiens clone 24674 mRNA sequence	8.9	0.08	upregulate stage
	411727	AW858443		gb:CM0-CT0341-260100-160-010 CT0341 Homo	1	1	upregulate stage
	411771	AW993247		gb:RC2-BN0033-180200-014-h09 BN0033 Homo	2.6	0.14	upregulate stage
	411787	AW863568		gb:MR3-SN0010-240300-102-c10 SN0010 Homo	1	1	upregulate stage
	411788	AW897793		gb:CM1-NN0063-280400-203-007 NN0063 Homo	3.7	0.15	upregulate stage
20	411826	AW947946		gb:PM0-MT0011-240300-001-a09 MT0011 Homo	3.25	0.13	upregulate stage
	411835	U29343	Hs.72550	hyaluronan-mediated motility receptor (R	1	1	upregulate stage
	411860	T89420		gb:yd98f04.s1 Soares fetal liver spleen	1	0.22	upregulate stage
	411874	AA096106	Hs.20403	ESTs	5.75	0.11	upregulate stage
	411917	AW876360	Hs.3592	Homo sapiens cDNA: FLJ22555 fis, clone H	1	0.33	upregulate stage
25	411928	AA888624	Hs.19121	adaptor-related protein complex 2, alpha	4.75	0.12	upregulate stage
	411932	AW876548		gb:RC3-PT0028-190100-012-h02 PT0028 Homo	1	0.38	upregulate stage
	411943	BE502436	Hs.7962	ESTs, Weakly similar to putative [C.eleg	3.82	0.23	upregulate stage
	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncog	4.65	0.15	upregulate stage
	411991	X58822	Hs.73010	interferon, omega 1	2.45	0.14	upregulate stage
30	412040	D85519	Hs.73086	neuropeptide Y receptor Y6 (pseudogene)	4.6	0.14	upregulate stage
	412088	AI689496	Hs.108932	ESTs	2.82	0.18	upregulate stage
	412134	AW895560		gb:QV4-NN0038-270400-187-g08 NN0038 Homo	6.4	0.1	upregulate stage
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	17.05	0.04	upregulate stage
	412231	AW902491	Hs.289088	heat shock 90kD protein 1, alpha	1	0.91	upregulate stage
35	412296	AW936233		gb:QV0-DT0020-090200-107-a06 DT0020 Homo	1	1	upregulate stage
	412327	AW937355		gb:QV3-DT0043-211299-044-a06 DT0043 Homo	1	1	upregulate stage
	412357	AW939537		gb:QV1-DT0072-110200-066-005 DT0072 Homo	1	0.24	upregulate stage
	412359	AW837985		gb:QV3-LT0048-140200-083-e05 LT0048 Homo	1	0.41	upregulate stage
	412367	AW945964		gb:QV0-ET0001-050500-228-e09 ET0001 Homo	1	0.22	upregulate stage
40	412529	BE271224	Hs.266273	Homo sapiens cDNA FLJ13346 fis, clone OV	4.45	0.14	upregulate stage
	412530	AA766268	Hs.266273	Homo sapiens cDNA FLJ13346 fis, clone OV	9.3	0.08	upregulate stage
	412537	AL031778	Hs.797	nuclear transcription factor Y, alpha	4.25	0.14	upregulate stage
	412547	W27161		gb:23a12 Human retina cDNA randomly prim	1	1	upregulate stage
	412559	T31474		gb:EST33147 Human Embryo Homo sapiens cD	1	0.26	upregulate stage
45	412636	NM_004415	Hs.74316	desmoplakin (DPI, DPL)	12.05	0.05	upregulate stage
	412648	AA115211	Hs.69658	EST	1	0.28	upregulate stage
	412668	AA456195	Hs.10056	ESTs	10.75	0.07	upregulate stage
	412671	AW977734		gb:EST389963 MAGE resequences, MAGO Homo	2.65	0.3	upregulate stage
	412673	AL042957	Hs.31845	ESTs	4.6	0.11	upregulate stage
50	412723	AA648459	Hs.179912	ESTs	2.55	0.11	upregulate stage
	412739	AA116018	Hs.271809	Homo sapiens cDNA: FLJ22406 fis, clone H	1.6	0.24	upregulate stage
	412744	N31101		gb:ys52a03.r1 Soares melanocyte 2NbHM Ho	2	0.23	upregulate stage
	412778	AA120882	Hs.159244	ESTs	1	1	upregulate stage
	412811	H06382	Hs.21400	ESTs	1	0.49	upregulate stage
55	412838	D61870		gb:HUM218F11B Clontech human aorta polyA	1	0.34	upregulate stage
	412854	BE004149	Hs.31161	ESTs	1	1	upregulate stage
	413075	D59828	Hs.70953	ESTs	1	0.77	upregulate stage
	413109	AW389845	Hs.110855	ESTs	3.93	0.1	upregulate stage
	413117	BE066107	Hs.138484	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.22	upregulate stage
60	413119	BE065941		gb:RC3-BT0319-100100-012-d12 BT0319 Homo	1	0.87	upregulate stage
	413141	BE166323		gb:QV4-HT0492-270100-086-e12 HT0492 Homo	5.45	0.12	upregulate stage
	413219	AA878200	Hs.118727	Homo sapiens cDNA FLJ13692 fis, clone PL	2.54	0.19	upregulate stage
	413228	AA127518	Hs.195870	ESTs	1	1	upregulate stage
	413273	U75679	Hs.75257	Hairpin binding protein, histone	5.05	0.11	upregulate stage
65	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.45	0.5	upregulate stage
	413294	BE144034		gb:MR0-HT0165-191199-004-a02 HT0165 Homo	1	1	upregulate stage
	413324	V00571	Hs.75294	corticotropin releasing hormone	6.95	0.03	upregulate stage
	413342	AA128535		gb:z124e04.r1 Soares_pregnant uterus_NbH	1	1	upregulate stage
	413430	R22479	Hs.24650	Homo sapiens cDNA FLJ13047 fis, clone NT	3	0.18	upregulate stage
70	413707	BE158679		gb:CM0-HT0395-280100-169-c04 HT0395 Homo	1	0.28	upregulate stage
	413743	BE161004		gb:PM0-HT0425-170100-002-h03 HT0425 Homo	1	1	upregulate stage
	413753	U17760	Hs.301103	Human DNA sequence from clone 272L16 on	22.7	0.03	upregulate stage
	413785	AW613780	Hs.13500	ESTs	9.9	0.07	upregulate stage
	413792	BE166924		gb:CM4-HT0501-240300-519-001 HT0501 Homo	1	1	upregulate stage
75	413804	T64682		gb:yc48b02.r1 Stralagena liver (937224)	0.99	0.75	upregulate stage
	413833	Z15005	Hs.75573	centromere protein E (312kD)	2.55	0.17	upregulate stage
	413854	BE174300	Hs.44581	heat shock protein hsp70-related protein	1.25	0.24	upregulate stage
	413918	AW015898	Hs.71245	ESTs	4	0.11	upregulate stage
	413968	AW500374	Hs.64056	ESTs	10.85	0.07	upregulate stage
	414091	T83742		gb:yd57g02.s1 Soares fetal liver spleen	8.9	0.1	upregulate stage
	414099	U11313	Hs.75760	sterol carrier protein 2	10.3	0.06	upregulate stage

	414116	AA587370	Hs.71584	ESTs	1	1	upregulate stage
	414127	AA431863	Hs.135270	ESTs	2.85	0.13	upregulate stage
	414169	AA136169	Hs.149335	ESTs	8.95	0.09	upregulate stage
5	414275	AW970254	Hs.889	Charot-Leyden crystal protein	7.05	0.05	upregulate stage
	414304	AI521276	Hs.165998	OKFZP564M2423 protein	1	0.24	upregulate stage
	414338	N80751	Hs.301471	ESTs	10.3	0.08	upregulate stage
	414447	AA147549	Hs.109909	ESTs	3.4	0.16	upregulate stage
	414494	AA768491	Hs.6783	Homo sapiens cDNA: FLJ22724 fis, clone H	3.4	0.18	upregulate stage
10	414520	AA148806	Hs.204046	ESTs	1	0.21	upregulate stage
	414569	AF109298	Hs.118258	prostate cancer associated protein 1	3.1	0.18	upregulate stage
	414575	H11257	Hs.295233	ESTs	3.1	0.15	upregulate stage
	414597	H67472	Hs.34274	ESTs	4.6	0.11	upregulate stage
	414643	H46177	Hs.119316	ESTs	1	0.28	upregulate stage
15	414658	X58528	Hs.76781	ATP-binding cassette, sub-family D (ALD)	7.75	0.08	upregulate stage
	414661	T97401	Hs.21929	ESTs	1	0.26	upregulate stage
	414683	S78296	Hs.76888	interlexin neuronal intermediate filamen	2.72	0.25	upregulate stage
	414735	BE468016	Hs.281904	ESTs	1	0.38	upregulate stage
	414737	AI160386	Hs.125087	ESTs	5.5	0.1	upregulate stage
20	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin	3.19	0.24	upregulate stage
	414774	X02419	Hs.77274	plasminogen activator, urokinase	1.45	0.49	upregulate stage
	414783	AW069569	Hs.75839	zinc finger protein 6 (CMPX1)	4.65	0.13	upregulate stage
	414799	AI752416	Hs.77326	insulin-like growth factor binding prote	1.7	0.46	upregulate stage
	414833	T07114		gb:EST05003 Fetal brain, Striatogene (cat	4.5	0.13	upregulate stage
25	414883	AA926960	Hs.77550	CDC28 protein kinase 1	3.36	0.22	upregulate stage
	414885	AA157531	Hs.269276	ESTs	2.7	0.21	upregulate stage
	414918	AI219207	Hs.72222	Homo sapiens cDNA FLJ13459 fis, clone PL	0.87	0.69	upregulate stage
	414985	C17372		gb:C17372 Clontech human aorta polyA+ mR	1	0.42	upregulate stage
30	415025	AW207091	Hs.72307	ESTs	5.3	0.06	upregulate stage
	415033	D31476	Hs.301448	Homo sapiens cDNA FLJ12152 fis, clone MA	1	1	upregulate stage
	415060	AJ223810	Hs.43213	ESTs, Weakly similar to IEF5_HUMAN TRANS	6.05	0.1	upregulate stage
	415068	Z19448	Hs.131887	ESTs, Weakly similar to ORF YNL227c [S.c	4.5	0.13	upregulate stage
	415095	D59592	Hs.34745	ESTs	1	0.44	upregulate stage
	415099	AI492170	Hs.77917	ubiquitin carboxyl-terminal esterase L3	2.27	0.29	upregulate stage
35	415104	D60076		gb:HUM084E10A Clontech human fetal brain	3.95	0.13	upregulate stage
	415114	D60468		gb:HUM111A06B Clontech human fetal brain	2.05	0.2	upregulate stage
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2	5.8	0.05	upregulate stage
	415139	AW975942	Hs.48524	ESTs	1.15	0.21	upregulate stage
	415148	Z36953	Hs.48527	ESTs	2.5	0.2	upregulate stage
40	415153	C03508	Hs.7000	ESTs	8.95	0.09	upregulate stage
	415178	D80503		gb:HUM080A02B Human fetal brain (TFujiwa	1	0.15	upregulate stage
	415217	H23983	Hs.26922	ESTs	1	0.31	upregulate stage
	415227	AW821113	Hs.72402	ESTs	6.3	0.11	upregulate stage
	415238	R37780	Hs.21422	ESTs	1	1	upregulate stage
45	415241	F02208	Hs.27214	ESTs	1	1	upregulate stage
	415295	R41450	Hs.6546	ESTs	1	0.63	upregulate stage
	415296	F05086		gb:HSC01A011 normalized infant brain cDN	5.65	0.1	upregulate stage
	415327	H22769	Hs.1861	membrane protein, palmitoylated 1 (55kD)	8.15	0.09	upregulate stage
	415330	Z44693	Hs.21422	ESTs	3	0.2	upregulate stage
50	415336	T77664	Hs.78362	Human clone 23839 mRNA sequence	1	0.87	upregulate stage
	415337	Z44881	Hs.9012	ESTs	8.8	0.07	upregulate stage
	415352	F06565		gb:HSC1CG051 normalized infant brain cDN	1	1	upregulate stage
	415364	F06771		gb:HSC1KD031 normalized infant brain cDN	1	1	upregulate stage
	415371	R15239		gb:yf89b02.r1 Soares infant brain 1NIB H	5.1	0.13	upregulate stage
55	415412	F08049	Hs.52132	ESTs	4.25	0.16	upregulate stage
	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A	4.1	0.15	upregulate stage
	415462	R52692	Hs.12698	ESTs	4.65	0.11	upregulate stage
	415496	R37637	Hs.12286	ESTs	5.4	0.13	upregulate stage
	415509	R40000	Hs.91968	ESTs	1	0.44	upregulate stage
60	415511	AI732617	Hs.182362	ESTs	9.3	0.03	upregulate stage
	415542	R13474	Hs.290263	ESTs	9.7	0.08	upregulate stage
	415569	Z43930		gb:HSC1OH121 normalized infant brain cDN	1	0.74	upregulate stage
	415600	F12664		gb:HSC3CG021 normalized infant brain cDN	1	0.43	upregulate stage
65	415616	F12945	Hs.12294	ESTs	1	1	upregulate stage
	415626	Z43847		gb:HSC1MC051 normalized infant brain cDN	1	1	upregulate stage
	415635	F13168		gb:HSC3JF101 normalized infant brain cDN	1	0.26	upregulate stage
	415750	AA167712		gb:zq39g08.s1 Striatogene hNT neuron (937	1	0.83	upregulate stage
	415786	AW419196	Hs.257924	Homo sapiens cDNA FLJ13782 fis, clone PL	9	0.08	upregulate stage
	415788	AW628686	Hs.73851	KIAA0217 protein	5.2	0.11	upregulate stage
70	415790	R23574	Hs.23545	ESTs	1	1	upregulate stage
	415799	AA653718	Hs.225841	DKFZP434D193 protein	4.25	0.12	upregulate stage
	415837	H05279	Hs.21758	ESTs	1	0.57	upregulate stage
	415857	AA866115	Hs.301646	Homo sapiens cDNA FLJ11381 fis, clone HE	8.05	0.07	upregulate stage
	415906	AI751357	Hs.288741	Homo sapiens cDNA: FLJ22256 fis, clone H	12.2	0.06	upregulate stage
	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	12.2	0.06	upregulate stage
75	415948	AA262226		gb:z24h06.r1 NCL_CGAP_GCB1 Homo sapiens	1	1	upregulate stage
	415979	H16427	Hs.271501	ESTs	4.85	0.13	upregulate stage
	415989	AI267700	Hs.111128	ESTs	4.45	0.08	upregulate stage

	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin 1	1	1	upregulate stage
	416052	R12816	Hs.21164	ESTs	1.45	0.24	upregulate stage
	416053	H16359	Hs.130648	ESTs	4.35	0.14	upregulate stage
5	416061	R45516	Hs.26119	ESTs	1	1	upregulate stage
	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	4.72	0.17	upregulate stage
	416097	BE387371	Hs.301304	Homo sapiens cDNA: FLJ21017 fis, clone C	5.75	0.11	upregulate stage
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (8.4	0.09	upregulate stage
	416135	AW473656	Hs.45119	ESTs	2.29	0.2	upregulate stage
10	416155	AI807264	Hs.205442	ESTs, Weakly similar to AF117610 1 inner	5.1	0.13	upregulate stage
	416173	R52782		gb:yg99d09.r1 Soares Infant brain 1N1B H	3.7	0.12	upregulate stage
	416195	AW131940	Hs.104030	ESTs	1.1	0.16	upregulate stage
	416196	W51955	Hs.73372	ESTs	3.25	0.14	upregulate stage
	416203	H27794	Hs.269055	ESTs	1	0.32	upregulate stage
15	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	4.15	0.12	upregulate stage
	416226	N55342	Hs.34372	ESTs	2.35	0.21	upregulate stage
	416239	AL038450	Hs.48948	ESTs	4.05	0.14	upregulate stage
	416241	N52639	Hs.32583	ESTs	5	0.09	upregulate stage
	416254	H51703	Hs.13640	ESTs	1	0.95	upregulate stage
20	416269	AA177138	Hs.161671	ESTs	4.07	0.2	upregulate stage
	416276	U41060	Hs.79136	LIV-1 protein, estrogen regulated	1.84	0.45	upregulate stage
	416280	H44180	Hs.181789	ESTs	1	1	upregulate stage
	416309	R84694	Hs.79194	cAMP responsive element binding protein	9.35	0.08	upregulate stage
	416324	H47983	Hs.1870	phenylalanine hydroxylase	5.15	0.13	upregulate stage
25	416332	H91284	Hs.244461	ESTs	1	1	upregulate stage
	416343	H49213		gb:yy19e04.r1 Soares fetal liver spleen	1	1	upregulate stage
	416353	T77127	Hs.191297	ESTs, Moderately similar to ALU6_HUMAN A	1.46	0.59	upregulate stage
	416395	R94575		gb:yy173e10.s1 Soares fetal liver spleen	9.2	0.09	upregulate stage
	416437	N48990	Hs.37204	ESTs	4.15	0.12	upregulate stage
30	416476	H58137	Hs.268639	ESTs	1	0.22	upregulate stage
	416537	T99086	Hs.144904	nuclear receptor co-repressor 1	5.45	0.12	upregulate stage
	416539	Y07909	Hs.79358	epithelial membrane protein 1	9.45	0.09	upregulate stage
	416575	W02414	Hs.38383	ESTs	4.95	0.1	upregulate stage
	416624	H69044		gb:yy77h05.s1 Soares fetal liver spleen	1	0.22	upregulate stage
35	416644	H70701	Hs.269135	ESTs	5.65	0.12	upregulate stage
	416658	U03272	Hs.79432	fibulin 2 (congenital contractural ara	9.65	0.05	upregulate stage
	416682	R99700	Hs.36152	ESTs	1	0.25	upregulate stage
	416690	H84078	Hs.108551	ESTs	5.35	0.13	upregulate stage
	416709	R99369	Hs.283108	hemoglobin, gamma G	5.4	0.13	upregulate stage
40	416712	N68576	Hs.81602	ESTs	1	0.25	upregulate stage
	416715	H79460	Hs.271722	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.32	upregulate stage
	416731	T58115	Hs.10336	ESTs	1	0.4	upregulate stage
	416734	H81213	Hs.14825	ESTs	3.8	0.16	upregulate stage
	416735	R11275	Hs.194485	ESTs	11.5	0.06	upregulate stage
45	416738	N29218	Hs.40290	ESTs	1	0.42	upregulate stage
	416856	N27833	Hs.269028	ESTs	2.6	0.22	upregulate stage
	416883	AW140128	Hs.184902	ESTs	11.3	0.07	upregulate stage
	416923	N32498	Hs.42829	ESTs	1	0.61	upregulate stage
	416936	N21352	Hs.42987	ESTs, Weakly similar to ORF2 [Mmusculus	1	1	upregulate stage
50	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	11.3	0.05	upregulate stage
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	5.04	0.15	upregulate stage
	417134	N51220	Hs.269068	ESTs	1	0.24	upregulate stage
	417185	NM_002484	Hs.81469	nucleotide binding protein 1 (E.coli Min	1.98	0.32	upregulate stage
	417218	AA005247	Hs.285754	mal proto-oncogene (hepatocyte growth fa	2.95	0.21	upregulate stage
55	417265	AL121369	Hs.281117	ESTs	1	0.3	upregulate stage
	417283	N62840	Hs.48648	ESTs	1.05	0.27	upregulate stage
	417308	H60720	Hs.81892	KIAA0101 gene product	9.2	0.09	upregulate stage
	417320	AA195667	Hs.287324	ESTs	2.8	0.16	upregulate stage
	417396	T98987		gb:ye66f02.r1 Soares fetal liver spleen	1	1	upregulate stage
60	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	2.75	0.09	upregulate stage
	417409	BE272506	Hs.82109	syndecan 1	1.92	0.44	upregulate stage
	417448	AA203135	Hs.130186	ESTs	6.45	0.1	upregulate stage
	417453	H73183	Hs.129885	ESTs, Moderately similar to unnamed prot	4.65	0.13	upregulate stage
65	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	1.59	0.49	upregulate stage
	417540	AA203600	Hs.152250	ESTs	1	1	upregulate stage
	417576	AA339449	Hs.82285	phosphoribosylglycnamide formyltransfer	5.65	0.1	upregulate stage
	417581	R26968	Hs.24104	ESTs, Weakly similar to ALU7_HUMAN ALU S	9.15	0.09	upregulate stage
	417596	R07343	Hs.226823	ESTs	4.35	0.14	upregulate stage
	417599	AA204688	Hs.136201	ESTs, Weakly similar to ALU7_HUMAN ALU S	0.94	0.9	upregulate stage
70	417620	R02530	Hs.191198	ESTs	9.1	0.07	upregulate stage
	417638	R12490	Hs.189779	ESTs	1	0.32	upregulate stage
	417650	T05870	Hs.100640	ESTs	1	0.22	upregulate stage
	417715	AW869587	Hs.86366	ESTs	6.31	0.09	upregulate stage
	417720	AA205625	Hs.208067	ESTs	4.65	0.11	upregulate stage
75	417742	R64719		gb:EST22d11 WATM1 Homo sapiens cDNA clon	4.15	0.13	upregulate stage
	417750	AI267720	Hs.260523	neuroblastoma RAS viral (v-ras) oncogene	9.98	0.08	upregulate stage
	417780	Z43482	Hs.82772	collagen, type XI, alpha 1	2.3	0.14	upregulate stage
	417789	R50978	Hs.267054	ESTs	1.05	0.19	upregulate stage

	417791	AW965339	Hs.111471	ESTs	5.35	0.1	upregulate stage
	417850	AA215724	Hs.82741	primase, polypeptide 1 (49kD)	1	1	upregulate stage
	417898	AA826198	Hs.291851	ESTs	2.15	0.21	upregulate stage
5	417975	AA641836	Hs.30085	Homo sapiens cDNA: FLJ23186 fis, clone L	3.7	0.13	upregulate stage
	418004	U37519	Hs.87539	aldehyde dehydrogenase 8	1.57	0.5	upregulate stage
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial)	17.9	0.02	upregulate stage
	418027	AB037807	Hs.83293	hypothetical protein	6.6	0.09	upregulate stage
	418030	BE207573	Hs.83321	neuromedin B	12.2	0.04	upregulate stage
10	418068	AW971155	Hs.293902	ESTs, Weakly similar to prollyl 4-hydroxy	4.26	0.14	upregulate stage
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	5.21	0.15	upregulate stage
	418134	AA397769	Hs.86617	ESTs	1	0.3	upregulate stage
	418153	R13696	Hs.112830	ESTs	1	0.3	upregulate stage
	418180	BE618087	Hs.83724	Human clone 23773 mRNA sequence	8.79	0.09	upregulate stage
15	418201	AA214345	Hs.98445	Homo sapiens cDNA: FLJ21652 fis, clone C	3.75	0.13	upregulate stage
	418203	X54942	Hs.83758	CDC28 protein kinase 2	13.85	0.04	upregulate stage
	418216	AA662240	Hs.283099	AF15q14 protein	9.75	0.07	upregulate stage
	418236	AW994005	Hs.172572	hypothetical protein FLJ20093	10.75	0.05	upregulate stage
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	6.25	0.12	upregulate stage
20	418259	AA215404	Hs.137289	ESTs	11.5	0.07	upregulate stage
	418268	AA810599	Hs.86643	ESTs	1	0.43	upregulate stage
	418296	C01566	Hs.86671	ESTs	1	0.45	upregulate stage
	418372	AA311833	Hs.84318	replication protein A1 (70kD)	9.04	0.08	upregulate stage
	418379	AA218940	Hs.137516	fidgetin-like 1	3.25	0.15	upregulate stage
25	418422	AW440068	Hs.59425	Homo sapiens cDNA: FLJ23323 fis, clone H	8.95	0.1	upregulate stage
	418454	AA315308	Hs.85266	gbr:EST187095 Colon carcinoma (HCC) cell	2.5	0.15	upregulate stage
	418462	BE001596	Hs.85266	Integrin, beta 4	1.33	0.59	upregulate stage
	418469	U34879	Hs.85279	hydroxysteroid (17-beta) dehydrogenase 1	1.21	0.71	upregulate stage
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (ma	2.69	0.23	upregulate stage
30	418480	AA223929	Hs.86902	ESTs	1	1	upregulate stage
	418498	T78248	Hs.85701	gbyd79f05.r1 Soares fetal liver spleen	1	0.47	upregulate stage
	418516	NM_006218	Hs.85701	phosphoinositide-3-kinase, catalytic, al	5.4	0.14	upregulate stage
	418546	AA224827	Hs.85701	gbcnc32g04.s1 NCI_CGAP_Pr2 Homo sapiens	2.72	0.23	upregulate stage
	418573	AA225188	Hs.85701	gbcnc21h04.r1 NCI_CGAP_Pr1 Homo sapiens	9.95	0.07	upregulate stage
35	418577	AA225247	Hs.269300	ESTs, Weakly similar to B34087 hypothell	1	0.77	upregulate stage
	418578	U92459	Hs.86204	glutamate receptor, metabotropic 8	1	1	upregulate stage
	418590	AI732672	Hs.252507	ESTs	1	0.59	upregulate stage
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	4.75	0.13	upregulate stage
	418612	AB037788	Hs.224961	cleavage and polyadenylation specific fa	1	0.23	upregulate stage
40	418624	AI734080	Hs.104211	ESTs	7.95	0.09	upregulate stage
	418661	NM_001949	Hs.1189	Human mRNA for KIAA0075 gene, partial cd	3	0.15	upregulate stage
	418663	AK001100	Hs.87013	Homo sapiens cDNA FLJ10238 fis, clone HE	17.2	0.04	upregulate stage
	418675	AW299723	Hs.87223	bone morphogenetic protein receptor, typ	1	1	upregulate stage
	418686	Z36830	Hs.87268	annexin A8	2.11	0.3	upregulate stage
45	418687	R61650	Hs.22581	ESTs	6.75	0.07	upregulate stage
	418693	AI750878	Hs.87409	thrombospondin 1	4.5	0.08	upregulate stage
	418704	AA227235	Hs.83286	ESTs	1	0.33	upregulate stage
	418712	Z42183	Hs.83286	gbr:HSC08F041 normalized infant brain cDN	1	0.91	upregulate stage
50	418717	AI334430	Hs.86984	ESTs	4.7	0.12	upregulate stage
	418723	AA504428	Hs.10487	ESTs, Weakly similar to Weak similarity	5.85	0.1	upregulate stage
	418738	AW388633	Hs.6682	ESTs	3.6	0.09	upregulate stage
	418752	AL133556	Hs.88144	hypothetical protein FLJ12476	1	1	upregulate stage
	418757	AI864193	Hs.169728	Homo sapiens cDNA FLJ13150 fis, clone NT	9.15	0.09	upregulate stage
	418844	M62982	Hs.1200	arachidonate 12-lipoxygenase	9.25	0.08	upregulate stage
55	418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	1.83	0.43	upregulate stage
	418876	AA740616	Hs.293874	ESTs	11.3	0.06	upregulate stage
	418903	AW969665	Hs.154848	ESTs	1	1	upregulate stage
	418915	AI474778	Hs.118977	ESTs	4.75	0.12	upregulate stage
	418939	AW630803	Hs.89497	lamin B1	2.6	0.13	upregulate stage
60	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	1.45	0.53	upregulate stage
	418976	AA933082	Hs.126883	ESTs	1	0.23	upregulate stage
	419059	T86216	Hs.89584	gbyd84a05.r1 Soares fetal liver spleen	1	0.38	upregulate stage
	419078	M93119	Hs.89584	Insulinoma-associated 1	1.25	0.18	upregulate stage
	419121	AA374372	Hs.89626	parathyroid hormone-like hormone	1	1	upregulate stage
65	419169	AW851980	Hs.262346	ESTs, Weakly similar to ORF2: function u	1.59	0.3	upregulate stage
	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	3.55	0.05	upregulate stage
	419218	AI248073	Hs.188723	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.27	upregulate stage
	419226	AI342491	Hs.87413	ESTs	1	0.37	upregulate stage
	419235	AW470411	Hs.288433	neurotrophin	11.9	0.07	upregulate stage
70	419286	AA236005	Hs.221303	ESTs	4.85	0.14	upregulate stage
	419327	AA521504	Hs.190179	ESTs	1	1	upregulate stage
	419355	AA428520	Hs.90061	progesterone binding protein	10.6	0.06	upregulate stage
	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	1.84	0.47	upregulate stage
	419413	AA237040	Hs.87589	ESTs	1	1	upregulate stage
	419436	AA991639	Hs.15036	ESTs, Highly similar to AF161358.1 HSPC0	6.6	0.1	upregulate stage
75	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	1.31	0.64	upregulate stage
	419472	AW978038	Hs.87648	gbr:EST390147 MAGE resequences, MAGO Homo	1	1	upregulate stage
	419475	AA243420	Hs.87648	ESTs	1.1	0.24	upregulate stage

5	419477	AA826279		gb:cd03g07.s1 NCI_CGAP_GCB1 Homo sapiens	1	0.56	upregulate stage
	419484	AA243474	Hs.272128	Homo sapiens cDNA FLJ13901 fis, clone TH	1	0.22	upregulate stage
	419506	N20812	Hs.42369	ESTs	1	1	upregulate stage
	419554	AI732138	Hs.104318	ESTs	1	0.5	upregulate stage
	419569	AI971651	Hs.91143	Jagged 1 (Alagille syndrome)	1	0.91	upregulate stage
10	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	8.1	0.08	upregulate stage
	419651	NM_007023	Hs.91971	cAMP-regulated guanine nucleotide exchan	1	1	upregulate stage
	419666	NM_014810	Hs.92200	KIAA0480 gene product	5.2	0.12	upregulate stage
	419737	H24185	Hs.92918	hypothetical protein	11.7	0.07	upregulate stage
	419743	AW408762	Hs.127478	ESTs	6.1	0.09	upregulate stage
15	419752	AA249573	Hs.152618	ESTs	1.8	0.17	upregulate stage
	419769	H27374	Hs.103483	ESTs	1	0.36	upregulate stage
	419805	AW966945		gb:EST379019 MAGE resequences, MAGJ Homo	1	0.34	upregulate stage
	419807	R77402		gb:Y17511.s1 Soares placenta Nb2HP Homo	1	0.67	upregulate stage
	419831	AW448930	Hs.5415	ESTs	7.05	0.1	upregulate stage
20	419833	AA251131	Hs.220697	ESTs	1.25	0.53	upregulate stage
	419834	AA251139		gb:zs03g12.s1 NCI_CGAP_GCB1 Homo sapiens	1	1	upregulate stage
	419923	AW081455	Hs.120219	ESTs	5.89	0.13	upregulate stage
	419945	AW290975	Hs.118923	ESTs	1	0.24	upregulate stage
	419962	AA830111	Hs.291917	ESTs	1	1	upregulate stage
25	419970	AW612022	Hs.263271	ESTs	9.15	0.09	upregulate stage
	419986	AI345455	Hs.78915	GA-binding protein transcription factor,	3.05	0.17	upregulate stage
	419998	AA252691		gb:zs26d09.r1 NCI_CGAP_GCB1 Homo sapiens	1	0.47	upregulate stage
	420016	AW016908	Hs.88025	ESTs	1	0.8	upregulate stage
	420047	AI478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	4.8	0.11	upregulate stage
30	420076	AA827860	Hs.293717	ESTs	5.35	0.12	upregulate stage
	420111	AA255652		gb:zs21h11.r1 NCI_CGAP_GCB1 Homo sapiens	5.3	0.11	upregulate stage
	420145	AA809860	Hs.256284	ESTs	1	1	upregulate stage
	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	14.8	0.04	upregulate stage
	420161	AI683069	Hs.175319	ESTs	4.7	0.11	upregulate stage
35	420184	AA188408	Hs.95565	hypothetical protein	4.35	0.15	upregulate stage
	420226	AA773709	Hs.152818	ubiquitin specific protease 8	3.1	0.16	upregulate stage
	420230	AL034344	Hs.298020	Homo sapiens cDNA FLJ11796 fis, clone HE	10.35	0.06	upregulate stage
	420236	AA256763	Hs.291111	ESTs	4.45	0.14	upregulate stage
	420270	AA257390		gb:zs35h07.r1 NCI_CGAP_GCB1 Homo sapiens	10.05	0.08	upregulate stage
40	420297	AI628272	Hs.88323	ESTs	9.45	0.09	upregulate stage
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	11.7	0.05	upregulate stage
	420392	AI242930	Hs.97393	KIAA0328 protein	1.7	0.22	upregulate stage
	420413	AW971624	Hs.120605	ESTs	1	1	upregulate stage
	420445	AA262213	Hs.193514	ESTs	1	1	upregulate stage
45	420471	AA262452	Hs.192268	ESTs	3.95	0.13	upregulate stage
	420479	AW183695	Hs.186572	ESTs	4.95	0.12	upregulate stage
	420493	AI635113	Hs.270366	Homo sapiens mRNA; cDNA DKFZp564H0616 (f	4.4	0.15	upregulate stage
	420552	AK000492	Hs.98806	hypothetical protein	11.55	0.06	upregulate stage
	420572	AL035593	Hs.99016	Human DNA sequence from clone 310J6 on c	1.35	0.22	upregulate stage
50	420643	W87731		gb:zh65g10.r1 Soares_fetal_liver_spleen_	1.25	0.25	upregulate stage
	420650	AA455706	Hs.44581	heat shock protein hsp70-related protein	7.3	0.09	upregulate stage
	420654	AA279091	Hs.104420	ESTs	1	0.27	upregulate stage
	420655	R74405	Hs.300886	ESTs	1	1	upregulate stage
	420717	AA284447	Hs.271887	ESTs	9	0.09	upregulate stage
55	420734	AW972872	Hs.293736	ESTs	5.2	0.13	upregulate stage
	420756	AA411800	Hs.189900	ESTs	1	1	upregulate stage
	420789	AI670057	Hs.199882	ESTs	8.85	0.06	upregulate stage
	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	4.6	0.12	upregulate stage
	420851	AA281062	Hs.250734	ESTs	8.35	0.08	upregulate stage
60	420880	AI809621	Hs.105620	ESTs	1	1	upregulate stage
	420923	AF097021	Hs.273321	differentially expressed in hematopoieti	10.4	0.03	upregulate stage
	420928	AA281809		gb:zt10e01.r1 NCI_CGAP_GCB1 Homo sapiens	1	1	upregulate stage
	420936	AA456112	Hs.99410	ESTs	8.71	0.07	upregulate stage
	420947	AA491044	Hs.47196	ESTs	1	0.38	upregulate stage
65	421017	AW979181	Hs.293221	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	1	upregulate stage
	421064	AI245432	Hs.101382	tumor necrosis factor, alpha-induced pro	1.26	0.62	upregulate stage
	421070	AA283185	Hs.19327	ESTs	2.2	0.14	upregulate stage
	421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C	1.69	0.28	upregulate stage
	421102	AI470093	Hs.89217	ESTs	2.65	0.19	upregulate stage
70	421103	AI625835	Hs.27104	ESTs	6	0.1	upregulate stage
	421114	AW975051	Hs.293156	ESTs	4.7	0.12	upregulate stage
	421118	AI471925	Hs.89257	ESTs	1	0.39	upregulate stage
	421155	H87879	Hs.102257	lysyl oxidase	1.15	0.18	upregulate stage
	421159	AW978316	Hs.136649	ESTs	1	0.44	upregulate stage
75	421187	NM_014721	Hs.102471	KIAA0680 gene product	5.7	0.11	upregulate stage
	421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	0.07	2.55	upregulate stage
	421221	AW276914	Hs.300877	ESTs	8.75	0.07	upregulate stage
	421229	AI056590	Hs.7086	Homo sapiens cDNA: FLJ23000 fis, clone L	1.64	0.49	upregulate stage
	421261	AA600853	Hs.98133	ESTs	10.9	0.07	upregulate stage
	421262	AA285746	Hs.9343	Homo sapiens cDNA FLJ14265 fis, clone PL	2.65	0.16	upregulate stage
	421278	AI387919	Hs.99691	ESTs	1	0.56	upregulate stage

5	421280	AA811804		gb:ob39a05.s1 NCI_CGAP_GCB1 Homo sapiens	1	0.34	upregulate stage
	421282	AA286914	Hs.183299	ESTs	9	0.08	upregulate stage
	421306	AA806207	Hs.125889	ESTs	1	0.95	upregulate stage
	421308	AA687322	Hs.192843	ESTs	2.85	0.15	upregulate stage
	421373	AA808229	Hs.167771	ESTs	2.45	0.14	upregulate stage
10	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	1.6	0.26	upregulate stage
	421381	AA361752		gb:EST71314 T-cell lymphoma Homo sapiens	5.05	0.09	upregulate stage
	421418	AA806639		gb:ob88g05.s1 NCI_CGAP_GCB1 Homo sapiens	6.55	0.1	upregulate stage
	421433	AI829192	Hs.134805	ESTs	9.9	0.07	upregulate stage
	421451	AA291377	Hs.50831	ESTs	11.9	0.06	upregulate stage
15	421491	H99999	Hs.42736	ESTs	3	0.2	upregulate stage
	421493	BE300341	Hs.104925	ectodermal-neural cortex (with BTB-like	2.51	0.32	upregulate stage
	421559	NM_014720	Hs.105751	Ste20-related serine/threonine kinase	9	0.09	upregulate stage
	421577	BE465451	Hs.105925	single-minded (Drosophila) homolog 1	5.75	0.12	upregulate stage
	421673	H54384	Hs.36892	ESTs	1	1	upregulate stage
20	421685	AF189723	Hs.106778	ATPase, Ca++ transporting, type 2C, memb	9.45	0.07	upregulate stage
	421708	AW754341		gb:CM0-CT0341-181299-130-h12 CT0341 Homo	1	0.47	upregulate stage
	421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (ach	1.97	0.33	upregulate stage
	421838	AW881089	Hs.108806	Homo sapiens mRNA; cDNA DKFZp566M0947 (f	7.05	0.1	upregulate stage
	421869	AB003592	Hs.109050	contactin 6	1	1	upregulate stage
25	421925	S80310	Hs.109620	acidic epididymal glycoprotein-like 1	1	1	upregulate stage
	421948	L42583	Hs.111758	keratin 6A	51.9	0.01	upregulate stage
	421958	AA357185	Hs.109918	ras homolog gene family, member H	10.17	0.07	upregulate stage
	421991	NM_014918	Hs.110488	KIAA0990 protein	4.5	0.17	upregulate stage
	422026	U80736	Hs.110826	trinucleotide repeat containing 9	6.5	0.08	upregulate stage
30	422072	AB018255	Hs.111138	KIAA0712 gene product	9.2	0.08	upregulate stage
	422094	AF129535	Hs.272027	F-box only protein 5	6.95	0.09	upregulate stage
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	1.66	0.17	upregulate stage
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	3.96	0.1	upregulate stage
	422182	AL043892	Hs.180582	Homo sapiens cDNA: FLJ21836 fis, clone H	2.8	0.16	upregulate stage
35	422204	AA339015		gb:EST44247 Fetal brain I Homo sapiens c	1	1	upregulate stage
	422261	AA307595	Hs.119908	nucleolar protein NOP5/NOP58	1	1	upregulate stage
	422271	AB038995	Hs.114159	RAB-8b protein	5.04	0.16	upregulate stage
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	3.46	0.24	upregulate stage
	422282	AF019225	Hs.114309	apolipoprotein L	4.54	0.14	upregulate stage
40	422322	AB022192	Hs.115240	peroxisome biogenesis factor 13	1	0.53	upregulate stage
	422330	D30783	Hs.115263	epiregulin	4.45	0.06	upregulate stage
	422342	AA309272		gb:EST180209 Liver, hepatocellular carci	2.25	0.19	upregulate stage
	422406	AF025441	Hs.116206	Opa-interacting protein 5	9.5	0.07	upregulate stage
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	7.35	0.04	upregulate stage
45	422491	AA338548	Hs.117546	neurofilin	0.64	1.24	upregulate stage
	422504	AA311407		gb:EST182167 Jurkat T-cells V Homo sapie	3.6	0.11	upregulate stage
	422505	AL120862	Hs.124165	ESTs	2.8	0.14	upregulate stage
	422508	AJ000327	Hs.117852	ATP-binding cassette, sub-family D (ALD)	5.25	0.14	upregulate stage
	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	2.57	0.31	upregulate stage
50	422540	AI050751	Hs.22895	Homo sapiens cDNA: FLJ23548 fis, clone L	1	0.59	upregulate stage
	422588	AA312730		gb:EST183651 Monocytes, stimulated II Ho	3	0.14	upregulate stage
	422678	AA247778	Hs.119155	Homo sapiens mRNA; cDNA DKFZp434B249 (fr	10.7	0.07	upregulate stage
	422762	AL031320	Hs.119976	Human DNA sequence from clone RP1-20N2 o	5.1	0.13	upregulate stage
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	5.94	0.1	upregulate stage
55	422823	D89974	Hs.121102	vanin 2	10	0.07	upregulate stage
	422892	AA988176	Hs.121553	hypothetical protein FLJ20641	1	0.27	upregulate stage
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	7.2	0.08	upregulate stage
	422964	AW439476	Hs.256895	ESTs	11.75	0.07	upregulate stage
	422981	AF026445	Hs.122752	TATA box binding protein (TBP)-associate	3.05	0.14	upregulate stage
60	423001	AA320014	Hs.208603	ESTs	9.1	0.09	upregulate stage
	423090	BE387529	Hs.123536	melanoma antigen, family E, 1, cancer/te	1	0.49	upregulate stage
	423100	AA323114		gb:EST25873 Cerebellum II Homo sapiens c	1	1	upregulate stage
	423121	AW864848		gb:PM2-SN0018-290300-003-c09 SN0018 Homo	2.8	0.19	upregulate stage
	423156	AA131493	Hs.124752	fibroblast growth factor 12B	1	0.27	upregulate stage
65	423198	M81933	Hs.1634	cell division cycle 25A	8.95	0.07	upregulate stage
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	1.2	0.57	upregulate stage
	423262	NM_005479	Hs.126057	frequently rearranged in advanced T-cell	9.75	0.07	upregulate stage
	423296	AW967193	Hs.3327	Homo sapiens cDNA: FLJ22219 fis, clone H	4.95	0.12	upregulate stage
	423309	BE006775	Hs.126782	sushi-repeat protein	1.58	0.34	upregulate stage
70	423347	AI660412	Hs.234557	ESTs	1	0.45	upregulate stage
	423359	NM_014170	Hs.127496	HSPC135 protein	1	0.69	upregulate stage
	423368	AA364195		gb:EST75015 Pineal gland II Homo sapiens	1	0.95	upregulate stage
	423389	AI471609	Hs.54347	ESTs	3.95	0.14	upregulate stage
	423430	AF112481	Hs.128501	RAD54, S. cerevisiae, homolog of, B	1.62	0.43	upregulate stage
75	423441	R68649	Hs.278359	absent in melanoma 1 like	6.25	0.1	upregulate stage
	423453	AW450737	Hs.128791	CGI-09 protein	8.45	0.09	upregulate stage
	423500	AF020763	Hs.129705	clone 1900 unknown protein	1	0.8	upregulate stage
	423578	AW960454	Hs.222830	ESTs	11.94	0.07	upregulate stage
	423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H	3.4	0.17	upregulate stage
	423632	AA328824		gb:EST32358 Embryo, 12 week I Homo sapie	1	0.71	upregulate stage
	423642	AW452650	Hs.157148	Homo sapiens cDNA FLJ11883 fis, clone HE	8.35	0.1	upregulate stage

5	423644	AA329048		gb:EST32875 Embryo, 12 week I Homo sapie	1	0.43	upregulate stage
	423648	AK000456	Hs.130546	hypothetical protein FLJ20449	10.4	0.07	upregulate stage
	423651	AF192913	Hs.130683	zinc finger protein 180 (HIZ168)	5.75	0.1	upregulate stage
	423654	AI674253	Hs.35828	ESTs	3.15	0.18	upregulate stage
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	29.7	0.02	upregulate stage
10	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.1	0.16	upregulate stage
	423745	AI809797	Hs.43222	ESTs	1	0.5	upregulate stage
	423748	AJ149048	Hs.30211	hypothetical protein FLJ22313	4.25	0.13	upregulate stage
	423753	Y11312	Hs.132463	phosphoinositide-3-kinase, class 2, beta	1.18	0.71	upregulate stage
	423758	AA338153	Hs.82124	laminin, beta 1	1	1	upregulate stage
15	423774	L39064	Hs.1702	interleukin 9 receptor	3.08	0.15	upregulate stage
	423818	AA332439		gb:EST36554 Embryo, 8 week I Homo sapien	1	0.38	upregulate stage
	423827	AI472828	Hs.172625	ESTs	1	0.43	upregulate stage
	423837	AW937063		gb:PM3-DT0037-231299-001-g11 DT0037 Homo	1.44	0.55	upregulate stage
	423912	BE091233		gb:PM0-BT0726-300300-001-H07 BT0726 Homo	1	1	upregulate stage
20	423938	AL049328	Hs.135642	Homo sapiens mRNA; cDNA DKFZp564E026 (fr	1	1	upregulate stage
	423942	AF209704	Hs.135723	glycolipid transfer protein	11.65	0.05	upregulate stage
	423944	T91433	Hs.128291	phosphodiesterase 10A	1	0.45	upregulate stage
	423946	AL137344	Hs.135892	Homo sapiens mRNA; cDNA DKFZp761I1311 (f	1	1	upregulate stage
	423956	W28203	Hs.136169	Homo sapiens clone 25215 mRNA sequence,	5.35	0.09	upregulate stage
25	424006	AF054815	Hs.137548	CD84 antigen (leukocyte antigen)	8.8	0.06	upregulate stage
	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	3.14	0.19	upregulate stage
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	2.6	0.26	upregulate stage
	424073	U03493	Hs.138959	gap junction protein, alpha 7, 45kD (con	1.8	0.22	upregulate stage
	424075	AI807320	Hs.227630	RE1-silencing transcription factor	9.1	0.06	upregulate stage
30	424087	N69333	Hs.21638	ESTs	1	1	upregulate stage
	424193	AK002005	Hs.142868	Homo sapiens cDNA FLJ11143 fis, clone PL	1	0.23	upregulate stage
	424353	AA339646		gb:EST44755 Fetal brain I Homo sapiens c	1	1	upregulate stage
	424364	AW383226	Hs.201189	ESTs, Weakly similar to DRPLA [H.sapiens	2.18	0.33	upregulate stage
	424406	D54120	Hs.146409	wingless-type MMTV integration site fami	2.05	0.17	upregulate stage
35	424420	BE614743	Hs.146688	prostaglandin E synthase	1.19	0.67	upregulate stage
	424425	AB031480	Hs.146824	SPR1 protein	1.42	0.54	upregulate stage
	424486	BE002477	Hs.278714	chloride intracellular channel 6	1	0.27	upregulate stage
	424490	AJ278016	Hs.55565	ankyrin repeat domain 3	2.02	0.39	upregulate stage
	424492	AI133482	Hs.165210	ESTs	3.15	0.14	upregulate stage
40	424505	AA446131	Hs.124918	Homo sapiens cDNA FLJ13186 fis, clone NT	11.55	0.05	upregulate stage
	424513	BE385864	Hs.149894	mitochondrial translational initiation f	2.65	0.23	upregulate stage
	424575	AL110217	Hs.150751	DKFZP572C163 protein	1	1	upregulate stage
	424583	AF017445	Hs.150926	fructose-1-phosphate guanylyltransferase	1.8	0.26	upregulate stage
	424589	AW854298		gb:RC3-CT0254-100500-211-c03 CT0254 Homo	0.85	0.94	upregulate stage
45	424602	AK002055	Hs.301129	Homo sapiens clone Z3859 mRNA sequence	2.85	0.2	upregulate stage
	424625	AW904466	Hs.151310	PDZ domain protein (Drosophila InaD-like	1	0.4	upregulate stage
	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub	1.41	0.52	upregulate stage
	424643	AF241850	Hs.151428	ret finger protein 2	9.75	0.07	upregulate stage
	424649	BE242035	Hs.151461	embryonic ectoderm development	5.85	0.13	upregulate stage
50	424653	AW977534	Hs.151469	calcium/calmodulin-dependent serine prot	1	0.56	upregulate stage
	424670	W61215	Hs.116651	epithelial V-like antigen 1	1.42	0.52	upregulate stage
	424690	BE538356	Hs.151777	Human translation initiation factor eIF-	4.3	0.1	upregulate stage
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	3.85	0.11	upregulate stage
	424702	AF250237	Hs.152009	G protein-coupled receptor 85	1	1	upregulate stage
55	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	4.05	0.09	upregulate stage
	424735	U31875	Hs.152677	Homo sapiens cDNA FLJ20338 fis, clone HE	1.04	0.59	upregulate stage
	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	1.11	0.65	upregulate stage
	424749	NM_002451	Hs.152817	methylinthadenosine phosphorylase	1	1	upregulate stage
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	18.5	0.03	upregulate stage
60	424841	AI280215	Hs.96885	ESTs	1	1	upregulate stage
	424860	W60828	Hs.153529	Homo sapiens clone 24540 mRNA sequence	1	1	upregulate stage
	424878	H57111	Hs.221132	ESTs	9.45	0.07	upregulate stage
	424879	AA348013	Hs.159354	ESTs	10.7	0.07	upregulate stage
	424888	AA348126	Hs.24882	ESTs	2.8	0.21	upregulate stage
65	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	7.75	0.07	upregulate stage
	424930	AA885344	Hs.96910	ESTs	1.45	0.38	upregulate stage
	424948	AA348810	Hs.190503	ESTs	3.2	0.12	upregulate stage
	424951	AW964082		gb:EST376155 MAGE resequences, MAGH Homo	8.75	0.09	upregulate stage
	424993	F07625		gb:HSC2CF021 normalized infant brain cDN	1	1	upregulate stage
70	425020	U09368	Hs.154205	zinc finger protein 140 (clone pTZ-39)	1	1	upregulate stage
	425024	R39235	Hs.12407	ESTs	2.65	0.13	upregulate stage
	425057	AA826434	Hs.96944	ESTs	1	0.22	upregulate stage
	425058	AL048716	Hs.154387	KIAA0103 gene product	9.5	0.07	upregulate stage
	425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	1.66	0.52	upregulate stage
75	425191	AF052146	Hs.155085	Homo sapiens clone 24653 mRNA sequence	1	0.32	upregulate stage
	425216	U81504	Hs.155172	adaptor-related protein complex 3, beta	7.05	0.1	upregulate stage
	425234	AW152225	Hs.165909	ESTs	19.7	0.04	upregulate stage
	425239	BE567924	Hs.155244	pre-mRNA splicing factor similar to S. c	1	0.69	upregulate stage
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	10.45	0.05	upregulate stage
	425304	AA463844	Hs.31339	fibroblast growth factor 11	1.57	0.51	upregulate stage
	425316	AA354977	Hs.191565	ESTs, Moderately similar to NSD1 protein	5.05	0.12	upregulate stage

	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	14.7	0.05	upregulate stage
	425362	AA355936		gb:EST64410 Jurkat T-cells V1 Homo sapie	1	1	upregulate stage
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	8.24	0.09	upregulate stage
5	425403	AL023753	Hs.156406	Human DNA sequence from clone 1198H6 on	1	0.22	upregulate stage
	425415	M13903	Hs.157091	involucrin	1.19	0.55	upregulate stage
	425420	BE536911	Hs.234545	ESTs, Weakly similar to AF155135 1 novel	2.85	0.13	upregulate stage
	425463	AK000740	Hs.157986	hypothetical protein FLJ20733	9	0.07	upregulate stage
	425465	L18964	Hs.1904	protein kinase C, iota	9.6	0.07	upregulate stage
10	425467	R16484	Hs.190075	ESTs	1	0.83	upregulate stage
	425492	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	3.2	0.15	upregulate stage
	425607	U09860	Hs.158333	protease, serine, 7 (enterokinase)	1	1	upregulate stage
	425608	AA360486	Hs.92448	ESTs	4.7	0.14	upregulate stage
	425614	AI334963	Hs.156256	ESTs	2.65	0.14	upregulate stage
15	425641	D79758	Hs.143355	Homo sapiens cDNA FLJ13207 fis, clone NT	4.86	0.1	upregulate stage
	425660	AA521184	Hs.105504	ESTs	1	0.31	upregulate stage
	425665	AK001050	Hs.159066	hypothetical protein FLJ10188	1.25	0.19	upregulate stage
	425672	AA361483		gb:EST70790 T-cell lymphoma Homo sapiens	1	1	upregulate stage
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript)	3.96	0.13	upregulate stage
20	425726	AF085808	Hs.159330	uroplakin 3	0.92	0.79	upregulate stage
	425742	AJ001454	Hs.159425	testican 3	1	1	upregulate stage
	425785	T27017	Hs.159528	Homo sapiens clone 24400 mRNA sequence	1	0.39	upregulate stage
	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	1.89	0.44	upregulate stage
	425843	BE313280	Hs.159627	death associated protein 3	3.1	0.15	upregulate stage
25	425852	AK001504	Hs.159651	death receptor 6	1.72	0.47	upregulate stage
	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	0.95	0.68	upregulate stage
	426010	AA136563	Hs.1975	Homo sapiens cDNA: FLJ21007 fis, clone C	1	0.34	upregulate stage
	426028	NM_001110	Hs.172028	a disinigrin and metalloproteinase doma	14.3	0.04	upregulate stage
	426101	AL049987	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	11.75	0.05	upregulate stage
30	426108	AA622037	Hs.166468	programmed cell death 5	3.23	0.18	upregulate stage
	426115	H08895	Hs.166733	leucylcystinyl aminopeptidase	1	0.32	upregulate stage
	426168	NM_003152	Hs.167503	signal transducer and activator of trans	1.97	0.4	upregulate stage
	426257	AL137201	Hs.168625	KIAA0979 protein	1	0.29	upregulate stage
	426261	AW242243	Hs.168670	peroxisomal farnesylated protein	2.8	0.16	upregulate stage
35	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	14.75	0.04	upregulate stage
	426451	AI908165	Hs.169946	GATA-binding protein 3	3.05	0.28	upregulate stage
	426462	U59111	Hs.169993	dermatan sulphate proteoglycan 3	1	0.36	upregulate stage
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	14.17	0.05	upregulate stage
	426514	BE616633	Hs.301122	bone morphogenetic protein 7 (osteogenic	1.15	0.47	upregulate stage
40	426561	AA381437		gb:EST94514 Activated T-cells I Homo sap	5.65	0.11	upregulate stage
	426711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma	11.05	0.05	upregulate stage
	426731	AW303411	Hs.130332	ESTs	2.4	0.21	upregulate stage
	426759	AI590401	Hs.21213	ESTs	9.5	0.06	upregulate stage
45	426786	AA319798	Hs.172247	eukaryotic translation elongation factor	9.25	0.09	upregulate stage
	426788	U66815	Hs.172280	SW/SNF related, matrix associated, acti	5.63	0.14	upregulate stage
	426818	AA554827	Hs.124841	ESTs, Weakly similar to ALU5_HUMAN ALU S	9	0.08	upregulate stage
	426824	D87717	Hs.172652	KIAA0013 gene product	1	0.87	upregulate stage
	426827	AW067805	Hs.172665	methyltetrahydrofolate dehydrogenase	8.95	0.09	upregulate stage
	426921	AA037145	Hs.172665	cleavage stimulation factor, 3' pre-RNA,	1	0.19	upregulate stage
50	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	1.15	0.72	upregulate stage
	426997	BE620738	Hs.173125	peptidylprolyl isomerase F (cyclophilin	11.06	0.06	upregulate stage
	427071	AA397958	Hs.192719	ESTs	5.75	0.08	upregulate stage
	427126	AA620613	Hs.191827	ESTs	2.55	0.18	upregulate stage
	427134	AA398409	Hs.173561	EST	3.4	0.18	upregulate stage
55	427142	AA398510	Hs.133148	ESTs	1	0.25	upregulate stage
	427259	AA400096		gb:zu69107.s1 Soares_testis_NHT Homo sap	1	0.22	upregulate stage
	427308	D26067	Hs.174905	KIAA0033 protein	5.9	0.1	upregulate stage
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	6.12	0.11	upregulate stage
	427356	AW023482	Hs.97849	ESTs	2.7	0.13	upregulate stage
60	427370	AI243615	Hs.97740	ESTs	3.6	0.14	upregulate stage
	427376	AA401533	Hs.19440	ESTs	2.1	0.16	upregulate stage
	427387	BE244966	Hs.177584	3-oxoacid CoA transferase	1	0.39	upregulate stage
	427470	AW999924	Hs.178357	Homo sapiens cDNA FLJ13657 fis, clone PL	3.4	0.16	upregulate stage
	427519	AW085233	Hs.180696	ESTs	8.23	0.1	upregulate stage
65	427521	AW973352	Hs.299056	ESTs	7.75	0.1	upregulate stage
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	5.7	0.15	upregulate stage
	427566	AI743515		gb:w172b08.x2 Soares_NFL_T_GBC_S1 Homo s	1	1	upregulate stage
	427581	NM_014788	Hs.179703	KIAA0129 gene product	11.45	0.06	upregulate stage
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	3.25	0.16	upregulate stage
70	427603	AI090838	Hs.98006	ESTs	1	1	upregulate stage
	427646	AI578042	Hs.271953	ESTs	5.7	0.11	upregulate stage
	427652	AI673025	Hs.43874	ESTs	1	0.34	upregulate stage
	427742	AA411880	Hs.190688	ESTs	2.4	0.16	upregulate stage
	427814	W28383	Hs.180900	Williams-Beuren syndrome chromosome regl	9.13	0.08	upregulate stage
75	427839	AA608823	Hs.98244	ESTs	1.9	0.19	upregulate stage
	427878	C05766	Hs.181022	CGI-07 protein	4.1	0.14	upregulate stage
	427922	AK001934	Hs.181112	HSPC126 protein	2.6	0.19	upregulate stage
	427933	AW974643	Hs.190571	ESTs	4.55	0.14	upregulate stage

	427934	AA810541	Hs.291866	ESTs	1	1	upregulate stage
	427944	AA417878	Hs.48401	ESTs, Weakly similar to ALU8_HUMAN ALU S	6.15	0.1	upregulate stage
	427961	AW293165	Hs.143134	ESTs	4.85	0.11	upregulate stage
5	427986	N45214	Hs.282387	Homo sapiens cDNA: FLJ21837 fis, clone H	3.55	0.13	upregulate stage
	428003	AL110200	Hs.181384	Homo sapiens mRNA; cDNA DKFZp568B0922 (f	1.45	0.36	upregulate stage
	428004	AA449563	Hs.300270	ESTs	3.95	0.12	upregulate stage
	428010	AA806554	Hs.185375	ESTs	1	0.38	upregulate stage
	428057	AI343641	Hs.185798	ESTs	10.1	0.06	upregulate stage
10	428058	AI821625	Hs.191602	ESTs	1	0.5	upregulate stage
	428071	AF212848	Hs.182339	ets homologous factor	6.4	0.09	upregulate stage
	428182	BE386042	Hs.293317	ESTs, Weakly similar to JM27 [H.sapiens]	1	0.23	upregulate stage
	428192	AA424051		gb:zv80d03.s1 Soares_total_fetus_Nb2HF8_	2.45	0.16	upregulate stage
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	9.25	0.04	upregulate stage
15	428403	AI393048	Hs.239894	leucine rich repeat (in FLI) Interactin	9.94	0.06	upregulate stage
	428436	BE080180		gb:RC4-BT0629-120200-011-b10 BT0629 Homo	1	1	upregulate stage
	428450	NM_014791	Hs.184339	KIAA0175 gene product	4.43	0.16	upregulate stage
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	9.2	0.07	upregulate stage
	428529	AW262022	Hs.106278	Homo sapiens cDNA FLJ12839 fis, clone NT	1	1	upregulate stage
20	428576	AW009330	Hs.167621	ESTs	1	0.3	upregulate stage
	428605	AB037862	Hs.186756	KIAA1441 protein	9.25	0.09	upregulate stage
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	3.8	0.08	upregulate stage
	428685	AF131853	Hs.189527	Homo sapiens clone 25016 mRNA sequence	1	1	upregulate stage
	428716	AL122118	Hs.190614	Homo sapiens mRNA; cDNA DKFZp43401221 (f	1	0.65	upregulate stage
25	428763	AW070204	Hs.178176	ESTs	1.6	0.23	upregulate stage
	428788	AF082283	Hs.193516	B-cell CLL/lymphoma 10	9.6	0.08	upregulate stage
	428829	R14050	Hs.194051	Homo sapiens mRNA; cDNA DKFZp566B213 (fr	5.45	0.11	upregulate stage
	428839	AI767756	Hs.82302	ESTs	10	0.06	upregulate stage
	428881	AI298368	Hs.98918	ESTs	1.4	0.18	upregulate stage
30	428954	AF100781	Hs.194678	WNT1 Inducible signaling pathway protein	1	1	upregulate stage
	428988	AA442900	Hs.27947	ESTs	3.05	0.13	upregulate stage
	429042	AW015489	Hs.235920	ESTs	1	0.56	upregulate stage
	429057	AF156557	Hs.194816	stromatin-like protein 1	0.95	0.93	upregulate stage
	429066	AA868555	Hs.178222	ESTs	6	0.11	upregulate stage
35	429072	AI376228	Hs.108043	Friend leukemia virus integration 1	1	1	upregulate stage
	429083	Y09397	Hs.227817	BCL2-related protein A1	11.12	0.03	upregulate stage
	429091	AA935658	Hs.187939	ESTs	8.9	0.08	upregulate stage
	429115	AA446728	Hs.289020	Homo sapiens cDNA FLJ14098 fis, clone MA	4.1	0.17	upregulate stage
	429127	AA749382	Hs.107233	ESTs	1	0.23	upregulate stage
40	429135	AA446966	Hs.99090	ESTs, Moderately similar to similar to K	1	1	upregulate stage
	429170	NM_001394	Hs.23359	dual specificity phosphatase 4	8.6	0.08	upregulate stage
	429174	BE559598	Hs.197803	KIAA0160 protein	8.4	0.05	upregulate stage
	429236	AA448407		gb:zv68d11.s1 Soares_testis_NHT Homo sap	1	0.36	upregulate stage
45	429268	AA205386	Hs.198481	RAR-related orphan receptor B	2.9	0.16	upregulate stage
	429300	AB011108	Hs.198891	serine/threonine-protein kinase PRP4 hom	4.25	0.15	upregulate stage
	429334	D63078	Hs.186180	Homo sapiens cDNA: FLJ23038 fis, clone L	2.95	0.11	upregulate stage
	429344	R94038	Hs.199538	inhibin, beta C	2.91	0.28	upregulate stage
	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	1.19	0.68	upregulate stage
	429376	AI867889	Hs.43227	ESTs	1	1	upregulate stage
50	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor	8.15	0.07	upregulate stage
	429450	AA824451	Hs.94292	Homo sapiens cDNA: FLJ23311 fis, clone H	3.3	0.17	upregulate stage
	429472	AW452421	Hs.15652	ESTs	1	1	upregulate stage
	429482	AF076974	Hs.203952	transformation/transcription domain-asso	1.52	0.59	upregulate stage
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	2.9	0.15	upregulate stage
55	429572	AW295375	Hs.39474	ESTs	1	0.95	upregulate stage
	429584	AI817785	Hs.183037	protein kinase, cAMP-dependent, regulato	6.55	0.1	upregulate stage
	429590	AI219490	Hs.44445	ESTs, Weakly similar to Kelch motif cont	1	1	upregulate stage
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	5.6	0.14	upregulate stage
	429601	AI804293	Hs.119406	ESTs, Weakly similar to AF143946 1 trans	1.36	0.58	upregulate stage
60	429602	AA521463	Hs.183424	ESTs	1	0.34	upregulate stage
	429617	X89984	Hs.211563	B-cell CLL/lymphoma 7A	10.8	0.07	upregulate stage
	429629	BE501732	Hs.30822	Homo sapiens cDNA FLJ13010 fis, clone NT	3.4	0.12	upregulate stage
	429631	AA455612	Hs.136710	EST	1	1	upregulate stage
	429644	AA455892	Hs.156379	ESTs	3.4	0.15	upregulate stage
65	429653	NM_005955	Hs.211581	metal-regulatory transcription factor 1	4.45	0.17	upregulate stage
	429664	L20433	Hs.211588	POU domain, class 4, transcription facto	1.17	0.74	upregulate stage
	429673	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	3.19	0.22	upregulate stage
	429689	AI383469	Hs.159300	ESTs	4.4	0.1	upregulate stage
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	4.25	0.13	upregulate stage
70	429813	AW139678	Hs.180791	ESTs	1	0.95	upregulate stage
	429828	AB019494	Hs.225767	IDN3 protein	4.2	0.14	upregulate stage
	429838	AW904907	Hs.108241	ESTs, Weakly similar to The KIAA0191 gen	3.25	0.14	upregulate stage
	429859	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor t	1	0.36	upregulate stage
	429913	AA460608	Hs.99552	ESTs	1.35	0.2	upregulate stage
75	429917	H80572		gb:yu76c02.r1 Soares fetal liver spleen	4.8	0.13	upregulate stage
	429921	AA526911	Hs.102756	ESTs	1	0.63	upregulate stage
	429950	AW081608	Hs.105053	ESTs	3.7	0.13	upregulate stage
	429971	AF079550	Hs.227098	glial cells missing (Drosophila) homolog	1	0.83	upregulate stage

	429979	AA463338		gb:zx97a10.r1 Soares_NhHMPu_S1 Homo sapi	1	0.32	upregulate stage
	429982	AW449534	Hs.99607	Homo sapiens cDNA FLJ13841 fis, clone TH	9.45	0.08	upregulate stage
	429986	AF092047	Hs.227277	sine oculis homeobox (Drosophila) homolo	0.78	0.58	upregulate stage
	430020	AI539029	Hs.99607	Homo sapiens cDNA FLJ13841 fis, clone TH	1	0.36	upregulate stage
5	430021	AA463913	Hs.221160	ESTs	1	0.56	upregulate stage
	430049	AW277085	Hs.99619	ESTs	3.55	0.17	upregulate stage
	430060	NM_002941	Hs.301198	roundabout (axon guidance receptor, Dros	1	0.59	upregulate stage
	430076	AA465115		gb:aa32c11.r1 NCL_CGAP_GC81 Homo sapiens	5.4	0.12	upregulate stage
10	430134	BE380149	Hs.105223	ESTs, Weakly similar to contains similar	3.6	0.13	upregulate stage
	430184	AB013802	Hs.234790	contactin 5	1	1	upregulate stage
	430195	AW969308	Hs.188594	ESTs	9.15	0.1	upregulate stage
	430279	R85974	Hs.16279	ESTs	1.2	0.52	upregulate stage
	430287	AW182459	Hs.125759	ESTs, Weakly similar to tumor suppressor	4.05	0.15	upregulate stage
15	430291	AV660345	Hs.238126	CGI-49 protein	7.2	0.08	upregulate stage
	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	11.9	0.06	upregulate stage
	430350	BE169639		gb:PM1-HT0527-280200-005-a05 HT0527 Homo	7.1	0.09	upregulate stage
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	5.9	0.11	upregulate stage
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	2.56	0.2	upregulate stage
	430488	D19589	Hs.4220	ESTs, Moderately similar to tetracycline	10.5	0.08	upregulate stage
20	430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSm8	11.2	0.06	upregulate stage
	430519	AF129534	Hs.49210	F-box only protein 4	5.35	0.11	upregulate stage
	430550	AK000062	Hs.243756	hypothetical protein FLJ20055	1	1	upregulate stage
	430551	BE065227		gb:RC1-BT0314-310300-015-b06 BT0314 Homo	1	1	upregulate stage
25	430553	AA481269	Hs.178381	ESTs	1	0.45	upregulate stage
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	4.75	0.14	upregulate stage
	430630	AW269920	Hs.2521	cystatin A (stefin A)	2.52	0.25	upregulate stage
	430634	AI860651	Hs.26685	ESTs	1.24	0.61	upregulate stage
	430637	BE160081	Hs.256290	S100 calcium-binding protein A11 (calgiz	1.79	0.47	upregulate stage
30	430640	AA482636		gb:zv29c06.r1 Soares ovary tumor NbHOT H	9.15	0.08	upregulate stage
	430665	BE350122	Hs.157367	ESTs	9.4	0.08	upregulate stage
	430726	AL031224	Hs.247850	Human DNA sequence from clone 336H9 on c	1	0.27	upregulate stage
	430733	AW975920	Hs.283361	ESTs	3.5	0.13	upregulate stage
	430781	AW088127	Hs.278636	ESTs	1	1	upregulate stage
	430791	AA486293	Hs.272068	ESTs, Moderately similar to allarmatival	1.61	0.42	upregulate stage
35	430817	AA487242	Hs.185105	ESTs	1	1	upregulate stage
	430888	BE155293	Hs.76064	ribosomal protein L27a	3.05	0.17	upregulate stage
	430918	NM_000843	Hs.248131	glutamate receptor, metabotropic 6	9.05	0.09	upregulate stage
	430926	L05597	Hs.248136	5-hydroxytryptamine (serotonin) receptor	1	0.91	upregulate stage
40	430994	AA490346	Hs.40530	ESTs	1.03	0.89	upregulate stage
	431009	BE149762	Hs.248213	gap junction protein, beta 6 (connexin 3	24.8	0.03	upregulate stage
	431023	AI283133	Hs.178925	ESTs	2.55	0.15	upregulate stage
	431030	AA830525	Hs.291988	ESTs	1	0.47	upregulate stage
	431041	AA490987	Hs.105276	ESTs	1	0.35	upregulate stage
45	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	1.65	0.45	upregulate stage
	431082	AA491600	Hs.161942	ESTs	9.85	0.06	upregulate stage
	431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	43.15	0.01	upregulate stage
	431146	Z83850	Hs.250649	Human DNA sequence from PAC 82J11 and co	1	0.4	upregulate stage
	431173	AW971198	Hs.294068	ESTs	6.3	0.12	upregulate stage
50	431245	AA496933	Hs.191687	ESTs	1	1	upregulate stage
	431253	R06428	Hs.226351	ESTs	1	0.8	upregulate stage
	431267	AW969661	Hs.124047	ESTs	1	0.31	upregulate stage
	431287	BE044989	Hs.274901	ESTs	1	1	upregulate stage
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	10.8	0.06	upregulate stage
55	431332	AA503297	Hs.117108	ESTs	6.55	0.1	upregulate stage
	431343	AW970503	Hs.300941	Homo sapiens cDNA FLJ11661 fis, clone HE	5.65	0.09	upregulate stage
	431346	AA371059	Hs.251636	ubiquitin specific protease 3	1.68	0.52	upregulate stage
	431347	AI133461	Hs.251664	insulin-like growth factor 2 (somatomedi	1.12	0.47	upregulate stage
	431381	AA577114	Hs.105727	ESTs	1	0.36	upregulate stage
60	431448	AL137517	Hs.288381	hypothetical protein DKFZp564O1278	3.72	0.13	upregulate stage
	431494	AA991355	Hs.129808	ESTs	2.75	0.18	upregulate stage
	431510	AA580082	Hs.112264	ESTs	3.75	0.13	upregulate stage
	431560	BE244135	Hs.260238	hypothetical protein FLJ10842	9.1	0.08	upregulate stage
	431571	AW500486	Hs.180610	splicing factor proline/glutamine rich (7.5	0.11	upregulate stage
65	431596	T34708	Hs.272927	Sec23 (S. cerevisiae) homolog A	8.2	0.08	upregulate stage
	431610	AK000972	Hs.264363	hypothetical protein FLJ10110	5.4	0.1	upregulate stage
	431613	AA018515	Hs.264482	Apg12 (autophagy 12, S. cerevisiae)-like	5.8	0.11	upregulate stage
	431630	NM_002204	Hs.265829	Integrin, alpha 3 (antigen CD49C, alpha	1.3	0.59	upregulate stage
	431663	NM_016569	Hs.267182	TBX3-iso protein	1.6	0.52	upregulate stage
70	431670	AW971287		gb:EST383376 MAGE resequences, MAGL Homo	1	1	upregulate stage
	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	9.1	0.05	upregulate stage
	431691	AI208511	Hs.292510	ESTs	4.15	0.12	upregulate stage
	431692	AL021331	Hs.267749	unc93 (C.elegans) homolog A	4.2	0.13	upregulate stage
	431694	AW970112	Hs.292697	ESTs	1	0.83	upregulate stage
75	431726	NM_015361	Hs.268053	KJAA0029 protein	10.1	0.07	upregulate stage
	431736	AI912234	Hs.151245	ESTs	9.9	0.08	upregulate stage
	431753	X76029	Hs.2841	neuromedin U	1	0.23	upregulate stage
	431781	AA515474	Hs.99908	nuclear receptor coactivator 4	1	0.36	upregulate stage

	431810	X67155	Hs.270845	kinesin-like 5 (mitotic kinesin-like pro	1	0.65	upregulate stage
	431814	BE256242	Hs.270847	della-tubulin	3.35	0.18	upregulate stage
	431817	X65233	Hs.271079	zinc finger protein 80 (pT17)	1	1	upregulate stage
5	431828	AA572994		gb:nrm33f12.s1 NCL CGAP_Lip2 Homo sapiens	4	0.12	upregulate stage
	431880	AJ700238	Hs.187486	ESTs	1	1	upregulate stage
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subunit)	2.89	0.27	upregulate stage
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	1	0.18	upregulate stage
	431951	AI086335	Hs.136470	ESTs	6.4	0.11	upregulate stage
10	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	9.09	0.07	upregulate stage
	431989	AW972870	Hs.291069	ESTs	1	0.23	upregulate stage
	431992	NM_002742	Hs.2891	protein kinase C, mu	3.9	0.15	upregulate stage
	432015	AL157504	Hs.159115	ESTs	6.05	0.09	upregulate stage
	432023	AW273128	Hs.214188	ESTs	0.99	0.86	upregulate stage
	432028	AJ272208	Hs.272354	interleukin 1 receptor accessory protein	1	0.48	upregulate stage
15	432039	AF220217	Hs.272374	Homo sapiens rsec15-like protein mRNA, p	1	0.24	upregulate stage
	432065	AA401039	Hs.2903	protein phosphatase 4 (formerly X), cata	1.38	0.64	upregulate stage
	432069	AW975868	Hs.294100	ESTs	4.25	0.15	upregulate stage
	432072	N62937	Hs.269109	ESTs	5.9	0.09	upregulate stage
20	432093	H28383		gb:yl52c03.r1 Soares breast 3NbH8st Homo	7.9	0.08	upregulate stage
	432136	AA157632	Hs.272630	vacuolar proton pump della polypeptide	1	0.28	upregulate stage
	432162	AA584062	Hs.272798	hypothetical protein FLJ20413	2.5	0.25	upregulate stage
	432169	Y00971	Hs.2910	phosphonobosyl pyrophosphate synthetase	6.1	0.11	upregulate stage
	432215	AL076609	Hs.2934	ribonucleotide reductase M1 polypeptide	2.44	0.29	upregulate stage
25	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	15	0.02	upregulate stage
	432235	AA531129	Hs.190297	ESTs	9.57	0.06	upregulate stage
	432237	AK001926	Hs.274132	hypothetical protein FLJ11064	1	0.44	upregulate stage
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	4.3	0.1	upregulate stage
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	3.95	0.15	upregulate stage
30	432338	AA534197	Hs.272693	ESTs	1	1	upregulate stage
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	1.97	0.4	upregulate stage
	432375	BE536069	Hs.2962	S100 calcium-binding protein P	1.16	0.58	upregulate stage
	432407	AA221036	Hs.285026	HERV-H LTR-associating 1	3.75	0.16	upregulate stage
	432410	X68561	Hs.2982	Sp4 transcription factor	1	1	upregulate stage
35	432415	T16971	Hs.289014	ESTs	7.3	0.07	upregulate stage
	432432	AA541323	Hs.115831	ESTs	5.35	0.13	upregulate stage
	432435	BE218886	Hs.282070	ESTs	5.35	0.1	upregulate stage
	432441	AW292425	Hs.163484	ESTs	19.4	0.04	upregulate stage
	432518	AI675836	Hs.94319	ESTs	1	0.59	upregulate stage
40	432580	X82018	Hs.3053	zinc finger protein with interaction dom	9.15	0.08	upregulate stage
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	10.15	0.05	upregulate stage
	432614	AA567163	Hs.185853	ESTs	1	0.33	upregulate stage
	432642	BE297635	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	10.5	0.07	upregulate stage
	432661	AW973823	Hs.283526	ESTs	1	1	upregulate stage
45	432666	AW204069	Hs.129250	ESTs, Weakly similar to unnamed protein	1	0.16	upregulate stage
	432669	AL043482	Hs.267115	ESTs	4.15	0.12	upregulate stage
	432673	AB028859	Hs.278605	ER-associated DNAJ; ER-associated Hsp40	10.24	0.06	upregulate stage
	432678	AA923424	Hs.135567	ESTs	1	0.69	upregulate stage
	432690	AF181490	Hs.278527	prenylcysteine lyase	4.55	0.12	upregulate stage
50	432724	X98266		gb:h.sapiens mRNA for ligase like protei	1	1	upregulate stage
	432758	NM_014091	Hs.278920	PRO1510 protein	1	1	upregulate stage
	432773	NM_014124	Hs.278935	PRO0255 protein	1	1	upregulate stage
	432789	D26361	Hs.3104	KIAA0042 gene product	3.46	0.22	upregulate stage
	432829	W60377	Hs.57772	ESTs	1.33	0.43	upregulate stage
55	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	4.5	0.14	upregulate stage
	432900	BE178025	Hs.7942	hypothetical protein FLJ20080	1	0.3	upregulate stage
	432917	NM_014125	Hs.279812	PRO0327 protein	6.33	0.12	upregulate stage
	432935	AW270239	Hs.213709	ESTs	3.85	0.11	upregulate stage
	432963	AA572859	Hs.225791	ESTs	1	0.19	upregulate stage
60	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	29.9	0.03	upregulate stage
	433005	AW939074		gb:QV1-DT0069-010200-057-c12 DT0069 Homo	1	0.59	upregulate stage
	433129	AA577814		gb:nrm24d03.s1 NCL CGAP_Gas1 Homo sapiens	1	1	upregulate stage
	433159	AB035898	Hs.150587	kinesin-like protein 2	6	0.1	upregulate stage
	433201	AB040896	Hs.211104	KIAA1463 protein	9.2	0.09	upregulate stage
65	433211	H11850	Hs.12808	MARK	1.6	0.45	upregulate stage
	433218	AI040372	Hs.278894	KIAA1482 protein	1	0.44	upregulate stage
	433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMAN A	5.45	0.12	upregulate stage
	433230	AW136134	Hs.220277	ESTs	7.3	0.09	upregulate stage
	433237	AB040930	Hs.297021	Homo sapiens cDNA FLJ13211 fis, clone NT	1	1	upregulate stage
70	433365	AF026944	Hs.293797	ESTs	4.95	0.08	upregulate stage
	433371	T25451		gb:PTH188 HTCDL1 Homo sapiens cDNA 5/3	4.75	0.12	upregulate stage
	433394	AI907753	Hs.93810	cerebral cavernous malformations 1	4.5	0.11	upregulate stage
	433424	R68252	Hs.163566	ESTs	1	1	upregulate stage
	433440	AF052127		gb:Homo sapiens clone 23850 mRNA sequenc	1	1	upregulate stage
75	433452	AW296906	Hs.142869	ESTs	9.82	0.08	upregulate stage
	433456	AA593447	Hs.124296	ESTs	9.45	0.08	upregulate stage
	433467	AI420457	Hs.50955	ESTs	1.11	0.74	upregulate stage
	433479	AW511459	Hs.245972	ESTs	3.35	0.13	upregulate stage

	433484	BE264397	Hs.148674	ESTs	1	0.27	upregulate stage
	433515	AA595800	Hs.190246	ESTs	3.05	0.14	upregulate stage
	433602	AI769948	Hs.24906	ESTs	1	1	upregulate stage
5	433613	AA836126	Hs.5669	ESTs	2.8	0.12	upregulate stage
	433625	AW955674	Hs.161762	ESTs	1	0.53	upregulate stage
	433658	L03678	Hs.156110	immunoglobulin kappa constant	9.65	0.05	upregulate stage
	433672	BE281165	Hs.288038	TLS-associated serine-arginine protein 1	7.9	0.08	upregulate stage
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	6.7	0.11	upregulate stage
10	433735	AA608955	Hs.109653	ESTs	8.95	0.08	upregulate stage
	433895	AI287912	Hs.3628	mitogen-activated protein kinase kinase	4.43	0.16	upregulate stage
	433904	AI399956	Hs.208956	ESTs	5.5	0.12	upregulate stage
	433929	AI375499	Hs.27379	ESTs	7	0.09	upregulate stage
	433966	AF113017	Hs.284301	PRO1268 protein	7.95	0.08	upregulate stage
	433967	AF113018	Hs.284302	PRO1621 protein	2.65	0.1	upregulate stage
15	434006	AF113688		gb:Homo sapiens clone FLB4630	7.85	0.08	upregulate stage
	434037	AF115601	Hs.283048	hypothetical protein PRO0128	8.81	0.09	upregulate stage
	434064	AL049045	Hs.180758	hypothetical protein PRO0082	8.35	0.09	upregulate stage
	434085	AF116673	Hs.250029	hypothetical protein PRO1925	1	1	upregulate stage
20	434092	AA625155		gb:at70d06.r1 Soares_NhHMPu_S1 Homo sapi	1	1	upregulate stage
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	11.5	0.06	upregulate stage
	434138	AA625804		gb:zu86h01.s1 Soares_testis_NHT Homo sap	3.55	0.11	upregulate stage
	434192	AW387314	Hs.34371	ESTs	1.65	0.22	upregulate stage
	434194	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	7.85	0.09	upregulate stage
	434217	AW014795	Hs.23349	ESTs	3.8	0.13	upregulate stage
25	434228	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	5.95	0.11	upregulate stage
	434271	AA897778	Hs.201677	ESTs	1	0.38	upregulate stage
	434280	BE005398		gb:CM1-BN0116-150400-189-h02 BN0116 Homo	9.45	0.07	upregulate stage
	434322	AI125686	Hs.152727	ESTs	2.65	0.18	upregulate stage
30	434351	AW974991	Hs.191852	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.61	upregulate stage
	434354	AW974912	Hs.292783	ESTs	1	1	upregulate stage
	434398	AA121098	Hs.3838	serum-inducible kinase	10.7	0.08	upregulate stage
	434464	BE063921	Hs.295971	ESTs	10.15	0.07	upregulate stage
	434466	AB037829	Hs.3862	regulator of nonsense transcripts 2; DKF	7.6	0.09	upregulate stage
	434484	W79839	Hs.104336	hypothetical protein	5.1	0.15	upregulate stage
35	434513	AF143888	Hs.18213	Homo sapiens clone IMAGE:121736 mRNA seq	1	1	upregulate stage
	434534	H90477	Hs.41407	ESTs	1	0.18	upregulate stage
	434540	NM_016045	Hs.5184	TH1 drosophila homolog	12.4	0.06	upregulate stage
	434569	AI311295	Hs.58609	ESTs	1.75	0.38	upregulate stage
	434575	AI133446	Hs.299964	ESTs	9.7	0.06	upregulate stage
40	434627	AI221894	Hs.39311	ESTs	1.65	0.17	upregulate stage
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	9	0.07	upregulate stage
	434663	AA641972	Hs.130058	ESTs	4.55	0.15	upregulate stage
	434731	AA648049	Hs.121518	ESTs	8.5	0.1	upregulate stage
	434765	AA831115	Hs.190473	ESTs	1	0.71	upregulate stage
45	434773	AA648962	Hs.152947	ESTs	10.55	0.08	upregulate stage
	434792	AA649253	Hs.132458	ESTs	5.45	0.11	upregulate stage
	434828	D90070	Hs.96	phorbol-12-myristate-13-acetate-induced	1	0.34	upregulate stage
	434876	AF160477	Hs.245781	Homo sapiens Ig superfamily receptor LNI	1.4	0.57	upregulate stage
50	434909	AI479212	Hs.17283	hypothetical protein FLJ10890	1	0.91	upregulate stage
	434926	BE543269	Hs.50252	Homo sapiens HSPC283 mRNA, partial cds	4.9	0.13	upregulate stage
	434939	AF161422	Hs.21590	Homo sapiens HSPC304 mRNA, partial cds	1	1	upregulate stage
	434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	10.75	0.07	upregulate stage
	434970	AW272262	Hs.250468	ESTs	9.05	0.08	upregulate stage
55	434980	AW770553	Hs.293640	ESTs	4.95	0.14	upregulate stage
	434997	AW975155	Hs.292163	ESTs	1	0.36	upregulate stage
	435013	H91923	Hs.110024	NADH:ubiquinone oxidoreductase MLRQ subu	1.16	0.71	upregulate stage
	435030	AI203316	Hs.148655	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.95	0.14	upregulate stage
	435047	AA454985	Hs.54973	cadherin-like protein VR20	3.31	0.2	upregulate stage
60	435061	AI651474	Hs.163944	ESTs	1.4	0.2	upregulate stage
	435080	AI831760	Hs.155111	ESTs	9.05	0.08	upregulate stage
	435087	AW975241	Hs.23567	ESTs	1	1	upregulate stage
	435108	AW975018	Hs.287440	Homo sapiens cDNA FLJ11692 fis, clone HE	1	0.2	upregulate stage
	435136	R27299	Hs.10172	ESTs	8.9	0.07	upregulate stage
65	435159	AA668879	Hs.116649	ESTs	1.35	0.25	upregulate stage
	435162	AI911044	Hs.213893	ESTs	1	1	upregulate stage
	435166	AI391470	Hs.158618	ESTs	5.5	0.12	upregulate stage
	435212	AW300100	Hs.164185	ESTs	1	1	upregulate stage
	435237	AI026836	Hs.114689	ESTs	8.75	0.1	upregulate stage
70	435255	W87434	Hs.105015	ESTs, Moderately similar to ALU1_HUMAN A	3.4	0.14	upregulate stage
	435256	AF193766	Hs.13872	cytokine-like protein C17	3.2	0.14	upregulate stage
	435257	AA677026	Hs.191217	ESTs	4.5	0.12	upregulate stage
	435298	AA677696	Hs.189196	ESTs	1	1	upregulate stage
	435307	W90610	Hs.192003	ESTs	1	0.87	upregulate stage
	435347	AW014873	Hs.116963	ESTs	2.45	0.14	upregulate stage
75	435382	N54493		gb:yy40g05.s1 Soares fetal liver spleen	1	0.56	upregulate stage
	435408	H07897	Hs.4302	ESTs	0.84	0.97	upregulate stage
	435491	T98543	Hs.191900	ESTs	1	0.3	upregulate stage

	435525	AI831297	Hs.123310	ESTs	3.25	0.15	upregulate stage
	435597	AW305188	Hs.163027	ESTs	1	0.57	upregulate stage
	435637	AF220051	Hs.110853	uncharacterized hematopoietic stem/proge	8.76	0.09	upregulate stage
5	435647	AI653240	Hs.49823	ESTs	3.19	0.25	upregulate stage
	435738	AA699633	Hs.269543	ESTs	2.9	0.16	upregulate stage
	435762	AW043836	Hs.212460	ESTs	1	1	upregulate stage
	435809	H90213	Hs.191330	ESTs	1.25	0.23	upregulate stage
	435826	AI554089	Hs.117880	ESTs	6.55	0.08	upregulate stage
10	435854	AJ278120	Hs.4996	DKFZP564D166 protein	2.76	0.29	upregulate stage
	435979	W03698	Hs.83513	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.25	upregulate stage
	435981	H74319	Hs.188620	ESTs	6.35	0.11	upregulate stage
	435990	AI015862	Hs.131793	ESTs	4.25	0.08	upregulate stage
	435999	AA703271	Hs.269903	ESTs, Moderately similar to ALU1_HUMAN A	1	1	upregulate stage
15	436016	AA806465	Hs.121536	ESTs	1.45	0.23	upregulate stage
	436023	T81819		gb:yd95f05.s1 Soares fetal liver spleen	9.15	0.07	upregulate stage
	436052	AI021983	Hs.271432	ESTs	1	0.23	upregulate stage
	436115	AW512033	Hs.102004	ESTs	1.9	0.21	upregulate stage
	436118	AI221173	Hs.145080	ESTs	1	1	upregulate stage
20	436120	AI248193	Hs.119860	ESTs	9.61	0.08	upregulate stage
	436149	AI754308	Hs.159452	ESTs	2.4	0.19	upregulate stage
	436156	AA705466	Hs.119900	ESTs	1	0.26	upregulate stage
	436170	AW450381	Hs.14529	ESTs	1	0.91	upregulate stage
	436202	AA706315	Hs.192057	ESTs	1	1	upregulate stage
25	436246	AW450963	Hs.119991	ESTs	3.85	0.11	upregulate stage
	436274	AA732755	Hs.120299	ESTs	2.85	0.13	upregulate stage
	436282	R91913	Hs.272104	ESTs	3.95	0.11	upregulate stage
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	6	0.09	upregulate stage
	436300	AA831601	Hs.275736	ESTs	1	1	upregulate stage
30	436326	BE085238	Hs.181244	major histocompatibility complex, class	2.49	0.28	upregulate stage
	436360	AI962796	Hs.136754	ESTs	2.4	0.17	upregulate stage
	436363	AA843926	Hs.124434	ESTs	3.35	0.1	upregulate stage
	436383	BE065178		gb:RC1-BT0314-020200-012-h01 BT0314 Homo	1	0.67	upregulate stage
	436396	AI683487	Hs.299112	Homo sapiens cDNA FLJ11441 fis, clone HE	4	0.15	upregulate stage
35	436408	AW274577	Hs.252954	ESTs	9.1	0.09	upregulate stage
	436422	AA716141	Hs.147027	ESTs	1	0.26	upregulate stage
	436429	AA357003	Hs.17546	hypothetical protein FLJ23499	1	1	upregulate stage
	436463	H06502	Hs.6656	ESTs	5.45	0.12	upregulate stage
	436476	AA326108	Hs.53631	ESTs, Weakly similar to enhancer-of-split	7.75	0.07	upregulate stage
40	436507	AA721209	Hs.201630	ESTs	2.45	0.18	upregulate stage
	436518	AA766433	Hs.122864	ESTs	3.15	0.21	upregulate stage
	436522	AA721381	Hs.129876	ESTs	4.75	0.1	upregulate stage
	436578	AI091435	Hs.134859	ESTs	3.4	0.12	upregulate stage
	436670	AI690021	Hs.201536	ESTs	6.85	0.11	upregulate stage
45	436740	AW975133		gb:EST387239 MAGE resequences, MAGN Homo	7.4	0.09	upregulate stage
	436764	AW976004	Hs.291731	ESTs	1	1	upregulate stage
	436785	AA745597	Hs.291400	ESTs	1	1	upregulate stage
	436823	AW749865	Hs.293645	ESTs	4.6	0.12	upregulate stage
	436831	AA830173	Hs.291918	ESTs	1.6	0.27	upregulate stage
50	436839	AA767346	Hs.291614	ESTs	1	1	upregulate stage
	436844	AA766458	Hs.122812	ESTs	1.5	0.28	upregulate stage
	436853	BE328074	Hs.148661	ESTs	5.05	0.14	upregulate stage
	436860	H12751	Hs.5327	PRO1914 protein	8.95	0.08	upregulate stage
	436925	AA742327	Hs.292687	ESTs	1	1	upregulate stage
55	437044	AL035864	Hs.69517	ESTs, Highly similar to differentially e	1.61	0.5	upregulate stage
	437087	AA745563		gb:ny60e04.s1 NCI_CGAP_Pr18 Homo sapiens	1	1	upregulate stage
	437144	AL049466	Hs.7859	ESTs	1	0.31	upregulate stage
	437170	R49202	Hs.181694	ESTs	8.7	0.08	upregulate stage
	437181	AI306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	4.4	0.05	upregulate stage
60	437207	T27503	Hs.15929	Homo sapiens cDNA FLJ12910 fis, clone NT	1.4	0.22	upregulate stage
	437214	BE092336		gb:IL2-BT0734-240400-072-A12 BT0734 Homo	5.65	0.09	upregulate stage
	437240	AA747537		gb:nx85c05.s1 NCI_CGAP_GCB1 Homo sapiens	1	0.45	upregulate stage
	437257	AI283085	Hs.290931	ESTs, Weakly similar to unknown [S.cerev	3.8	0.14	upregulate stage
	437258	AL041243	Hs.174104	ESTs	9.72	0.08	upregulate stage
65	437267	AW511443	Hs.258110	ESTs	4.25	0.12	upregulate stage
	437274	AA747965		gb:nx79a10.s1 NCI_CGAP_Ew1 Homo sapiens	1	0.19	upregulate stage
	437288	AA748182	Hs.160377	ESTs	1	0.61	upregulate stage
	437311	AA370041	Hs.9456	SWI/SNF related, matrix associated, acti	3.1	0.17	upregulate stage
	437324	AL162077		gb:Homo sapiens mRNA; cDNA DKFZp761A219	1	0.25	upregulate stage
70	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	7.95	0.07	upregulate stage
	437356	BE622396	Hs.284252	Homo sapiens mRNA; cDNA DKFZp762O1615 (f	1	1	upregulate stage
	437438	AL359620	Hs.14217	hypothetical protein DKFZp762P2111	9.15	0.09	upregulate stage
	437471	AL390169		gb:Homo sapiens mRNA; cDNA DKFZp547D064	1	1	upregulate stage
	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	1.1	0.56	upregulate stage
75	437567	AW627990	Hs.288954	Homo sapiens cDNA: FLJ21466 fis, clone C	1	1	upregulate stage
	437575	AW954355	Hs.36529	ESTs	10.25	0.06	upregulate stage
	437717	AA804765	Hs.132853	ESTs	1	0.77	upregulate stage
	437722	AW292947	Hs.122872	ESTs	9.75	0.05	upregulate stage

	437752	AA767376	Hs.291631	ESTs	6.7	0.08	upregulate stage
	437770	AA767881	Hs.122897	ESTs	2.57	0.24	upregulate stage
	437798	AW811767		gb:RC2-ST0165-300999-011-g02 ST0165 Homo	1	1	upregulate stage
	437799	RS1083	Hs.90787	ESTs	1	1	upregulate stage
5	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.sa	1.77	0.3	upregulate stage
	437886	BE264111	Hs.31314	retinoblastoma-binding protein 7	8.8	0.08	upregulate stage
	437887	AA811524	Hs.29263	Homo sapiens cDNA FLJ11896 fis, clone HE	3.8	0.17	upregulate stage
	437889	AA830524	Hs.124357	ESTs	1	0.69	upregulate stage
	437937	AI917222	Hs.121655	ESTs	1	0.38	upregulate stage
10	437938	AI950087		gb:wq05c02.x1 NCL_CGAP_Kid12 Homo sapien	1.37	0.52	upregulate stage
	437983	AI303023	Hs.30211	hypothetical protein FLJ22313	8.82	0.08	upregulate stage
	438011	BE466173	Hs.145696	splicing factor (CC1.3)	9	0.09	upregulate stage
	438032	BE045824	Hs.152992	ESTs	5.65	0.13	upregulate stage
	438069	N80701	Hs.33790	ESTs	3.25	0.13	upregulate stage
15	438077	AA777330	Hs.50429	ESTs	1	1	upregulate stage
	438081	H49546	Hs.298964	ESTs	3.75	0.11	upregulate stage
	438102	AA777793	Hs.137580	xylulokinase (H. Influenzae) homolog	1	1	upregulate stage
	438112	W85729	Hs.194279	ESTs	1	0.33	upregulate stage
	438113	AI467908	Hs.8882	ESTs	1.21	0.55	upregulate stage
20	438119	AW963217	Hs.203961	ESTs, Moderately similar to AF116721 89	11.75	0.07	upregulate stage
	438144	AA778894	Hs.118364	ESTs	1	1	upregulate stage
	438153	AI268632	Hs.146159	ESTs	1	1	upregulate stage
	438171	AW976507	Hs.293515	ESTs	2.82	0.24	upregulate stage
25	438271	L21934	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	1	1	upregulate stage
	438290	AA843719	Hs.122341	ESTs	3.9	0.13	upregulate stage
	438321	AA576635	Hs.6153	CGI-48 protein	9.4	0.08	upregulate stage
	438325	AA804258	Hs.123229	ESTs	4.65	0.11	upregulate stage
	438334	AA806992	Hs.291686	ESTs	1	1	upregulate stage
30	438366	AA805760		gb:ns43f01.s1 NCL_CGAP_GC81 Homo sapiens	1	0.34	upregulate stage
	438370	AA843242	Hs.48523	ESTs	4	0.14	upregulate stage
	438374	AA321866	Hs.6193	Homo sapiens mRNA; cDNA DKFZp434C1717 (f	1	0.84	upregulate stage
	438377	AA806070	Hs.291716	ESTs	1	0.24	upregulate stage
	438378	AW970529	Hs.86434	Homo sapiens cDNA: FLJ21816 fis, clone H	6.65	0.11	upregulate stage
35	438401	AL046321	Hs.197484	ESTs	1	1	upregulate stage
	438403	AA806607	Hs.292206	ESTs	2.75	0.14	upregulate stage
	438412	AA806776	Hs.130814	ESTs	1	1	upregulate stage
	438448	AA807344	Hs.172932	Homo sapiens mRNA for partial 3'UTR, seq	1	0.34	upregulate stage
	438451	AI081972	Hs.220261	ESTs	5.7	0.09	upregulate stage
40	438473	H07986	Hs.136901	ESTs	1	1	upregulate stage
	438487	AI684733	Hs.88820	HDCMC28P protein	1	0.21	upregulate stage
	438529	AW007287	Hs.28538	Homo sapiens cDNA: FLJ21086 fis, clone C	1	0.36	upregulate stage
	438534	AW204052	Hs.123644	ESTs	1	0.37	upregulate stage
	438693	AA814360	Hs.249595	ESTs	3.55	0.15	upregulate stage
45	438698	AW297855	Hs.125815	ESTs	3.12	0.22	upregulate stage
	438728	AA815202	Hs.25657	ESTs	1	0.67	upregulate stage
	438746	AI885815	Hs.184727	ESTs	1.5	0.35	upregulate stage
	438805	AA826048	Hs.117887	ESTs	9.35	0.07	upregulate stage
	438812	AA826199	Hs.44287	ESTs	1	0.57	upregulate stage
50	438817	AI023799	Hs.163242	ESTs	4.2	0.08	upregulate stage
	438886	AA827728	Hs.126705	ESTs, Weakly similar to AF149422 2 unkno	4.05	0.12	upregulate stage
	438913	AI380429	Hs.172445	ESTs	5.4	0.11	upregulate stage
	438950	H23789	Hs.144530	ESTs	1	1	upregulate stage
	438961	H42135	Hs.101848	ESTs	7.85	0.08	upregulate stage
55	438990	AF085890		gb:Homo sapiens full length insert cDNA	1	0.83	upregulate stage
	439026	R98978	Hs.117767	ESTs	1	0.27	upregulate stage
	439052	AF085917	Hs.37921	ESTs	1	0.22	upregulate stage
	439057	H59623	Hs.271561	ESTs	1	1	upregulate stage
	439176	AI446444	Hs.190394	ESTs	5.8	0.12	upregulate stage
60	439179	AA831250	Hs.292693	ESTs	1	1	upregulate stage
	439183	AW970600		gb:EST382681 MAGE resequences, MAGK Homo	4.5	0.13	upregulate stage
	439208	AK000299	Hs.180952	dynactin p62 subunit	11.9	0.06	upregulate stage
	439212	AF087995	Hs.134877	ESTs	11.4	0.07	upregulate stage
	439223	AW238299	Hs.23945	ESTs	2.79	0.26	upregulate stage
65	439312	AA833902	Hs.270745	ESTs	8.9	0.08	upregulate stage
	439330	AF086147		gb:Homo sapiens full length insert cDNA	1	0.19	upregulate stage
	439351	W37688	Hs.55158	ESTs, Weakly similar to weak similarity	1	0.31	upregulate stage
	439430	AF124250	Hs.6564	breast cancer anti-estrogen resistance 3	3.9	0.15	upregulate stage
	439444	AI277652	Hs.54578	ESTs	11	0.07	upregulate stage
70	439453	BE254974	Hs.6566	thyroid hormone receptor interactor 13	12.21	0.05	upregulate stage
	439476	AA836340	Hs.165490	ESTs	1	0.65	upregulate stage
	439492	AF086310	Hs.103159	ESTs	5.43	0.1	upregulate stage
	439527	AW298119	Hs.202536	ESTs	5.25	0.1	upregulate stage
	439550	H10438		gb:ym08d10.s1 Soares infant brain 1N18 H	3.2	0.18	upregulate stage
75	439560	BE555647	Hs.74899	hypothetical protein FLJ12820	1.81	0.32	upregulate stage
	439565	AF086386	Hs.145599	ESTs	8.96	0.07	upregulate stage
	439592	AF086413	Hs.58399	ESTs	1	1	upregulate stage
	439605	AF086431	Hs.134805	ESTs	9.15	0.09	upregulate stage

5	439606	W79123	Hs.58561	ESTs, Weakly similar to KI01_HUMAN PROBA	8.45	0.06	upregulate stage
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	5.43	0.14	upregulate stage
	439780	AL109688		gb:Homo sapiens mRNA full length insert	5	0.09	upregulate stage
	439851	AI149520	Hs.144453	ESTs	2.75	0.21	upregulate stage
	439862	AI571647	Hs.146170	hypothetical protein FLJ22969	6.3	0.11	upregulate stage
10	439926	AW014875	Hs.137007	ESTs	33.5	0.02	upregulate stage
	439942	AW993791	Hs.94881	ESTs	9.9	0.08	upregulate stage
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	5.59	0.15	upregulate stage
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	6.95	0.07	upregulate stage
	439987	AA860116	Hs.223232	ESTs	2.45	0.17	upregulate stage
15	439999	AA115811	Hs.6838	ras homolog gene family, member E	8.75	0.07	upregulate stage
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	1.68	0.41	upregulate stage
	440012	AA861072		gb:ak32e05.s1 Scores_testis_NHT Homo sap	1	1	upregulate stage
	440126	AA975145	Hs.66194	ESTs	1	1	upregulate stage
	440194	R43809	Hs.22688	ESTs	1	1	upregulate stage
20	440228	AF125392	Hs.7089	insulin induced protein 2	1	1	upregulate stage
	440249	AI246590	Hs.125325	ESTs	1.74	0.44	upregulate stage
	440284	AA912032	Hs.181059	ESTs	1	1	upregulate stage
	440334	BE276112	Hs.7165	zinc finger protein 259	9.45	0.09	upregulate stage
	440348	AW015802	Hs.47023	ESTs	1	0.33	upregulate stage
25	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	3.75	0.16	upregulate stage
	440366	F08229	Hs.125273	ESTs	3.5	0.12	upregulate stage
	440462	T71629	Hs.100554	ESTs	1.54	0.52	upregulate stage
	440527	AV657117	Hs.184164	ESTs	3.75	0.14	upregulate stage
	440613	AI733034	Hs.137079	ESTs	3.9	0.11	upregulate stage
30	440705	AA904244	Hs.153205	ESTs	3.9	0.14	upregulate stage
	440856	AW993377	Hs.130390	ESTs	8.95	0.09	upregulate stage
	440899	AW449445	Hs.172690	diacylglycerol kinase, alpha (80kD)	2.55	0.2	upregulate stage
	440917	AA909851	Hs.160025	ESTs	1	0.17	upregulate stage
	440980	AL042005	Hs.1117	tripeptidyl peptidase II	8.9	0.09	upregulate stage
35	440994	AI160011	Hs.193341	ESTs	1.29	0.58	upregulate stage
	441092	T99289	Hs.126556	EST	4.9	0.11	upregulate stage
	441107	AA917075	Hs.190520	ESTs	5.9	0.09	upregulate stage
	441131	AI733222	Hs.126632	ESTs	9.55	0.09	upregulate stage
	441143	AI027604	Hs.159650	ESTs	3.8	0.13	upregulate stage
40	441205	AW137827	Hs.176904	ESTs	4.75	0.12	upregulate stage
	441206	BE552314	Hs.131823	ESTs, Weakly similar to TERA HUMAN [H.s]	1	1	upregulate stage
	441264	AA927170	Hs.23290	ESTs	4.3	0.14	upregulate stage
	441318	AI078234	Hs.176130	ESTs	1.74	0.45	upregulate stage
	441334	AI700529	Hs.117954	ESTs	1	1	upregulate stage
45	441346	AA931077	Hs.186889	Homo sapiens cDNA FLJ12021 fis, clone HE	1	1	upregulate stage
	441378	AA931826	Hs.126846	ESTs	4.5	0.1	upregulate stage
	441383	AW294408	Hs.222058	ESTs	1	1	upregulate stage
	441421	AA356792	Hs.301786	ESTs	1	0.24	upregulate stage
	441470	BE503874	Hs.301986	ESTs	0.63	0.93	upregulate stage
50	441474	AW274946	Hs.144476	ESTs	1	1	upregulate stage
	441484	AA935481	Hs.58972	ESTs	1	0.33	upregulate stage
	441485	AI792988	Hs.189133	ESTs	4.25	0.1	upregulate stage
	441508	AW015203	Hs.232237	ESTs	1	1	upregulate stage
	441562	AW578981	Hs.52184	hypothetical protein FLJ20618	4.05	0.12	upregulate stage
55	441599	AW473352	Hs.127221	ESTs	1	0.29	upregulate stage
	441612	AI802629	Hs.113660	Homo sapiens cDNA FLJ11631 fis, clone HE	8.75	0.08	upregulate stage
	441616	BE569122	Hs.74111	RNA-binding protein (autoantigenic)	1.14	0.71	upregulate stage
	441643	AI740504	Hs.205128	ESTs	1	0.33	upregulate stage
	441677	AW271702	Hs.93739	ESTs	1	0.28	upregulate stage
60	441693	AA384673	Hs.7943	RPB5-mediating protein	1	0.43	upregulate stage
	441703	AW390054	Hs.192843	ESTs	9.85	0.08	upregulate stage
	441732	AW298818	Hs.127341	ESTs	4.6	0.14	upregulate stage
	441759	C16126	Hs.161377	ESTs	4.55	0.13	upregulate stage
	441762	AW592203	Hs.144769	ESTs	1	0.83	upregulate stage
65	441790	AW294909	Hs.132208	ESTs	9	0.08	upregulate stage
	441794	AW197794	Hs.253338	ESTs	4.5	0.12	upregulate stage
	441799	AW252276	Hs.127872	ESTs	1	0.22	upregulate stage
	441801	AW242799	Hs.211874	ESTs	8	0.06	upregulate stage
	441904	AI633205	Hs.128104	ESTs	2	0.19	upregulate stage
70	441955	AA972327	Hs.142903	ESTs	0.87	0.96	upregulate stage
	441989	AA306207	Hs.286241	Homo sapiens cDNA: FLJ22698 fis, clone H	9.17	0.07	upregulate stage
	441990	T66139	Hs.113631	ESTs	3.55	0.12	upregulate stage
	442029	AW956698	Hs.14456	neural precursor cell expressed, develop	4.65	0.14	upregulate stage
	442030	W67167	Hs.109080	ESTs	1	0.35	upregulate stage
75	442064	AI422867	Hs.88594	ESTs	8.8	0.08	upregulate stage
	442071	BE048433	Hs.276043	ESTs	9.15	0.09	upregulate stage
	442093	AA976049	Hs.128454	ESTs	1	1	upregulate stage
	442194	AA984389	Hs.205088	ESTs	1	0.83	upregulate stage
	442202	BE272862	Hs.106534	Homo sapiens cDNA: FLJ22625 fis, clone H	9.9	0.08	upregulate stage
	442203	AI921423	Hs.250146	ESTs	1	1	upregulate stage
	442214	AI681733	Hs.129003	ESTs	2.2	0.26	upregulate stage

	442216	AI733468	Hs.129006	ESTs	1	1	upregulate stage
	442295	AI827248	Hs.224388	Homo sapiens cDNA FLJ11469 fis, clone HE	1.49	0.31	upregulate stage
	442319	BE048144	Hs.177677	CGI-102 protein	1	0.29	upregulate stage
5	442432	BE093589	Hs.38178	Homo sapiens cDNA: FLJ23468 fis, clone H	22.95	0.03	upregulate stage
	442510	AF150179	Hs.249890	ESTs	1	0.63	upregulate stage
	442518	AF150226		gb:AF150226 Human mRNA from cd34+ stem c	1	1	upregulate stage
	442539	AL119506	Hs.58220	Homo sapiens cDNA: FLJ23005 fis, clone L	1	0.23	upregulate stage
	442552	R20624	Hs.83572	son of sevenless (Drosophila) homolog 1	9	0.08	upregulate stage
10	442562	BE379584	Hs.34789	ESTs	6.55	0.1	upregulate stage
	442564	AI590207	Hs.188378	ESTs	1	1	upregulate stage
	442577	AA292998	Hs.163900	ESTs	1.41	0.52	upregulate stage
	442590	AI002686	Hs.130313	ESTs	1	0.36	upregulate stage
	442597	AI499214	Hs.130925	ESTs	1	1	upregulate stage
15	442611	BE077155	Hs.177537	ESTs	4.35	0.15	upregulate stage
	442612	AI005233	Hs.130631	ESTs	1	0.28	upregulate stage
	442619	AA447492	Hs.20183	ESTs, Weakly similar to AF164793 1 prote	7.85	0.09	upregulate stage
	442642	R61853	Hs.226429	ESTs	1	1	upregulate stage
	442650	AW138174	Hs.130651	ESTs	4.1	0.09	upregulate stage
20	442696	BE566962	Hs.7063	Homo sapiens cDNA: FLJ20913 fis, clone A	2.65	0.16	upregulate stage
	442712	BE465168	Hs.131011	ESTs	2.51	0.23	upregulate stage
	442760	BE075297	Hs.10067	ESTs, Weakly similar to KIAA1205 protein	8	0.1	upregulate stage
	442769	AW243058	Hs.131155	ESTs	1	0.3	upregulate stage
	442785	AW296625	Hs.131188	ESTs	1	0.27	upregulate stage
	442806	AW294522	Hs.149991	ESTs	9.6	0.08	upregulate stage
25	442856	H56735	Hs.282958	Homo sapiens cDNA FLJ13611 fis, clone PL	4.3	0.11	upregulate stage
	442861	AA243837	Hs.57787	ESTs	3.9	0.12	upregulate stage
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	3.85	0.15	upregulate stage
	442879	AF032922	Hs.8813	synlaxin binding protein 3	3.95	0.14	upregulate stage
30	442883	AW195774	Hs.253199	ESTs	1	1	upregulate stage
	442961	BE614474	Hs.289074	Homo sapiens cDNA FLJ13986 fis, clone Y7	11.55	0.07	upregulate stage
	442966	AI394036	Hs.132237	ESTs, Weakly similar to dual specificity	2.95	0.16	upregulate stage
	442980	AA857025	Hs.8878	kinesin-like 1	1	0.24	upregulate stage
	442992	AI914699	Hs.13297	ESTs	6.1	0.14	upregulate stage
35	442994	AI026718	Hs.16954	ESTs	8.9	0.07	upregulate stage
	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	5.7	0.11	upregulate stage
	443113	AI040885	Hs.132908	ESTs	3.9	0.14	upregulate stage
	443119	AA312264	Hs.7980	ESTs, Moderately similar to ALU4_HUMAN A	8.73	0.08	upregulate stage
	443171	BE281128	Hs.9030	TONDU	3.18	0.22	upregulate stage
40	443211	AI128388	Hs.143655	ESTs	6.55	0.08	upregulate stage
	443242	BE243910	Hs.9082	nucleoporin p54	11.05	0.06	upregulate stage
	443243	AI452496	Hs.132056	ESTs	8.9	0.09	upregulate stage
	443247	BE614387	Hs.47378	ESTs, Moderately similar to hypothetical	10.95	0.05	upregulate stage
	443270	NM_004272	Hs.9192	Homer, neuronal immediate early gene, 1B	3.75	0.2	upregulate stage
45	443299	AI733642	Hs.133042	ESTs	1	0.69	upregulate stage
	443362	AI053464	Hs.166505	ESTs	2.9	0.16	upregulate stage
	443383	AI792453	Hs.166507	ESTs	5	0.14	upregulate stage
	443411	AW134566	Hs.65320	ESTs	1	0.59	upregulate stage
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	2.68	0.31	upregulate stage
50	443447	AI094222	Hs.166572	ESTs	1	0.38	upregulate stage
	443542	AI927065	Hs.146040	ESTs	5.65	0.13	upregulate stage
	443557	AV645987	Hs.145681	ESTs	1	1	upregulate stage
	443584	AI807036	Hs.101619	ESTs	1	0.36	upregulate stage
	443606	AI078654	Hs.199424	ESTs	1.15	0.33	upregulate stage
55	443634	H73972	Hs.134460	ESTs	3.05	0.16	upregulate stage
	443640	AI872643	Hs.134218	ESTs	3.65	0.12	upregulate stage
	443715	AI583187	Hs.9700	cyclin E1	5.65	0.11	upregulate stage
	443799	AA150320	Hs.9800	protein kinase Njmu-R1	1.8	0.19	upregulate stage
	443899	AW842283	Hs.79933	cyclin I	4.65	0.13	upregulate stage
60	443917	AW503739	Hs.72325	Human DNA sequence from clone RP1-187J11	1	1	upregulate stage
	443919	AI091284	Hs.135224	ESTs	8.05	0.07	upregulate stage
	443967	AW294013	Hs.200942	ESTs	5.55	0.13	upregulate stage
	443977	AL120986	Hs.150627	ESTs	4	0.14	upregulate stage
	443979	AV647366	Hs.282365	ESTs	1	1	upregulate stage
65	444020	R92962	Hs.35052	ESTs	10.45	0.08	upregulate stage
	444105	AW189097	Hs.166597	ESTs	6.29	0.1	upregulate stage
	444129	AW294292	Hs.256212	ESTs	1	0.77	upregulate stage
	444152	AI125694	Hs.149305	Homo sapiens cDNA FLJ14264 fis, clone PL	1.64	0.48	upregulate stage
	444163	AI126098		gb:qc54g07.x1 Soares_placenta_8to9weeks_	1.12	0.81	upregulate stage
70	444166	AV648429	Hs.282393	ESTs	1	1	upregulate stage
	444270	AI138580	Hs.255220	EST	1	0.47	upregulate stage
	444271	AW452569	Hs.149804	ESTs	3.2	0.12	upregulate stage
	444282	AI138955		gb:xd79b07.x1 Soares_testis_NHT Homo sap	1	1	upregulate stage
	444333	AI262567	Hs.253801	trinucleotide repeat containing 15	1	0.77	upregulate stage
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	6.9	0.06	upregulate stage
75	444378	R41339	Hs.12569	ESTs	1	0.32	upregulate stage
	444381	BE387335	Hs.283713	ESTs, Weakly similar to CA54_HUMAN COLLA	2.85	0.26	upregulate stage
	444431	AW513324	Hs.42280	ESTs	6.27	0.12	upregulate stage

	444437	AI377961	Hs.44041	ESTs	9.9	0.07	upregulate stage
	444444	AI149332	Hs.14855	ESTs	1.16	0.47	upregulate stage
	444525	AW593778	Hs.259699	ESTs	1	0.5	upregulate stage
5	444584	AI168422		gb:ok30e11.x1 Soares_NSF_F8_9W_OT_PA_P_S	3.6	0.15	upregulate stage
	444599	AI174377	Hs.143796	ESTs	1	0.44	upregulate stage
	444646	AI184565		gb:qd60b08.x1 Soares_testis_NHT Homo sap	1	1	upregulate stage
	444649	AW207523	Hs.197628	ESTs	9.35	0.06	upregulate stage
	444675	AI186380	Hs.244621	ESTs	9.88	0.08	upregulate stage
10	444698	AI188139	Hs.147050	ESTs	1	0.36	upregulate stage
	444743	AA045648	Hs.11817	nucleoside diphosphate linked moi	2.1	0.15	upregulate stage
	444762	AI733700	Hs.143883	ESTs	3.9	0.14	upregulate stage
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	1.44	0.53	upregulate stage
	444783	AK001468	Hs.52180	anillin (Drosophila Scraps homolog), act	6.65	0.07	upregulate stage
15	444838	AV651680	Hs.208558	ESTs	4.84	0.14	upregulate stage
	444849	AI199438	Hs.148480	ESTs	3.05	0.17	upregulate stage
	444950	AI950256	Hs.224875	ESTs	1	0.51	upregulate stage
	445027	AV652692	Hs.282498	ESTs	11.1	0.08	upregulate stage
	445091	AI652154	Hs.147294	ESTs	1	1	upregulate stage
20	445098	AL050272	Hs.12305	DKFZP566B183 protein	9.75	0.07	upregulate stage
	445101	T75202	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (f	10.9	0.07	upregulate stage
	445250	AI597838	Hs.175621	ESTs	9.8	0.08	upregulate stage
	445258	AI635931	Hs.147613	ESTs	3.05	0.13	upregulate stage
	445390	AI222165	Hs.144923	ESTs	10.6	0.06	upregulate stage
25	445396	BE181792		gb:CV1-HT0639-070500-193-g06 HT0639 Homo	1	0.29	upregulate stage
	445413	AA151342	Hs.12677	CGI-147 protein	4.65	0.12	upregulate stage
	445436	AI224105	Hs.151408	ESTs	1.35	0.22	upregulate stage
	445444	AA380876	Hs.270	pleckstrin homology, Sec7 and coiled/coi	10.7	0.07	upregulate stage
	445483	AI307150	Hs.148845	ESTs	1	1	upregulate stage
30	445496	AB007860	Hs.12802	development and differentiation enhancin	12.05	0.06	upregulate stage
	445525	BE149866	Hs.14831	ESTs	10.65	0.06	upregulate stage
	445527	W39694	Hs.83288	ESTs	4.85	0.1	upregulate stage
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	9.7	0.06	upregulate stage
	445546	AW468821	Hs.156054	ESTs	4.2	0.13	upregulate stage
	445576	AI793233	Hs.145608	ESTs	1	0.31	upregulate stage
35	445623	AI245366	Hs.149158	ESTs	1	1	upregulate stage
	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapi	4.7	0.13	upregulate stage
	445668	AI557114	Hs.181591	EST	1	0.34	upregulate stage
	445766	AI623607	Hs.282977	Homo sapiens cDNA FLJ13490 fis, clone PL	1	0.23	upregulate stage
40	445770	AL119499	Hs.13285	neuronal potassium channel alpha subunit	1	1	upregulate stage
	445778	AA196443	Hs.86043	Homo sapiens cDNA FLJ13558 fis, clone PL	9.7	0.07	upregulate stage
	445787	AI253167	Hs.145395	ESTs, Weakly similar to ALUC_HUMAN !!!	3.1	0.13	upregulate stage
	445814	H92020	Hs.101624	ESTs	1	1	upregulate stage
	445818	BE045321	Hs.136017	ESTs	1	1	upregulate stage
45	445829	AI452457	Hs.145526	ESTs	1	0.37	upregulate stage
	445832	AI261545		gb:qx30a07.x1 NCI_CGAP_Kid11 Homo sapien	3.21	0.22	upregulate stage
	445873	AA250970	Hs.251946	Homo sapiens cDNA: FLJ23107 fis, clone L	5.25	0.12	upregulate stage
	445880	AV655474	Hs.131058	ESTs	1.05	0.27	upregulate stage
	445883	AF070559	Hs.13413	Homo sapiens clone 24463 mRNA sequence	1	1	upregulate stage
50	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	3.25	0.15	upregulate stage
	445939	BE018658	Hs.141003	Homo sapiens cDNA: FLJ21691 fis, clone C	8.85	0.08	upregulate stage
	446019	AI362520	Hs.94133	ESTs	9.75	0.08	upregulate stage
	446054	AB014537	Hs.13604	KIAA0637 gene product	10.25	0.07	upregulate stage
	446062	AA211738	Hs.282974	ESTs, Weakly similar to transformation-r	1	1	upregulate stage
55	446080	AI221741	Hs.117777	ESTs	9.75	0.09	upregulate stage
	446082	AI274139	Hs.156452	ESTs	1.37	0.4	upregulate stage
	446099	T93096	Hs.17126	ESTs	2.4	0.31	upregulate stage
	446119	D29527		gb:HUMNK667 Human epidermal keratinocyte	1	1	upregulate stage
60	446120	N26080	Hs.43741	ESTs	1	0.31	upregulate stage
	446126	AW085909	Hs.47413	ESTs	9.35	0.08	upregulate stage
	446127	AA333608	Hs.13980	ubiquitously transcribed tetrapepti	1	0.25	upregulate stage
	446152	AI292036	Hs.150028	ESTs	4.7	0.12	upregulate stage
	446196	AI744888	Hs.149470	ESTs	1	0.83	upregulate stage
	446229	AI744954	Hs.14449	KIAA1609 protein	2.4	0.36	upregulate stage
65	446248	AI283014	Hs.149638	ESTs	1	1	upregulate stage
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	10.85	0.07	upregulate stage
	446303	X77244	Hs.14732	malic enzyme 1, NADP(+) dependent, cytos	1	1	upregulate stage
	446312	BE087853		gb:QV1-BT0681-290400-181-h05 BT0681 Homo	11.75	0.06	upregulate stage
	446332	AK001635	Hs.14838	hypothetical protein FLJ10773	6.45	0.1	upregulate stage
70	446356	AI816736	Hs.14896	DHHC1 protein	8.9	0.08	upregulate stage
	446362	AW612481	Hs.255914	ESTs	7.6	0.1	upregulate stage
	446398	AI681317	Hs.150074	ESTs	1	1	upregulate stage
	446411	AI298828	Hs.153439	ESTs	1	0.37	upregulate stage
	446474	AI301227	Hs.150186	ESTs	3.35	0.13	upregulate stage
	446501	AI302616	Hs.150819	ESTs	4.25	0.12	upregulate stage
75	446507	AA352554	Hs.15164	nuclear DNA-binding protein	11.25	0.06	upregulate stage
	446526	H89616	Hs.296290	Homo sapiens cDNA FLJ13357 fis, clone PL	10.25	0.07	upregulate stage
	446555	AV659046	Hs.201847	ESTs	1	1	upregulate stage

	446577	AB040933	Hs.15420	KIAA1500 protein	1	0.51	upregulate stage
	446629	AJ436046	Hs.156148	Homo sapiens cDNA: FLJ23082 fis, clone L	1	0.25	upregulate stage
	446636	AC002563	Hs.15767	cltron (rho-interacting, serine/threonin	2.54	0.28	upregulate stage
5	446682	AW205632	Hs.211198	ESTs	4	0.18	upregulate stage
	446701	AK001621	Hs.15921	hypothetical protein FLJ10759	1.32	0.69	upregulate stage
	446718	AV660019	Hs.282676	ESTs	1	1	upregulate stage
	446719	W39500	Hs.47305	ESTs, Weakly similar to LONN_HUMAN MITOC	9.65	0.07	upregulate stage
	446720	AI439136	Hs.140546	ESTs	4.55	0.12	upregulate stage
10	446765	AV660348	Hs.282688	ESTs	1	0.91	upregulate stage
	446771	AA128965	Hs.60679	TATA box binding protein (TBP)-associate	11.2	0.06	upregulate stage
	446821	W03766	Hs.301482	ESTs	8.9	0.09	upregulate stage
	446830	BE179030	Hs.64239	Human DNA sequence from clone RP5-1174N9	10.65	0.07	upregulate stage
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	14.05	0.05	upregulate stage
15	446853	AV660630	Hs.87627	disrupter of silencing 10	9.7	0.09	upregulate stage
	446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ12534 fis, clone NT	11.05	0.06	upregulate stage
	446922	BE175605		gb:RC5-HT0580-100500-022-H07 HT0580 Homo	2.75	0.16	upregulate stage
	446950	AA305800	Hs.293454	ESTs, Weakly similar to Similarity to Ye	9.6	0.06	upregulate stage
	446988	AW339533	Hs.272108	ESTs	1	0.29	upregulate stage
20	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	1.75	0.51	upregulate stage
	447052	AV661911	Hs.282735	ESTs	1	1	upregulate stage
	447065	AI829014	Hs.158678	ESTs	1	0.25	upregulate stage
	447069	AI359927	Hs.157722	ESTs	1	0.4	upregulate stage
	447078	AW885727	Hs.301570	ESTs	4.4	0.13	upregulate stage
25	447080	AI418781	Hs.300144	ESTs	1	0.31	upregulate stage
	447081	Y13896	Hs.17287	potassium inwardly-rectifying channel, s	3.55	0.12	upregulate stage
	447118	AB014599	Hs.17411	KJAA0699 protein	10.15	0.07	upregulate stage
	447153	AA805202	Hs.173912	eukaryotic translation initiation factor	6.2	0.12	upregulate stage
	447154	H52284	Hs.293545	ESTs	1	0.24	upregulate stage
30	447159	AI685286	Hs.280386	EST	1.25	0.25	upregulate stage
	447215	BE617056	Hs.283000	ESTs	2.4	0.16	upregulate stage
	447228	AW192200	Hs.158188	ESTs	1	0.29	upregulate stage
	447258	BE047911		gb:tz44a05.y1 NCI_CGAP_Bm52 Homo sapien	1.15	0.23	upregulate stage
	447286	AW197097	Hs.183858	transcriptional intermediary factor 1	1	1	upregulate stage
35	447289	AW247017	Hs.36978	melanoma antigen, family A, 3	1	1	upregulate stage
	447334	AA515032	Hs.91109	ESTs	9.15	0.08	upregulate stage
	447342	AI199268	Hs.19322	ESTs	5.95	0.09	upregulate stage
	447343	AA256641	Hs.236894	ESTs, Highly similar to LRP1_HUMAN LOW-D	2.11	0.33	upregulate stage
	447376	AI376747		gb:tc35h05.x1 Scores_total_fetus_Nb2HF8_	1	0.33	upregulate stage
40	447397	BE247676	Hs.18442	E-1 enzyme	5.3	0.14	upregulate stage
	447430	AI742989	Hs.206112	ESTs	3.65	0.13	upregulate stage
	447444	AK000318	Hs.18616	hypothetical protein FLJ20311	9.2	0.08	upregulate stage
	447519	U46258	Hs.23448	ESTs	14.4	0.05	upregulate stage
	447522	BE143888		gb:MR0-HT0165-081199-001-b04 HT0165 Homo	1.7	0.18	upregulate stage
45	447578	AA912347	Hs.136585	ESTs	1.5	0.3	upregulate stage
	447606	AI588954	Hs.170995	ESTs	2.7	0.16	upregulate stage
	447688	N87079	Hs.19236	NADH dehydrogenase (ubiquinone) 1 beta s	4.55	0.12	upregulate stage
	447701	BE619526	Hs.255527	ESTs, Weakly similar to unnamed protein	1.63	0.46	upregulate stage
	447741	AI421737	Hs.167253	ESTs	1	1	upregulate stage
50	447748	AI422023	Hs.161338	ESTs	3.9	0.11	upregulate stage
	447827	U73727	Hs.19718	protein tyrosine phosphatase, receptor t	1.44	0.59	upregulate stage
	447881	BE620886	Hs.23037	ESTs	12.15	0.06	upregulate stage
	447963	AI452973	Hs.165900	ESTs, Weakly similar to ALUC_HUMAN !!!!	8.9	0.08	upregulate stage
	447977	AI457097	Hs.255906	ESTs	1	1	upregulate stage
55	447978	AI457098	Hs.280848	ESTs	1	1	upregulate stage
	447982	H22953	Hs.137551	ESTs	4.25	0.13	upregulate stage
	448032	AW511770	Hs.246868	ESTs	1	1	upregulate stage
	448045	AJ297436	Hs.20166	prostate stem cell antigen	2.22	0.29	upregulate stage
60	448058	AI458998	Hs.170424	ESTs	1	0.51	upregulate stage
	448062	AW295923	Hs.255472	ESTs	5.9	0.08	upregulate stage
	448138	AW847925	Hs.170736	ESTs	1	1	upregulate stage
	448154	AL120320	Hs.203230	ESTs	9.85	0.07	upregulate stage
	448165	NM_005591	Hs.202379	metollic recombination (S. cerevisiae) 11	7.3	0.09	upregulate stage
	448168	AW605999	Hs.22549	hypothetical protein FLJ12799	1	0.77	upregulate stage
65	448236	AA890449	Hs.20766	oxysterol 7alpha-hydroxylase	1	0.47	upregulate stage
	448256	BE614149	Hs.20814	CGI-27 protein	11.95	0.07	upregulate stage
	448289	AW390251	Hs.202402	ESTs	1	0.47	upregulate stage
	448356	AL120837	Hs.20993	high-glucose-regulated protein 8	11	0.07	upregulate stage
	448357	N20169	Hs.108923	ESTs	1.34	0.61	upregulate stage
70	448408	AA322866	Hs.21107	neuroiligin	1.7	0.24	upregulate stage
	448455	AI252625	Hs.269860	ESTs	8.8	0.09	upregulate stage
	448459	AW069838	Hs.171055	ESTs	1	0.27	upregulate stage
	448464	AI522053	Hs.196093	ESTs	10.35	0.06	upregulate stage
	448468	BE560361	Hs.171072	ESTs	1	1	upregulate stage
75	448502	AW805285	Hs.239699	ESTs	9.3	0.08	upregulate stage
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	4.75	0.13	upregulate stage
	448556	AW885606	Hs.5064	ESTs	9.8	0.08	upregulate stage
	448569	BE382657	Hs.21486	signal transducer and activator of trans	2.14	0.35	upregulate stage

	448632	BE614269		gb:601504311T1 NIH_MGC_71 Homo sapiens c	1	1	upregulate stage
	448643	AI557531		gb:pt2.1-06.D06.r tumor2 Homo sapiens cD	3.6	0.14	upregulate stage
	448649	T94590	Hs.222855	ESTs	1.95	0.21	upregulate stage
5	448663	BE614599	Hs.105823	H.sapiens gene from PAC 42616, similar t	4.3	0.12	upregulate stage
	448680	AW245890	Hs.21753	JM5 protein	0.97	0.93	upregulate stage
	448725	AA193251	Hs.40289	ESTs	2.6	0.19	upregulate stage
	448729	BE614535	Hs.138580	ESTs, Weakly similar to ALUS_HUMAN ALU S	3.25	0.16	upregulate stage
	448743	AB032962	Hs.21896	KIAA1136 protein	1.9	0.19	upregulate stage
10	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	1.78	0.44	upregulate stage
	448914	AI927656	Hs.196459	ESTs	2.75	0.19	upregulate stage
	448946	AI652855	Hs.155796	ESTs	9.7	0.07	upregulate stage
	448958	AB020651	Hs.22653	KIAA0844 protein	1	0.18	upregulate stage
	448974	AL049390	Hs.22689	Homo sapiens mRNA; cDNA DKFZp586O1318 (f	5.85	0.11	upregulate stage
15	448979	AI611378	Hs.192610	ESTs	1	1	upregulate stage
	449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)	5.2	0.11	upregulate stage
	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	1	0.33	upregulate stage
	449053	AI625777	Hs.270344	ESTs	5.73	0.12	upregulate stage
	449057	AB037784	Hs.22941	KIAA1363 protein	9.25	0.07	upregulate stage
20	449148	AW836577	Hs.287564	Homo sapiens cDNA FLJ13345 fis, clone OV	7.2	0.09	upregulate stage
	449203	AI634578	Hs.282121	ESTs	7	0.1	upregulate stage
	449207	AL044222	Hs.23255	nucleoporin 155kD	2.34	0.36	upregulate stage
	449219	AI637581	Hs.195012	ESTs	1	1	upregulate stage
	449230	BE613348	Hs.23348	S-phase kinase-associated protein 2 (p45	3.08	0.25	upregulate stage
25	449246	AW411209	Hs.23363	hypothetical protein FLJ10983	4.79	0.16	upregulate stage
	449318	AW236021	Hs.108788	ESTs, Weakly similar to zeste [D.melanog	2.8	0.16	upregulate stage
	449328	AI962493	Hs.197647	ESTs	2.55	0.17	upregulate stage
	449343	AI151418	Hs.272458	protein phosphatase 3 (formerly 2B), cal	4.75	0.12	upregulate stage
	449344	AI640355		gb:wa17c04.x1 NCI_CGAP_Kid11 Homo sapien	2.1	0.22	upregulate stage
30	449351	AW016537	Hs.200760	ESTs	2.45	0.14	upregulate stage
	449370	AK002114	Hs.23495	hypothetical protein FLJ11252	1.55	0.14	upregulate stage
	449424	AW448937	Hs.197030	ESTs	4.05	0.12	upregulate stage
	449425	AW103433	Hs.195684	ESTs	4.6	0.12	upregulate stage
	449434	AW294858	Hs.197641	ESTs	1	0.29	upregulate stage
35	449437	AI702038	Hs.100057	Homo sapiens cDNA: FLJ22902 fis, clone K	2.38	0.34	upregulate stage
	449474	AA019344	Hs.2055	ubiquitin-activating enzyme E1 (A1S9T an	5.9	0.12	upregulate stage
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.45	0.1	upregulate stage
	449528	H63337	Hs.38178	Homo sapiens cDNA: FLJ23468 fis, clone H	2.85	0.18	upregulate stage
	449565	AI824925	Hs.197066	ESTs	1	1	upregulate stage
40	449568	AL157479	Hs.23740	KIAA1598 protein	10.15	0.06	upregulate stage
	449618	AB074659	Hs.14366	Homo sapiens cDNA FLJ12819 fis, clone NT	11.7	0.06	upregulate stage
	449639	AA001968	Hs.59956	ESTs, Highly similar to MGR7_HUMAN METAB	1	1	upregulate stage
	449666	AA002047		gb:zh84e05.r1 Soares_fetal_liver_spleen_	1.85	0.33	upregulate stage
	449704	AK000733	Hs.23900	GTPase activating protein	2.82	0.3	upregulate stage
45	449722	BE280074	Hs.23960	cyclin B1	6.44	0.12	upregulate stage
	449764	N93104	Hs.54895	ESTs, Weakly similar to ZNF91L [H.sapien	1	1	upregulate stage
	449784	AW161319	Hs.12915	ESTs	6.25	0.11	upregulate stage
	449829	N51440	Hs.47261	ESTs	1	0.57	upregulate stage
	449843	R85337	Hs.24030	solute carrier family 31 (copper transpo	10.2	0.07	upregulate stage
50	449892	N73608	Hs.50309	ESTs	6.5	0.1	upregulate stage
	449894	AK001578	Hs.24129	hypothetical protein FLJ10716	4.55	0.12	upregulate stage
	449919	AI674685	Hs.200141	ESTs	5.3	0.11	upregulate stage
	450020	AI680684	Hs.282219	ESTs	1	1	upregulate stage
	450033	R43010	Hs.269452	ESTs, Weakly similar to JH0148 nucleotin	1	0.65	upregulate stage
55	450063	AI681509	Hs.277133	ESTs	4.2	0.17	upregulate stage
	450083	AA131795	Hs.142001	ESTs	3.9	0.16	upregulate stage
	450116	AA005355	Hs.222882	ESTs	1	1	upregulate stage
	450121	AL040174	Hs.288927	Homo sapiens cDNA: FLJ22944 fis, clone K	1	1	upregulate stage
	450135	AI810816	Hs.201142	ESTs	4.95	0.14	upregulate stage
60	450144	T63961	Hs.301851	ESTs	2.75	0.13	upregulate stage
	450149	AW969781	Hs.293440	ESTs, Moderately similar to ZIC2 protein	3.75	0.14	upregulate stage
	450151	AI088196	Hs.295233	ESTs	2.51	0.28	upregulate stage
	450152	AI138635	Hs.22968	ESTs	2.45	0.15	upregulate stage
	450195	AA007352	Hs.256042	ESTs	4.1	0.14	upregulate stage
65	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	1	0.3	upregulate stage
	450238	T89693	Hs.138777	ESTs	12.2	0.07	upregulate stage
	450257	AW820313		gb:QV2-ST0296-150200-028-d02 ST0296 Homo	1	1	upregulate stage
	450313	AI038989	Hs.24809	hypothetical protein FLJ10826	4.35	0.15	upregulate stage
	450314	AA574309	Hs.283402	TCR eta	10.1	0.07	upregulate stage
70	450350	T97817	Hs.174880	ESTs	3.65	0.1	upregulate stage
	450411	D61167	Hs.202156	ESTs	1	0.67	upregulate stage
	450447	AF212223	Hs.25010	hypothetical protein P15-2	10.75	0.07	upregulate stage
	450448	D54299	Hs.36244	ESTs	1	1	upregulate stage
	450449	AI696596	Hs.202068	ESTs	1	1	upregulate stage
75	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	11.45	0.05	upregulate stage
	450573	AW964334		gb:EST376407 MAGC resequences, MAGH Homo	1.2	0.2	upregulate stage
	450628	AW382884	Hs.204715	ESTs	4.95	0.13	upregulate stage
	450636	AI703076	Hs.201959	ESTs	1	0.69	upregulate stage

	450655	AI707846	Hs.279860	hypothetical protein FLJ20030	1	1	upregulate stage
	450684	AA808358	Hs.36830	ESTs	1	0.34	upregulate stage
	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	9.51	0.09	upregulate stage
5	450722	AI732318	Hs.101120	ESTs	1	0.87	upregulate stage
	450751	AI733251	Hs.126853	ESTs, Weakly similar to JU0033 hypotheti	1	1	upregulate stage
	450772	BE326391	Hs.280146	ESTs, Weakly similar to JU0033 hypotheti	1	1	upregulate stage
	450800	BE395161	Hs.243963	ESTs, Weakly similar to ALU5_HUMAN ALU S	8.7	0.08	upregulate stage
	450824	R09055	Hs.269204	ESTs	3.03	0.22	upregulate stage
10	450832	AW970602	Hs.105421	ESTs	6.15	0.08	upregulate stage
	450870	AA011471		gb:z101h08.r1 Soares_fetal_liver_spleen_	1.15	0.23	upregulate stage
	450937	R49131	Hs.26267	ATP-dependant Interferon response protei	9.75	0.08	upregulate stage
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	3.32	0.26	upregulate stage
	451052	AA281504	Hs.24444	ESTs, Moderately similar to ALUE_HUMAN !	9.25	0.08	upregulate stage
15	451067	BE172186	Hs.180789	S164 protein	2.8	0.21	upregulate stage
	451088	AA015600	Hs.82415	ESTs	1	0.32	upregulate stage
	451094	AI949825	Hs.260395	ESTs	4.45	0.14	upregulate stage
	451096	BE383234	Hs.25925	Homo sapiens clone 23860 mRNA sequence	4.15	0.14	upregulate stage
	451126	H30600	Hs.40910	ESTs	1	1	upregulate stage
20	451161	AA211329	Hs.26006	hypothetical protein FLJ10559	2.15	0.16	upregulate stage
	451166	T98171	Hs.185675	ESTs	9.26	0.08	upregulate stage
	451222	AA018386	Hs.64341	ESTs	1	0.36	upregulate stage
	451225	AI433694	Hs.293608	ESTs	9.19	0.08	upregulate stage
	451228	AI767166	Hs.207025	ESTs	1	1	upregulate stage
25	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	7.35	0.11	upregulate stage
	451266	AA016292	Hs.290849	ESTs	1	0.33	upregulate stage
	451276	AW294386	Hs.236533	ESTs, Highly similar to dJ742C19.2 [H.sa	1	1	upregulate stage
	451277	AK001123	Hs.26176	hypothetical protein FLJ10261	11.7	0.06	upregulate stage
	451291	R39288	Hs.6702	ESTs	1	1	upregulate stage
30	451326	AW296946	Hs.300967	ESTs	10.55	0.07	upregulate stage
	451347	AI288679	Hs.101139	ESTs	1	1	upregulate stage
	451359	H85334		gb:ys90e05.r1 Soares retina N2b5HR Homo	2.7	0.15	upregulate stage
	451365	AI791783		gb:op20h10.y5 NCI_CGAP_Co12 Homo sapiens	8.9	0.09	upregulate stage
	451386	AB029006	Hs.26334	spastic paraplegia 4 (autosomal dominant	2.45	0.19	upregulate stage
35	451440	AA017599	Hs.293817	ESTs	1	1	upregulate stage
	451487	AA018072		gb:ze51g02.r1 Soares retina N2b5HR Homo	5.7	0.1	upregulate stage
	451492	AA018119	Hs.297824	ESTs, Highly similar to C1K1_HUMAN VOLTA	1	1	upregulate stage
	451495	H86887		gb:y07a01.r1 Soares retina N2b5HR Homo	4.25	0.13	upregulate stage
	451535	AW970577		gb:EST382658 MAGE resequences, MAGK Homo	6.8	0.12	upregulate stage
40	451553	AA018454	Hs.269211	ESTs, Weakly similar to B34087 hypotheti	1	1	upregulate stage
	451562	H04150	Hs.107708	ESTs	4.65	0.11	upregulate stage
	451580	AW138195	Hs.184326	CDC10 (cell division cycle 10, S. cerevi	1	0.42	upregulate stage
	451592	AI805416	Hs.213897	ESTs	2.8	0.17	upregulate stage
	451651	AI097337	Hs.88977	hypothetical protein dJ511E16.2	1	0.18	upregulate stage
45	451658	AW195351	Hs.250520	ESTs	9.55	0.07	upregulate stage
	451684	AF218751	Hs.26813	CDA14	3.7	0.15	upregulate stage
	451690	AW451469	Hs.209990	ESTs	10.86	0.07	upregulate stage
	451724	AI903765		gb:U1-BT037-301298-102 BT037 Homo saplen	8.85	0.09	upregulate stage
	451743	AW074266	Hs.23071	ESTs	2.17	0.35	upregulate stage
50	451794	AA019799	Hs.111911	ESTs	1	1	upregulate stage
	451844	T61430		gb:yc06a03.s1 Stratagene lung (937210) H	6.5	0.11	upregulate stage
	451903	W19617	Hs.261003	ESTs, Moderately similar to B34087 hypot	2.2	0.21	upregulate stage
	451914	AI822115	Hs.270618	ESTs, Weakly similar to KIAA0822 protein	11.67	0.07	upregulate stage
	451938	AI354355	Hs.16697	down-regulator of transcription 1, TBP-b	11.65	0.06	upregulate stage
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	1	0.95	upregulate stage
55	451971	AA021185	Hs.226306	ESTs	1	1	upregulate stage
	451998	AW594129	Hs.213666	ESTs	1	0.26	upregulate stage
	452028	AK001859	Hs.27595	hypothetical protein FLJ10997	1	0.21	upregulate stage
	452036	NM_003966	Hs.27621	sema domain, seven thrombospondin repeal	1.76	0.41	upregulate stage
60	452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	8.9	0.07	upregulate stage
	452122	AF216833	Hs.1710	ATP-binding cassette, sub-family B (MDR/	1	0.47	upregulate stage
	452163	AI863140		gb:tz43h12.x1 NCI_CGAP_Brn52 Homo sapien	1	0.2	upregulate stage
	452179	H16725	Hs.27463	ESTs	3	0.13	upregulate stage
	452198	AI097560	Hs.61210	ESTs	1	0.28	upregulate stage
65	452206	AW340281	Hs.33074	ESTs, Moderately similar to ALU1_HUMAN A	12.4	0.07	upregulate stage
	452234	AW084176	Hs.223296	ESTs	6.8	0.09	upregulate stage
	452240	AI591147	Hs.61232	ESTs	3.75	0.07	upregulate stage
	452247	AL137432	Hs.28564	hypothetical protein DKFZp761E1824	3.9	0.15	upregulate stage
	452250	BE618654	Hs.28507	hypothetical protein A-211C6.1	8.75	0.09	upregulate stage
70	452256	AK000933	Hs.28561	Homo sapiens cDNA FLJ10071 fis, clone HE	5.2	0.09	upregulate stage
	452266	AI767250	Hs.165240	ESTs	10.45	0.06	upregulate stage
	452277	AL049013	Hs.28783	KIAA1223 protein	8.9	0.05	upregulate stage
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	8.2	0.04	upregulate stage
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	3.5	0.13	upregulate stage
75	452328	AA805679	Hs.61271	ESTs	3.5	0.14	upregulate stage
	452331	AA598509	Hs.29117	H.sapiens mRNA for pur alpha extended 3'	11.75	0.07	upregulate stage
	452345	AA293279	Hs.29173	hypothetical protein FLJ20515	1.08	0.73	upregulate stage
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	10.15	0.07	upregulate stage

5	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	1	0.17	upregulate stage
	452404	AW450675	Hs.212709	ESTs	3.63	0.2	upregulate stage
	452430	AF118083	Hs.29494	PRO1912 protein	1	0.41	upregulate stage
	452436	BE077546	Hs.31447	ESTs	10	0.07	upregulate stage
	452457	AW052499		gb:MR0-CT0065-100899-001-d02 CT0065 Homo	1	0.13	upregulate stage
10	452461	N78223	Hs.108106	transcription factor	8.1	0.06	upregulate stage
	452518	AA280722	Hs.24758	ESTs	9.3	0.08	upregulate stage
	452519	BE008701		gb:RC0-BN0132-270300-021-a03 BN0132 Homo	1	0.19	upregulate stage
	452524	AW135499	Hs.29796	Homo sapiens mRNA; cDNA DKFZp434D1319 (f	1	0.45	upregulate stage
	452531	AA429462	Hs.293946	ESTs	2.94	0.22	upregulate stage
15	452547	AA335295	Hs.74120	adipose specific 2	1.51	0.53	upregulate stage
	452560	BE077084		gb:RCS-BT0603-220200-013-C07 BT0603 Homo	5.35	0.11	upregulate stage
	452571	W31518	Hs.34665	ESTs	2.55	0.11	upregulate stage
	452607	AJ160029	Hs.61438	ESTs	4.75	0.11	upregulate stage
	452677	BE167202	Hs.212065	ESTs	1	0.32	upregulate stage
20	452680	AW138410	Hs.45051	ESTs	1	1	upregulate stage
	452724	R84810	Hs.30464	cyclin E2	1	0.27	upregulate stage
	452738	AL133800		gb:DKFZp761A0614_r1 761 (synonym: hamy2)	3.45	0.15	upregulate stage
	452741	BE392914	Hs.30503	Homo sapiens cDNA FLJ111344 fis, clone PL	3.05	0.16	upregulate stage
	452747	BE153855	Hs.61460	ESTs	2.54	0.28	upregulate stage
25	452761	BE244742	Hs.30532	CGI-77 protein	3.85	0.14	upregulate stage
	452825	AJ921523		gb:wo26d09.x1 NCI_CGAP_Gas4 Homo sapiens	1	1	upregulate stage
	452831	AW864089	Hs.135145	ESTs	2.4	0.19	upregulate stage
	452846	AA082160	Hs.204295	ESTs	8.9	0.08	upregulate stage
	452850	H23230	Hs.22481	ESTs	4.75	0.14	upregulate stage
30	452859	AJ300555	Hs.288158	Homo sapiens cDNA: FLJ23591 fis, clone L	9.15	0.08	upregulate stage
	452862	AW378065	Hs.8587	ESTs	5.95	0.07	upregulate stage
	452899	M96739	Hs.30956	Human NSCL-1 mRNA sequence	1.04	0.9	upregulate stage
	452902	AJ926501	Hs.249729	ESTs	6.8	0.1	upregulate stage
	452909	NM_015368	Hs.30985	pannexin 1	5.6	0.1	upregulate stage
35	452931	AW190011	Hs.158006	hypothetical protein	1	0.53	upregulate stage
	452934	AA581322	Hs.4213	ESTs	1.44	0.55	upregulate stage
	452956	AW003578	Hs.231872	ESTs	1	0.22	upregulate stage
	452974	BE090803	Hs.61506	ESTs	1.75	0.18	upregulate stage
	453011	N62952	Hs.46473	ESTs	1	1	upregulate stage
40	453050	AW136479	Hs.224046	ESTs	1	0.39	upregulate stage
	453074	AA031813	Hs.271880	ESTs	1	1	upregulate stage
	453076	AJ978583	Hs.232161	ESTs	3.75	0.14	upregulate stage
	453123	AJ953718	Hs.221849	ESTs	6.6	0.11	upregulate stage
	453134	AA032211	Hs.118493	ESTs	1.68	0.42	upregulate stage
45	453135	T07886	Hs.31834	Homo sapiens clone 25129 mRNA sequence	1	1	upregulate stage
	453137	AJ954733	Hs.223640	ESTs	1	0.51	upregulate stage
	453144	AW268807	Hs.61646	ESTs	1	0.26	upregulate stage
	453153	N53893	Hs.24360	ESTs	5	0.13	upregulate stage
	453156	BE463762	Hs.223784	ESTs	2.8	0.15	upregulate stage
50	453204	R10799	Hs.191990	ESTs	9.5	0.05	upregulate stage
	453228	AW628325	Hs.232327	ESTs	1	1	upregulate stage
	453274	AA018511	Hs.32769	Homo sapiens mRNA full length insert cDN	1	1	upregulate stage
	453293	AA382267	Hs.10653	ESTs	8.4	0.09	upregulate stage
	453321	AJ984381	Hs.232521	ESTs	6.7	0.1	upregulate stage
55	453329	T97205	Hs.17998	ESTs	8.9	0.08	upregulate stage
	453389	BE273648	Hs.32963	cadherin 6, type 2, K-cadherin (fetal kd	1	0.18	upregulate stage
	453437	H10751	Hs.79981	Human clone 23560 mRNA sequence	1	0.83	upregulate stage
	453450	AW797627	Hs.89474	ADP-ribosylation factor 6	7.09	0.08	upregulate stage
	453459	BE047032	Hs.257789	ESTs	2.35	0.3	upregulate stage
60	453476	AJ840500	Hs.24633	SAM domain, SH3 domain and nuclear local	2.75	0.16	upregulate stage
	453651	AA971698	Hs.159397	x 010 protein	8.95	0.08	upregulate stage
	453653	AW505554	Hs.300284	ESTs	4.6	0.1	upregulate stage
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	3.4	0.1	upregulate stage
	453776	R15749	Hs.31677	ESTs	1	1	upregulate stage
65	453846	AL157586		gb:DKFZp761H0216_r1 761 (synonym: hamy2)	1	0.95	upregulate stage
	453884	AA355925	Hs.36232	KIAA0186 gene product	10.25	0.06	upregulate stage
	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	4.75	0.12	upregulate stage
	453913	AW004683	Hs.233502	ESTs	3.65	0.14	upregulate stage
	453925	AW021088	Hs.181614	ESTs	3.7	0.13	upregulate stage
70	453931	AL121278	Hs.25144	ESTs	3.45	0.18	upregulate stage
	453945	NM_005171	Hs.36908	activating transcription factor 1	6.35	0.12	upregulate stage
	454032	W31790	Hs.194293	ESTs	6.15	0.07	upregulate stage
	454049	AW022885		gb:dt45e05.y1 Morton Fetal Cochlea Homo	2.8	0.15	upregulate stage
	454069	AW025160	Hs.34161	ESTs, Moderately similar to ALU1_HUMAN A	1	0.32	upregulate stage
75	454099	AW082974		gb:IL1-ST0041-020899-001-H08 ST0041 Homo	1	1	upregulate stage
	454111	AW081681	Hs.269064	ESTs	2.8	0.18	upregulate stage
	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	9.4	0.05	upregulate stage
	454259	AL110136	Hs.47679	Homo sapiens mRNA; cDNA DKFZp564I112 (fr	6.2	0.11	upregulate stage
	454327	BE064097		gb:QV3-BT0297-231199-020-h08 BT0297 Homo	1	1	upregulate stage
	454331	AW372937		gb:QV3-BT0381-161299-042-a09 BT0381 Homo	1	0.43	upregulate stage
	454380	AW858722		gb:RC3-CT0347-281199-011-c04 CT0347 Homo	1	0.29	upregulate stage

5	454524	AW857191	gb:RC2-CT0304-080100-011-b12 CT0304 Homo	10.55	0.08	upregulate stage
	454592	AW810112	gb:MR4-ST0124-100400-006-e07 ST0124 Homo	1	0.37	upregulate stage
	454648	AW811960	gb:RC2-ST0168-240300-017-f09 ST0168 Homo	1	0.4	upregulate stage
	454687	AW814473	gb:MR3-ST0203-010200-109-c11 ST0203 Homo	1	1	upregulate stage
	454692	AW813350	gb:MR3-ST0192-100100-024-g07 ST0192 Homo	4.45	0.14	upregulate stage
10	454702	BE145915	gb:MR0-HT0208-221299-204-h08 HT0208 Homo	9.65	0.08	upregulate stage
	454729	AW817003	gb:QVO-ST0247-040100-081-f03 ST0247 Homo	1	0.8	upregulate stage
	454789	BE156314	gb:QVO-HT0367-150200-114-d02 HT0367 Homo	1	0.31	upregulate stage
	454797	BE161168	gb:PM0-HT0425-170100-002-a10 HT0425 Homo	4.1	0.14	upregulate stage
	454863	AW835610	gb:QV4-LT0016-090200-100-c02 LT0016 Homo	1	1	upregulate stage
15	454893	AW837753	gb:CM1-LT0042-310100-112-g03 LT0042 Homo	4.45	0.18	upregulate stage
	454898	AW838125	gb:QV2-LT0051-240300-097-e12 LT0051 Homo	1	1	upregulate stage
	454951	AW847464	gb:RC3-CT0208-270999-021-h12 CT0208 Homo	7.4	0.1	upregulate stage
	454956	AW847725	gb:IL3-CT0213-180200-041-H10 CT0213 Homo	1	0.23	upregulate stage
	455047	AW852530	gb:PM1-CT0243-071099-001-g06 CT0243 Homo	4.25	0.13	upregulate stage
20	455128	AW861555	gb:RC2-CT0321-110100-013-b05 CT0321 Homo	2.9	0.13	upregulate stage
	455201	AW847884	gb:PM1-MT0010-200300-001-g08 MT0010 Homo	3.15	0.16	upregulate stage
	455207	AW994394	gb:RC3-BN0036-060400-014-h12 BN0036 Homo	1	0.18	upregulate stage
	455331	AW897292	gb:CM0-NN0057-150400-338-b02 NN0057 Homo	1	0.87	upregulate stage
	455351	AW901942	gb:QVO-NN1022-100400-190-b04 NN1022 Homo	1	0.39	upregulate stage
25	455380	BE160188	gb:QV1-HT0413-010200-059-g05 HT0413 Homo	1.96	0.33	upregulate stage
	455414	AW936969	gb:RC1-DT0029-160200-013-f10 DT0029 Homo	1	1	upregulate stage
	455428	AW938204	gb:QVO-DT0048-170200-124-f01 DT0048 Homo	1	0.67	upregulate stage
	455573	BE004988	gb:MR2-BN0114-100500-020-b04 BN0114 Homo	1	1	upregulate stage
	455586	BE070794	gb:RC3-BT0501-130100-011-h02 BT0501 Homo	1	1	upregulate stage
30	455595	BE008343	gb:CM0-BN0154-080400-325-g10 BN0154 Homo	1	1	upregulate stage
	455610	BE011703	gb:CM3-BN0223-100500-177-h09 BN0223 Homo	6.05	0.12	upregulate stage
	455647	BE064415	gb:RC4-BT0311-241199-012-b03 BT0311 Homo	1	1	upregulate stage
	455650	BE064655	gb:RC1-BT0313-301299-012-c09 BT0313 Homo	1	0.67	upregulate stage
	455657	BE065209	gb:RC1-BT0314-310300-015-b12 BT0314 Homo	1.87	0.4	upregulate stage
35	455669	BE065903	gb:RC2-BT0318-241199-011-g02 BT0318 Homo	2.85	0.2	upregulate stage
	455678	BE066007	gb:RC3-BT0319-120200-014-d09 BT0319 Homo	2.8	0.18	upregulate stage
	455761	BE080895	gb:QV1-BT0631-280200-084-e01 BT0631 Homo	1	0.48	upregulate stage
	455799	BE169911	Hs.14570 Homo sapiens cDNA: FLJ22530 fis, clone H	5.7	0.11	upregulate stage
	455831	BE144966	gb:RC6-HT0187-201099-031-c04 HT0187 Homo	1	1	upregulate stage
40	455874	BE152283	gb:QV4-HT0316-191199-039-b01 HT0316 Homo	1	0.67	upregulate stage
	455903	BE155185	gb:PM1-HT0350-231299-005-g05 HT0350 Homo	1	0.31	upregulate stage
	455938	BE159432	gb:MR0-HT0407-140200-009-e06 HT0407 Homo	2.4	0.15	upregulate stage
	455950	BE161004	gb:PM0-HT0425-170100-002-h03 HT0425 Homo	1	0.44	upregulate stage
	455951	BE161001	gb:PM0-HT0425-170100-002-f10 HT0425 Homo	1	0.38	upregulate stage
45	455965	BE167014	gb:CM2-HT0502-140200-088-d08 HT0502 Homo	1	1	upregulate stage
	455981	BE177000	gb:RC4-HT0587-070400-015-b07 HT0587 Homo	1	0.57	upregulate stage
	456034	AW450979	gb:U1-H-B13-ala-a-12-0-U1.s1 NCL_CGAP_Su	8.29	0.05	upregulate stage
	456046	R51494	Hs.71818 ESTs	3.15	0.17	upregulate stage
	456122	R11813	gb:Yf53a04.r1 Soares Infant brain 1N18 H	1.3	0.31	upregulate stage
50	456212	N51636	gb:Yf87b01.s1 Soares_multiple_sclerosis_	4.45	0.14	upregulate stage
	456265	AJ968210	Hs.173623 ESTs	1	0.34	upregulate stage
	456285	R67585	Hs.268748 ESTs	1	0.83	upregulate stage
	456320	AJ734064	Hs.136212 ESTs	1	1	upregulate stage
	456353	AJ042330	Hs.87128 ESTs, Weakly similar to similar to YBS4	5.15	0.11	upregulate stage
55	456486	AA676544	Hs.171545 HIV-1 Rev binding protein	1	0.27	upregulate stage
	456493	AA261830	gb:z517g09.r1 NCL_CGAP_GCB1 Homo sapiens	1	0.8	upregulate stage
	456504	AK000532	Hs.98491 Homo sapiens cDNA FLJ20525 fis, clone KA	1	0.29	upregulate stage
	456508	AA502764	Hs.123469 ESTs, Weakly similar to AF208855 1 BM-01	17.7	0.05	upregulate stage
	456519	AA279917	Hs.88678 ESTs, Weakly similar to Unknown [H.sapie	2.3	0.18	upregulate stage
60	456536	AW135986	Hs.257859 ESTs	9.45	0.06	upregulate stage
	456592	R91600	gb:Yf10c02.r1 Soares fetal liver spleen	4.5	0.14	upregulate stage
	456621	T35958	Hs.107614 DKFZP564I1171 protein	1	0.2	upregulate stage
	456682	AW500321	Hs.246766 Homo sapiens cDNA FLJ12360 fis, clone MA	1	0.24	upregulate stage
	456726	H43102	Hs.144183 ESTs	1	0.69	upregulate stage
65	456736	AW248217	Hs.1619 achaete-scute complex (Drosophila) homol	0.89	0.91	upregulate stage
	456786	AK002084	Hs.132851 hypothetical protein FLJ11222	3.2	0.13	upregulate stage
	456800	AL118754	gb:DKFZp761P1910_r1 761 (synonym: hamy2)	1	0.69	upregulate stage
	456823	AL161979	Hs.146128 Homo sapiens mRNA; cDNA DKFZp761G1823 (f	8.95	0.07	upregulate stage
	456844	AJ264155	Hs.152981 CDP-diacylglycerol synthase (phosphatida	5.55	0.1	upregulate stage
70	456999	AA319798	Hs.172247 eukaryotic translation elongation factor	11.3	0.07	upregulate stage
	457015	AA688058	Hs.261544 ESTs	9.25	0.08	upregulate stage
	457030	AJ301740	Hs.173381 dihydropyrimidinase-like 2	2.65	0.17	upregulate stage
	457158	AA135370	Hs.188536 Homo sapiens cDNA: FLJ21635 fis, clone C	1	1	upregulate stage
	457190	AJ753247	Hs.29643 Homo sapiens cDNA FLJ13103 fis, clone NT	1	0.87	upregulate stage
75	457309	AF131843	Hs.239340 Homo sapiens clone 24987 mRNA sequence	2.6	0.15	upregulate stage
	457376	AJ026984	Hs.293662 ESTs	1	1	upregulate stage
	457402	AW452648	Hs.149342 activation-induced cytidine deaminase	2.9	0.16	upregulate stage
	457435	AW972024	Hs.154645 ESTs, Weakly similar to tyrosine kinase	1	0.36	upregulate stage
	457437	AW969732	gb:EST381810 MAGE resequences, MAGK Homo	2.5	0.14	upregulate stage
	457465	AW301344	Hs.195969 ESTs	6.3	0.1	upregulate stage
	457467	AW974815	Hs.292786 ESTs	1	1	upregulate stage

	457474	AW972935		gb:EST385031 MAGE resequences, MAGM Homo	1	0.29	upregulate stage
	457530	AW973713	Hs.293596	ESTs	1	0.39	upregulate stage
	457637	AI288373	Hs.149875	ESTs	1	1	upregulate stage
5	457643	AI375499	Hs.27379	ESTs	3.25	0.19	upregulate stage
	457650	AA649162	Hs.236456	ESTs	8.9	0.08	upregulate stage
	457661	AA917801	Hs.128596	ESTs	0.96	0.9	upregulate stage
	457692	AA744046	Hs.133350	ESTs	1	1	upregulate stage
	457857	AW814892	Hs.273104	ESTs	1	1	upregulate stage
10	457892	AA744389		gb:ny51e10.s1 NCL_CGAP_Pr18 Homo sapiens	8.7	0.06	upregulate stage
	457902	AI624876	Hs.75862	MAD (mothers against decapentaplegic, Dr	2.2	0.21	upregulate stage
	457943	AA765625	Hs.155690	ESTs	3.55	0.1	upregulate stage
	457948	AI498640	Hs.159354	ESTs	2.65	0.19	upregulate stage
	457964	NM_016353	Hs.5943	rec	1.5	0.17	upregulate stage
	458004	AW976942	Hs.153057	ESTs	1	0.87	upregulate stage
15	458027	L49054	Hs.85195	ESTs, Highly similar to t(3;5)(q25.1;p34	3.45	0.12	upregulate stage
	458079	AI796870	Hs.54277	ESTs	11.5	0.05	upregulate stage
	458158	AW296778	Hs.300357	ESTs, Highly similar to dJ416F21.2 [H.sa	1	1	upregulate stage
	458171	AI420016	Hs.192090	ESTs	0.69	1.09	upregulate stage
20	458172	BE007237		gb:PM0-BN0139-050500-003-g09 BN0139 Homo	3	0.16	upregulate stage
	458186	AA904244	Hs.153205	ESTs	4.6	0.15	upregulate stage
	458242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ121869 fis, clone H	3.1	0.16	upregulate stage
	458270	T66139	Hs.113631	ESTs	1	0.67	upregulate stage
	458282	AA984075	Hs.22580	alkylglycerone phosphate synthase	1	1	upregulate stage
25	458287	AA987556	Hs.12867	ESTs	5.05	0.13	upregulate stage
	458580	Z30118	Hs.293788	ESTs, Moderately similar to unnamed prot	1	0.28	upregulate stage
	458586	AI683479	Hs.65390	ESTs	8.2	0.07	upregulate stage
	458608	AW444662	Hs.202247	ESTs	1	0.27	upregulate stage
	458632	AI744445	Hs.24650	Homo sapiens cDNA FLJ13047 fis, clone NT	1.05	0.23	upregulate stage
30	458663	AV658444	Hs.280776	Homo sapiens cDNA FLJ13684 fis, clone PL	5.05	0.13	upregulate stage
	458670	AI301987	Hs.233398	ESTs	8.9	0.08	upregulate stage
	458680	N73773	Hs.282950	ESTs	1	0.23	upregulate stage
	458720	AV662037	Hs.124740	ESTs	1	0.3	upregulate stage
	458722	AA741545	Hs.282832	ESTs	3.2	0.11	upregulate stage
35	458747	BE618395	Hs.257391	ESTs, Weakly similar to GTPase-activatin	3.3	0.14	upregulate stage
	458760	AI498631	Hs.111334	fertilin, light polypeptide	11	0.07	upregulate stage
	458781	AI444821		gb:RET487 subtracted retina cDNA library	6.05	0.12	upregulate stage
	458801	N98648	Hs.276860	ESTs	4.45	0.13	upregulate stage
	458880	AA046742		gb:z48c09.r1 Soares retina N2b4HR Homo	9	0.08	upregulate stage
40	458886	AI247487	Hs.103277	ESTs	1	0.3	upregulate stage
	458946	AA009716	Hs.42311	ESTs	8.7	0.08	upregulate stage
	459023	AW968226	Hs.60798	ESTs	2.95	0.15	upregulate stage
	459028	AI940577		gb:IL5-HT0009-120799-001-G07 HT0009 Homo	2.6	0.17	upregulate stage
	459030	H86658	Hs.107699	ESTs, Weakly similar to hypothetical pro	1	1	upregulate stage
45	459058	H85939	Hs.209605	ESTs	1	1	upregulate stage
	459128	AI902169		gb:IL-BT002-221198-051 BT002 Homo sapien	1	0.26	upregulate stage
	459182	BE178517		gb:PM1-HT0603-090300-001-e09 HT0603 Homo	1	1	upregulate stage
	459204	AW194501	Hs.13219	ESTs	2.85	0.16	upregulate stage
	459256	AW967468	Hs.99821	Homo sapiens mRNA; cDNA DKFZp564C046 (fr	10.65	0.07	upregulate stage
50	459319	NM_000059		gb:Homo sapiens breast cancer 2, early o	1	1	upregulate stage
	459395	Z30300	Hs.281935	ESTs	4.05	0.14	upregulate stage
	459459	AA460445		gb:zx66h11.r1 Soares_total_fetus_Nb2HF8_	4.8	0.13	upregulate stage
	459464	AA854847		gb:aj77h02.s1 Soares_parathyroid_tumor_N	1	0.38	upregulate stage
	459492	AL118619		gb:DKFZp761E2410_r1 761 (synonym: hamy2)	1	1	upregulate stage
55	459530	AW770811		gb:h49d07.x1 NCL_CGAP_Co17 Homo sapiens	1	1	upregulate stage
	401519				12.65	0.06	upregulate stage
	402474				25.55	0.03	upregulate stage
	402727				16.25	0.05	upregulate stage
	405411				12.95	0.05	upregulate stage
60	406636	L12064		gb:Homo sapiens (clone WR4.12VL) anti-th	14.42	0.03	upregulate stage
	406685	M18728		gb:Human nonspecific crossreacting antig	15.75	0.03	upregulate stage
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	16.3	0.04	upregulate stage
	407242	M18728		gb:Human nonspecific crossreacting antig	12.58	0.03	upregulate stage
	407347	AA829847	Hs.167347	ESTs, Weakly similar to ALU8_HUMAN ALU S	12.91	0.06	upregulate stage
65	407796	AA195509	Hs.272239	lymphocyte activation-associated protein	14.2	0.06	upregulate stage
	408243	Y00787	Hs.624	interleukin 8	18.52	0.02	upregulate stage
	408380	AF123050	Hs.44532	diubiquitin	16	0.03	upregulate stage
	408618	AK000637	Hs.46624	HSPC043 protein	12.6	0.06	upregulate stage
	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	15.5	0.03	upregulate stage
70	409417	AA156247	Hs.295908	ESTs, Weakly similar to ALU7_HUMAN ALU S	12.55	0.04	upregulate stage
	410315	AI638871	Hs.17625	ESTs	14	0.05	upregulate stage
	410324	AW292539	Hs.30177	ESTs	15.65	0.05	upregulate stage
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	12.6	0.05	upregulate stage
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	16.45	0.03	upregulate stage
	413281	AA861271	Hs.34396	ESTs	12.95	0.04	upregulate stage
75	414004	AA737033	Hs.7155	ESTs, Weakly similar to 2115357A TYK1 pr	15.25	0.04	upregulate stage
	414161	AA136106	Hs.184852	KIAA1553 protein	13.25	0.06	upregulate stage
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	12.5	0.05	upregulate stage

	414219	W20010	Hs.75823	ALL-1-fused gene from chromosome 1q	12.71	0.05	upregulate stage
	414493	AL133921	Hs.76272	retinoblastoma-binding protein 2	13.05	0.05	upregulate stage
	414522	AW518944	Hs.76325	Homo sapiens cDNA: FLJ23125 fis, clone L	30.45	0.02	upregulate stage
5	414602	AW630088	Hs.76550	Homo sapiens mRNA: cDNA DKFZp564B1264 (f	29	0.02	upregulate stage
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	13.2	0.05	upregulate stage
	416114	AI695549	Hs.183868	glucuronidase, beta	14.7	0.04	upregulate stage
	416179	R19015	Hs.79067	MAD (mothers against decapentaplegic, Dr	13	0.06	upregulate stage
	416391	AI878927	Hs.79284	mesoderm specific transcript (mouse) hom	13.3	0.04	upregulate stage
10	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	15.55	0.04	upregulate stage
	416980	AA381133	Hs.80684	high-mobility group (nonhistone chromoso	23.85	0.03	upregulate stage
	417258	N58885	Hs.294040	ESTs	15.05	0.06	upregulate stage
	417274	N92036	Hs.81848	RAD21 (S. pombe) homolog	23.05	0.04	upregulate stage
	417353	AA375752	Hs.76362	general transcription factor IIA, 2 (12k	13	0.05	upregulate stage
15	417615	BE548641	Hs.82314	hypoxanthine phosphoribosyltransferase 1	19.45	0.04	upregulate stage
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	12.45	0.03	upregulate stage
	417777	AI823763	Hs.7055	ESTs	12.6	0.06	upregulate stage
	417821	BE245149	Hs.82643	protein tyrosine kinase 9	20.8	0.04	upregulate stage
	417928	AA209344	Hs.282973	ESTs	14.65	0.05	upregulate stage
20	418699	BE539639	Hs.173030	ESTs, Weakly similar to ALU8_HUMAN ALU S	13	0.05	upregulate stage
	418791	AA935633	Hs.194628	ESTs	12.95	0.06	upregulate stage
	419145	N99638		gb2a39g11.1 r1 Soares fetal liver spleen	13.2	0.05	upregulate stage
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	12.6	0.05	upregulate stage
	422150	AI867118	Hs.2953	ribosomal protein S15a	13.55	0.05	upregulate stage
25	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	15.7	0.05	upregulate stage
	424673	AA345051	Hs.294092	ESTs	16.9	0.04	upregulate stage
	424848	AI263231	Hs.145607	ESTs	15.2	0.05	upregulate stage
	424865	AF011333	Hs.153563	lymphocyte antigen 75	12.85	0.04	upregulate stage
	425053	AF046024	Hs.154320	ubiquitin-activating enzyme E1C (homolog	13.25	0.06	upregulate stage
30	425787	AA363867	Hs.155029	ESTs	17.55	0.05	upregulate stage
	426252	BE176980	Hs.28917	ESTs	12.95	0.05	upregulate stage
	426329	AL389951	Hs.271623	nucleoporin 50kD	13.8	0.05	upregulate stage
	427127	AW802282	Hs.22265	pyruvate dehydrogenase phosphatase	13.85	0.05	upregulate stage
	427351	AW402593	Hs.123253	Homo sapiens cDNA: FLJ22009 fis, clone H	12.8	0.06	upregulate stage
35	427979	BE379776	Hs.181309	proteasome (prosome, macropain) subunit,	16.95	0.05	upregulate stage
	428044	AA093322	Hs.182225	RNA binding motif protein 3	14.65	0.05	upregulate stage
	428428	AL037544	Hs.184298	cyclin-dependent kinase 7 (homolog of Xa	17.15	0.05	upregulate stage
	428840	M15590	Hs.194148	v-yes-1 Yamaguchi sarcoma viral oncogene	16.8	0.05	upregulate stage
	430191	AI149880	Hs.188809	ESTs	14.5	0.05	upregulate stage
40	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	14.9	0.05	upregulate stage
	430853	AI734179	Hs.105676	ESTs	13.55	0.06	upregulate stage
	431049	AA846576	Hs.103267	hypothetical protein FLJ22548 similar to	16.2	0.04	upregulate stage
	431211	M86849	Hs.5566	gap junction protein, beta 2, 26kD (conn	27	0.01	upregulate stage
	431341	AA307211	Hs.251531	proteasome (prosome, macropain) subunit,	13.45	0.06	upregulate stage
45	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	21.2	0.03	upregulate stage
	431770	BE221880	Hs.268555	5'-3' exonuclease 2	13.05	0.06	upregulate stage
	431863	AA188185	Hs.271871	spindlin	15.6	0.05	upregulate stage
	434263	N34895	Hs.44648	ESTs	14.25	0.05	upregulate stage
	434651	BE616902	Hs.285313	core promoter element binding protein	17.95	0.05	upregulate stage
50	436286	AA804442	Hs.3459	Homo sapiens cDNA: FLJ22003 fis, clone H	14.95	0.05	upregulate stage
	436385	BE551618	Hs.144097	ESTs	13.85	0.06	upregulate stage
	437192	AW975786	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	12.75	0.06	upregulate stage
	438000	AI825880	Hs.5985	non-kinase Cdc42 effector protein SPEC2	15.3	0.04	upregulate stage
	439941	AI392640	Hs.18272	ESTs	17.42	0.05	upregulate stage
55	440086	NM_005402	Hs.288757	v-rat simian leukemia viral oncogene hom	12.59	0.05	upregulate stage
	440116	AI798851	Hs.9403	ESTs	14.5	0.05	upregulate stage
	441020	W79283	Hs.35962	ESTs	12.4	0.04	upregulate stage
	441633	AW958544	Hs.112242	ESTs	15.85	0.03	upregulate stage
	441980	AK001441	Hs.8055	hypothetical protein FLJ10579	13.6	0.05	upregulate stage
60	442043	BE567620	Hs.99210	ESTs	12.5	0.06	upregulate stage
	442053	R35343	Hs.24968	Human DNA sequence from clone RP1-233G16	12.65	0.06	upregulate stage
	442271	AF000652	Hs.8180	syndecan binding protein (syntenin)	15.15	0.05	upregulate stage
	443303	U67319	Hs.9216	caspase 7, apoptosis-related cysteine pr	13.4	0.05	upregulate stage
	445033	AV652402	Hs.155145	ESTs	13.3	0.05	upregulate stage
65	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	30.5	0.02	upregulate stage
	446847	T51454	Hs.82845	Human clone Z3815 mRNA sequence	13.8	0.04	upregulate stage
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	15.15	0.04	upregulate stage
	448712	W01046	Hs.181634	Homo sapiens cDNA: FLJ23602 fis, clone L	13.2	0.05	upregulate stage
	448772	AW390822	Hs.24639	ESTs	12.75	0.06	upregulate stage
70	448926	AI798164	Hs.140903	ESTs, Moderately similar to neuronal thr	13.35	0.06	upregulate stage
	449962	AA004879	Hs.187820	ESTs	12.79	0.05	upregulate stage
	450139	AK001838	Hs.296323	Homo sapiens cDNA FLJ10976 fis, clone PL	14.76	0.06	upregulate stage
	451035	AU076785	Hs.430	plastin 1 (I isoform)	17.65	0.04	upregulate stage
	451334	AI122691	Hs.13268	ESTs	14.7	0.05	upregulate stage
75	452567	D87120	Hs.29882	predicted osteoblast protein	12.45	0.06	upregulate stage
	453258	AW293134	Hs.32597	ring finger protein (C3H2C3 type) 6	13.4	0.05	upregulate stage
	453331	AI240655	Hs.8895	ESTs	12.6	0.05	upregulate stage
	400365	Y10259	Hs.274501	H.sapiens ACTH receptor mRNA 3'UTR	2.2	0.17	upregulate stage

401256				2	0.16	upregulate stage
402075				1	0.1	upregulate stage
403029				1.75	0.16	upregulate stage
403047				3.3	0.1	upregulate stage
403426				1.7	0.18	upregulate stage
403754				2.8	0.12	upregulate stage
403822				1.2	0.14	upregulate stage
407835	AK002081	Hs.40337	hypothetical protein	1.9	0.15	upregulate stage
407980	AA046309		gb:zf12f01.s1 Soares_fetal_heart_NbHH19W	1.35	0.1	upregulate stage
408081	AW451597	Hs.167409	ESTs	2.3	0.18	upregulate stage
408408	AF070571	Hs.44690	Homo sapiens clone 24739 mRNA sequence	1.65	0.12	upregulate stage
408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	1	0.2	upregulate stage
409810	AW500895		gb:U1-HF-BPOp-air-a-02-Q-U1.r1 NIH_MGC_5	2.25	0.2	upregulate stage
410094	BE147897	Hs.58593	general transcription factor IIF, polype	4.05	0.12	upregulate stage
410603	AA086219	Hs.68714	ESTs	1.9	0.18	upregulate stage
410763	AF279145	Hs.8966	tumor endothelial marker 8	4.15	0.13	upregulate stage
411418	BE241870		gb:TCAAP2E0047 Pediatric acute myelogeno	1.6	0.22	upregulate stage
411691	AW857199		gb:RC2-CT0304-080100-011-106 CT0304 Homo	1.45	0.24	upregulate stage
411750	BE562298	Hs.71827	KIAA0112 protein; homolog of yeast ribos	2.2	0.2	upregulate stage
411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	1.75	0.06	upregulate stage
412102	H56435	Hs.75935	KIAA0077 protein	1.7	0.2	upregulate stage
412303	AW936336		gb:QV4-DT0021-281299-070-g11 DT0021 Homo	1	0.17	upregulate stage
412312	AW936686		gb:PM2-DT0023-080300-004-g01 DT0023 Homo	3.4	0.16	upregulate stage
412598	AI681997	Hs.107057	ESTs	2.25	0.2	upregulate stage
413383	AA128978	Hs.154706	Homo sapiens cDNA FLJ13594 fis, clone PL	2.3	0.17	upregulate stage
413406	AW452823	Hs.135268	ESTs	3.52	0.14	upregulate stage
413618	BE154078		gb:PMO-HT0339-200400-010-F04 HT0339 Homo	1	0.18	upregulate stage
416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	1.05	0.12	upregulate stage
417708	N74392	Hs.50495	ESTs	2	0.16	upregulate stage
417974	AA210765		gb:zz90c06.r1 NCI_CGAP_GCB1 Homo sapiens	1.7	0.18	upregulate stage
418604	AA225632	Hs.190016	ESTs	3.75	0.13	upregulate stage
418631	AA225921	Hs.115105	ESTs	1.75	0.2	upregulate stage
418830	BE513731	Hs.88959	Human DNA sequence from clone 967N21 on	3.8	0.09	upregulate stage
418893	N32264	Hs.44330	ESTs	2.35	0.14	upregulate stage
418950	T78517	Hs.13941	ESTs	2.15	0.19	upregulate stage
419044	AI799135	Hs.87164	Homo sapiens cDNA FLJ14001 fis, clone Y7	1.85	0.15	upregulate stage
420082	N43741	Hs.203148	ESTs	3.8	0.14	upregulate stage
420653	AI224532	Hs.88550	ESTs	2.05	0.16	upregulate stage
421112	AW243875	Hs.265427	ESTs	3.3	0.13	upregulate stage
421683	AI147535	Hs.143769	ESTs	2	0.14	upregulate stage
421799	AW972292	Hs.292998	ESTs	2.35	0.15	upregulate stage
422177	AA720878	Hs.201375	ESTs	3.3	0.14	upregulate stage
422429	AA310527		gb:EST181333 Jurkat T-cells V Homo saple	3.45	0.12	upregulate stage
422956	BE545072	Hs.122579	hypothetical protein FLJ10461	2.15	0.11	upregulate stage
424026	AI798295	Hs.123218	ESTs	3.8	0.14	upregulate stage
425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	1	0.09	upregulate stage
425761	AW664214	Hs.196729	ESTs	2	0.19	upregulate stage
426427	M86699	Hs.169840	TTK protein kinase	2.1	0.16	upregulate stage
427558	D49493	Hs.2171	growth differentiation factor 10	2.15	0.14	upregulate stage
427635	BE397988	Hs.179982	tumor protein p53-binding protein	3.9	0.11	upregulate stage
428766	AA477989	Hs.98800	ESTs	3.8	0.12	upregulate stage
429761	AI276780	Hs.135173	ESTs	1.9	0.17	upregulate stage
430132	AA204686	Hs.234149	hypothetical protein FLJ20647	5.05	0.11	upregulate stage
430253	AK001514	Hs.236844	hypothetical protein FLJ10652	3.55	0.15	upregulate stage
430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	2.5	0.14	upregulate stage
431187	AW971146	Hs.293187	ESTs	3.95	0.13	upregulate stage
431364	AW971382	Hs.294016	ESTs, Weakly similar to alpha-1(XVII) c	1.8	0.15	upregulate stage
431401	AA504626	Hs.105735	ESTs	1.65	0.22	upregulate stage
431419	AL041844	Hs.277522	ESTs, Weakly similar to FYVE finger-cont	1.45	0.16	upregulate stage
432361	AI378582	Hs.159585	ESTs	2.15	0.14	upregulate stage
432810	AA863400	Hs.23054	ESTs	3.7	0.08	upregulate stage
432926	AA570416	Hs.32271	hypothetical protein FLJ10846	2	0.2	upregulate stage
433108	AB002446		gb:Homo sapiens mRNA from chromosome 5q2	2.35	0.14	upregulate stage
434153	AF118072	Hs.283916	Homo sapiens PRO1716 mRNA, complete cds	1	0.14	upregulate stage
435202	AI971313	Hs.170204	KIAA0551 protein	1.25	0.16	upregulate stage
435313	AI769400	Hs.169729	ESTs	2	0.18	upregulate stage
435359	T60843	Hs.189679	ESTs	3.6	0.11	upregulate stage
435488	H57954	Hs.34394	ESTs	2.2	0.22	upregulate stage
436583	AW293909	Hs.156935	ESTs	1.4	0.19	upregulate stage
436862	AI821940	Hs.264622	ESTs, Moderately similar to ALU8_HUMAN A	3.2	0.12	upregulate stage
437485	AI149570	Hs.127363	ESTs	2.05	0.22	upregulate stage
437854	AL119723		gb:DKFZp761A2124_r1 761 (synonym: hamy2)	2.75	0.15	upregulate stage
438316	AA789249		gb:aj27g08.s1 Soares_testis_NHT Homo sap	2.45	0.13	upregulate stage
438390	AI422017		gb:tf45f12.x1 NCI_CGAP_Bm23 Homo sapien	3.1	0.13	upregulate stage
438915	AA280174	Hs.23282	ESTs	1.35	0.12	upregulate stage
439983	AA858394	Hs.117955	ESTs	4	0.13	upregulate stage
442048	AA974603		gb:op34f05.s1 Soares_NFL_T_GBC_S1 Homo s	5.55	0.09	upregulate stage

	442369	AI565071	Hs.159983	ESTs	3.85	0.14	upregulate stage
	442748	AI016713	Hs.135787	ESTs	2.35	0.23	upregulate stage
	443717	BE163884	Hs.282331	ESTs	2.5	0.18	upregulate stage
5	445935	AA287537	Hs.167585	ESTs	1	0.2	upregulate stage
	446078	AI339982	Hs.156051	ESTs	2.25	0.24	upregulate stage
	446139	H77395	Hs.39749	ESTs	2.15	0.18	upregulate stage
	446183	AA354991	Hs.14222	Homo sapiens mRNA; cDNA DKFZp761P019 (tr	3.45	0.14	upregulate stage
	448253	H25899	Hs.201591	ESTs	1.65	0.18	upregulate stage
10	448956	AK001674	Hs.22630	cofactor required for Spl transcription	2.2	0.14	upregulate stage
	449199	AI990122	Hs.196988	ESTs	1.25	0.23	upregulate stage
	449558	AA001765	Hs.157079	KIAA1227 protein	1	0.16	upregulate stage
	449576	AW014631	Hs.225068	ESTs	2.3	0.19	upregulate stage
	449859	T98077	Hs.18214	ESTs	6.3	0.07	upregulate stage
15	450434	AA166950	Hs.18645	ESTs, Weakly similar to partial CDS [C.e	1.65	0.22	upregulate stage
	450625	AW970107		gb:EST382188 MAGE resequences, MAGK Homo	1.35	0.19	upregulate stage
	451337	AI400209	Hs.60787	ESTs	1.6	0.16	upregulate stage
	451686	AA059246	Hs.110293	ESTs	3.4	0.14	upregulate stage
	452079	AA830908	Hs.15825	ESTs	1.9	0.23	upregulate stage
20	452220	BE158006	Hs.212296	ESTs	3.1	0.17	upregulate stage
	453918	AW005123	Hs.231975	ESTs	1	0.21	upregulate stage
	455350	AW901809		gb:QVO-NN1020-170400-195-h02 NN1020 Homo	2	0.2	upregulate stage
	456511	AA282330	Hs.145668	ESTs	1.15	0.12	upregulate stage
	456986	D38299	Hs.170917	prostaglandin E receptor 3 (subtype EP3)	1.65	0.18	upregulate stage
25	457427	AW971287		gb:EST383376 MAGE resequences, MAGL Homo	2.35	0.16	upregulate stage
	460296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	1	0.27	upregulate stage
	460409	AF153341	Hs.283954	Homo sapiens winged helix/forkhead trans	2.33	0.2	upregulate stage
	460471				7.45	0.09	upregulate stage
	460641				0.71	0.31	upregulate stage
30	460749				7.25	0.1	upregulate stage
	460751				5.35	0.09	upregulate stage
	460761				5.9	0.1	upregulate stage
	460843				5.85	0.07	upregulate stage
	461045				2.42	0.17	upregulate stage
35	461049				1.2	0.19	upregulate stage
	461192				2.47	0.3	upregulate stage
	461203				6.73	0.08	upregulate stage
	461205				6.63	0.1	upregulate stage
	461276				6.95	0.1	upregulate stage
40	461561				2.2	0.13	upregulate stage
	461604				1	0.19	upregulate stage
	462245				7.65	0.09	upregulate stage
	462296				1	0.33	upregulate stage
	462530				5.1	0.13	upregulate stage
45	462812				1.65	0.17	upregulate stage
	462820				1	0.34	upregulate stage
	462892				1	1	upregulate stage
	463344				6.5	0.08	upregulate stage
	464156				3.7	0.11	upregulate stage
50	464290				4.45	0.09	upregulate stage
	464538				8.38	0.09	upregulate stage
	464676				8.3	0.09	upregulate stage
	464977				0.9	0.35	upregulate stage
	465033				1.52	0.31	upregulate stage
55	465109	N47812	Hs.81360	CGI-35 protein	6.2	0.1	upregulate stage
	465654				1.95	0.06	upregulate stage
	466081				3	0.07	upregulate stage
	466270				6.09	0.13	upregulate stage
	466399				1.55	0.41	upregulate stage
60	466475				6.2	0.12	upregulate stage
	466485				1	0.48	upregulate stage
	466741	AA058357	Hs.74466	carcinoembryonic antigen-related cell ad	5.4	0.07	upregulate stage
	466867	AA157857	Hs.182265	keratin 19	2.26	0.37	upregulate stage
	467173	T64349		gb:yc10d08.s1 Stratagene lung (937210) H	3.35	0.11	upregulate stage
65	467230	AA157857	Hs.182265	keratin 19	2.15	0.38	upregulate stage
	467266	AJ235664		gb:Homo sapiens mRNA for immunoglobulin	2.1	0.09	upregulate stage
	467783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	3.25	0.11	upregulate stage
	467825	NM_006152	Hs.40202	lymphoid-restricted membrane protein	6.25	0.08	upregulate stage
	467870	AB032990	Hs.40719	hypothetical protein KIAA1164	4.5	0.12	upregulate stage
70	467877	AW016811	Hs.234478	Homo sapiens cDNA: FLJ22648 fis, clone H	3.3	0.15	upregulate stage
	467968	NM_004863	Hs.59403	serine palmitoyltransferase, long chain	7.35	0.1	upregulate stage
	468162	AA993833	Hs.118527	ESTs	6.2	0.09	upregulate stage
	468363	NM_003389	Hs.44396	coronin, actin-binding protein, 2A	5.35	0.14	upregulate stage
	468576	NM_003542	Hs.46423	H4 histone family, member G	7.28	0.1	upregulate stage
75	468673	BE208517	Hs.184109	ribosomal protein L37a	2.53	0.24	upregulate stage
	468684	R61377	Hs.12727	hypothetical protein FLJ21610	1	0.3	upregulate stage
	469361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	7.7	0.06	upregulate stage
	469592	BE280951	Hs.55058	EH-domain containing 4	3.95	0.1	upregulate stage

	409744	AW675258	Hs.56265	Homo sapiens mRNA; cDNA DKFZp586P2321 (f	1.55	0.16	upregulate stage
	410141	R07775	Hs.287657	Homo sapiens cDNA: FLJ21291 fis, clone C	4.1	0.18	upregulate stage
	410232	AW372451	Hs.61184	CGI-79 protein	3.65	0.14	upregulate stage
5	410269	AW613597		gb:hh79g12.x1 NCI_CGAP_GU1 Homo sapiens	7.55	0.09	upregulate stage
	410297	AA148710	Hs.159441	ESTs	3.8	0.1	upregulate stage
	410337	M83822	Hs.62354	cell division cycle 4-like	4.35	0.19	upregulate stage
	410418	D31382	Hs.63325	transmembrane protease, serine 4	1.42	0.4	upregulate stage
	410541	AA065003	Hs.64179	hypothetical protein	1.61	0.48	upregulate stage
10	410724	AW799269		gb:RC0-UM0051-210300-012-01 UM0051 Homo	6.65	0.12	upregulate stage
	410785	AW803341		gb:IL2-UM0079-090300-050-D03 UM0079 Homo	1.4	0.16	upregulate stage
	410968	AA199907	Hs.67397	homeo box A1	3.05	0.1	upregulate stage
	411162	AW819944		gb:QV0-ST0294-240300-172-e03 ST0294 Homo	2	0.23	upregulate stage
	411173	R81571		gb:yj02h10.r1 Soares placenta Nb2HP Homo	7.2	0.1	upregulate stage
15	411243	AB039886	Hs.69319	CA11	0.36	0.93	upregulate stage
	411407	R00903		gb:ye87a07.r1 Soares fetal liver spleen	8	0.09	upregulate stage
	411704	AI499220	Hs.71573	hypothetical protein FLJ10074	1.75	0.22	upregulate stage
	412121	AB033061	Hs.73287	KIAA1235 protein	5.3	0.11	upregulate stage
	412123	BE251328	Hs.73291	hypothetical protein FLJ10881	6.9	0.1	upregulate stage
20	412129	M21984	Hs.73454	troponin T3, skeletal, fast	0.27	1.06	upregulate stage
	412354	AW939148		gb:QV1-DT0069-110200-067-d06 DT0069 Homo	6.9	0.11	upregulate stage
	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	2.88	0.21	upregulate stage
	412700	BE222433	Hs.201262	ESTs	2.85	0.15	upregulate stage
	412706	R97106	Hs.167546	ESTs	3.75	0.16	upregulate stage
25	412935	BE267045	Hs.75064	tubulin-specific chaperone c	7	0.09	upregulate stage
	413402	T24065		gb:seq2245 HMSWMYK Homo sapiens cDNA clo	6.3	0.12	upregulate stage
	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	3.45	0.11	upregulate stage
	413445	BE141022		gb:MR0-HT0067-201099-002-d10 HT0067 Homo	3.9	0.13	upregulate stage
	413587	AA156164	Hs.271833	Homo sapiens cDNA FLJ13473 fis, clone PL	7.63	0.09	upregulate stage
30	413800	AI129238	Hs.192235	ESTs	3.2	0.18	upregulate stage
	413859	AW992356	Hs.8364	pyruvate dehydrogenase kinase, isoenzyme	2.54	0.33	upregulate stage
	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	1.75	0.21	upregulate stage
	413991	H44725	Hs.71300	ESTs	1.3	0.21	upregulate stage
	414052	AW578849	Hs.283552	ESTs, Weakly similar to unnamed protein	8.1	0.07	upregulate stage
35	414203	BE262170		gb:601150419F1 NIH_MGC_19 Homo sapiens c	1.45	0.14	upregulate stage
	414343	AL036166	Hs.75914	coated vesicle membrane protein	1	0.23	upregulate stage
	414664	AA587775	Hs.66295	Homo sapiens HSPC311 mRNA, partial cds	1	0.36	upregulate stage
	414987	AA524394	Hs.165544	ESTs	1.51	0.51	upregulate stage
	414993	AW819403	Hs.77724	KIAA0586 gene product	2.72	0.23	upregulate stage
40	415276	U88666	Hs.78353	SFRS protein kinase 2	6.95	0.1	upregulate stage
	415303	R11813		gb:yf53a04.r1 Soares infant brain 1NIB H	8.1	0.09	upregulate stage
	415392	Z44067		gb:HSC1RF051 normalized infant brain cDN	5.66	0.11	upregulate stage
	415572	F12294		gb:HSC38B051 normalized infant brain cDN	5.7	0.11	upregulate stage
	415773	R21651		gb:yh19g02.r1 Soares placenta Nb2HP Homo	5.3	0.11	upregulate stage
45	416012	AF061959	Hs.78961	protein phosphatase 1, regulatory (inhib	2.19	0.28	upregulate stage
	416074	R40174	Hs.21209	ESTs	7.61	0.11	upregulate stage
	416182	NM_004354	Hs.79069	cyclin G2	1	0.39	upregulate stage
	416518	H60730	Hs.18917	ESTs	6.6	0.1	upregulate stage
	416782	L35035	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	3.9	0.17	upregulate stage
50	416987	D86957	Hs.80712	KIAA0202 protein	2.54	0.31	upregulate stage
	417094	NM_006895	Hs.81182	histamine N-methyltransferase	4.26	0.12	upregulate stage
	417275	X63578	Hs.81849	parvalbumin	1	0.12	upregulate stage
	417395	BE564245	Hs.82084	Integrin beta 3 binding protein (beta3-e	8.4	0.08	upregulate stage
	417683	AW566008	Hs.239154	Homo sapiens cDNA FLJ12814 fis, clone NT	2.2	0.17	upregulate stage
55	417759	R13567	Hs.12548	ESTs	8.18	0.09	upregulate stage
	417848	AA206581	Hs.39457	ESTs	8.6	0.08	upregulate stage
	417985	AA187545	Hs.83114	crystallin, zeta (quinone reductase)	7	0.11	upregulate stage
	418073	R39789	Hs.119714	EST	6.3	0.11	upregulate stage
	418394	AF132818	Hs.84728	Kruppel-like factor 5 (intestinal)	1.63	0.46	upregulate stage
60	418406	X73501	Hs.84905	cytokeratin 20	3.5	0.02	upregulate stage
	418555	AA172115	Hs.87159	Homo sapiens cDNA FLJ12577 fis, clone NT	6.75	0.06	upregulate stage
	418636	AW749855		gb:QV4-BT0534-281299-053-c05 BT0534 Homo	4.1	0.11	upregulate stage
	418786	AI796317	Hs.203594	Homo sapiens uncharacterized gastric pro	7.5	0.08	upregulate stage
	418827	BE327311	Hs.47166	HT021	5.6	0.13	upregulate stage
65	418948	AI217097		gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	1.5	0.22	upregulate stage
	419551	AW582256	Hs.91011	anterior gradient 1 (Xenopus laevis) hom	2.44	0.29	upregulate stage
	419590	AF005043	Hs.91390	poly (ADP-ribose) glycohydrolase	8.08	0.1	upregulate stage
	419693	AA133749	Hs.92323	FXYD domain-containing ion transport reg	1.64	0.48	upregulate stage
	419712	AA360838	Hs.179909	Homo sapiens cDNA: FLJ22995 fis, clone K	5.4	0.11	upregulate stage
70	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	7.9	0.06	upregulate stage
	419720	AA249131	Hs.143607	hypothetical protein FLJ11068	2.95	0.15	upregulate stage
	419791	AI579909	Hs.105104	ESTs	2.45	0.2	upregulate stage
	419872	AI422951	Hs.146162	ESTs	4.25	0.17	upregulate stage
	419903	T16938	Hs.87902	ESTs	2.5	0.22	upregulate stage
75	419932	AA281594		gb:z03a01.r1 NCI_CGAP_GCB1 Homo sapiens	6.1	0.12	upregulate stage
	420026	AI831190	Hs.166676	ESTs	3.4	0.14	upregulate stage
	420187	AK001714	Hs.95744	hypothetical protein similar to ankryrin	4.03	0.18	upregulate stage
	420193	AI460080	Hs.202869	ESTs	1	0.28	upregulate stage

	420281	AI623693	Hs.191533	ESTs	6.6	0.11	upregulate stage
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	6	0.09	upregulate stage
	420370	Y13645	Hs.97234	uroplakin 2	1.2	0.45	upregulate stage
5	420383	T55154	Hs.144880	ESTs	3.8	0.12	upregulate stage
	420450	AW968989	Hs.177726	ESTs	2.75	0.14	upregulate stage
	420588	AF000982	Hs.147916	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	8.1	0.09	upregulate stage
	420763	AA419392	Hs.178354	ESTs	8	0.09	upregulate stage
	420838	AW118210	Hs.5244	ESTs	8.65	0.07	upregulate stage
10	420981	L40904	Hs.100724	peroxisome proliferative activated recep	1.98	0.32	upregulate stage
	421013	M62397	Hs.1345	mutated in colorectal cancers	1	0.29	upregulate stage
	421072	AI215069	Hs.89113	ESTs	5.8	0.12	upregulate stage
	421110	AJ250717	Hs.1355	cathepsin E	5.45	0.03	upregulate stage
	421141	AW117261	Hs.125914	ESTs	2.75	0.16	upregulate stage
15	421338	AA287443	Hs.105115	gbz552c10.r1 NCL CGAP_GCB1 Homo sapiens	7.45	0.09	upregulate stage
	421508	NM_004833	Hs.105115	absent in melanoma 2	4.21	0.19	upregulate stage
	421634	AA437414	Hs.106283	hypothetical protein FLJ10262	7.79	0.08	upregulate stage
	421674	T10707	Hs.296355	neuronal PAS domain protein 2	7.5	0.1	upregulate stage
	421810	AK001718	Hs.108530	hypothetical protein FLJ10856	8.45	0.08	upregulate stage
20	421855	F06504	Hs.27384	ESTs	2.9	0.16	upregulate stage
	421898	AA259011	Hs.109268	hypothetical protein FLJ12552	7.05	0.11	upregulate stage
	422156	N34524	Hs.300893	ESTs, Weakly similar to envelope protein	3.75	0.16	upregulate stage
	422225	BE245652	Hs.118281	zinc finger protein 266	2.95	0.17	upregulate stage
	422243	AW803733	Hs.250655	prothymosin, alpha (gene sequence 28)	8.15	0.08	upregulate stage
	422511	AJ076442	Hs.117938	collagen, type XVII, alpha 1	2.21	0.17	upregulate stage
25	422634	NM_016010	Hs.118821	CGI-62 protein	1.3	0.29	upregulate stage
	422988	AW673847	Hs.97321	ESTs	4.15	0.11	upregulate stage
	423081	AF262992	Hs.123159	sperm associated antigen 4	2.82	0.3	upregulate stage
	423596	AA328195	Hs.234101	ESTs, Weakly similar to CTL1 protein [H.	2.75	0.19	upregulate stage
30	423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	1.95	0.13	upregulate stage
	423979	AF229181	Hs.136844	CS box-containing WD protein	7.12	0.11	upregulate stage
	424005	AB033041	Hs.137507	KIAA1215 protein	1.71	0.37	upregulate stage
	424014	AA333653	Hs.24790	KIAA1573 protein	4.85	0.12	upregulate stage
	424028	AF065084	Hs.153692	KIAA0686 protein	8.5	0.07	upregulate stage
35	424194	BE245833	Hs.169854	hypothetical protein SP192	6.1	0.1	upregulate stage
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	6.59	0.11	upregulate stage
	424550	AI650541	Hs.115298	ESTs	3.25	0.12	upregulate stage
	424631	AA688021	Hs.179808	ESTs	5.45	0.11	upregulate stage
	424659	AW891298	Hs.301877	ESTs, Weakly similar to hSIAH2 [H.sapien	3.55	0.15	upregulate stage
40	424704	AI263293	Hs.152096	cytochrome P450, subfamily IIJ (arachido	8.45	0.06	upregulate stage
	424775	AB014540	Hs.153026	SWAP-70 protein	6.65	0.11	upregulate stage
	424800	AL035588	Hs.153203	MyoD family inhibitor	1.94	0.3	upregulate stage
	425066	M82882	Hs.154365	E74-like factor 1 (ets domain transcript	2.85	0.19	upregulate stage
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (tr	5.2	0.1	upregulate stage
45	425277	NM_001241	Hs.155478	cyclin T2	6	0.13	upregulate stage
	425508	AA991551	Hs.97013	ESTs	5.67	0.1	upregulate stage
	425689	W16480	Hs.24283	ESTs	4.55	0.13	upregulate stage
	425721	AC002115	Hs.159309	uroplakin 1A	0.71	0.8	upregulate stage
	426069	H10807	Hs.30998	ESTs	3.4	0.17	upregulate stage
50	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	6.84	0.09	upregulate stage
	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	6.7	0.1	upregulate stage
	426227	U67058	Hs.168102	Human proteinase activated receptor-2 mR	3.05	0.14	upregulate stage
	426603	AA382291	Hs.171731	gb:EST95683 Testis 1 Homo sapiens cDNA 5	1.8	0.26	upregulate stage
55	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	0.96	0.36	upregulate stage
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	1.32	0.49	upregulate stage
	426902	AI125334	Hs.97408	ESTs	5.05	0.07	upregulate stage
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	2.95	0.12	upregulate stage
	427001	NM_006482	Hs.173135	dual-specificity tyrosine-(Y)-phosphoryl	4.9	0.13	upregulate stage
	427087	BE073913	Hs.173515	uncharacterized hypothalamus protein HT0	0.57	0.86	upregulate stage
60	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	1.86	0.31	upregulate stage
	427399	NM_014883	Hs.177664	KIAA0914 gene product	5	0.13	upregulate stage
	427450	AB014526	Hs.178121	KIAA0626 gene product	5.3	0.09	upregulate stage
	427490	Z95152	Hs.178695	mitogen-activated protein kinase 13	6.37	0.13	upregulate stage
	427737	AA435988	Hs.178066	ESTs, Weakly similar to AF068289 5 HDCME	5.7	0.11	upregulate stage
65	428042	AA419529	Hs.183752	gb:zv03d12.r1 Soares_NhHMPu_S1 Homo sapi	1.65	0.14	upregulate stage
	428336	AA503115	Hs.183752	microseminoprotein, beta-	5.37	0.05	upregulate stage
	428337	AA644508	Hs.183752	gb:af73c01.r1 Soares_NhHMPu_S1 Homo sapi	3.4	0.13	upregulate stage
	428365	AA295331	Hs.183861	Homo sapiens cDNA FLJ20042 fis, clone CO	1	0.17	upregulate stage
	428471	X57348	Hs.184510	stratifin	1.81	0.39	upregulate stage
70	428583	AA430589	Hs.101374	ESTs, Moderately similar to ALU5_HUMAN A	7.55	0.11	upregulate stage
	428670	AA431682	Hs.134832	ESTs	8.05	0.1	upregulate stage
	428785	AI015953	Hs.125265	ESTs	1.65	0.15	upregulate stage
	429332	AF030403	Hs.199263	Ste-20 related kinase	2.64	0.26	upregulate stage
	429343	AK000785	Hs.199480	epsin 3	3.15	0.27	upregulate stage
75	429556	AW139399	Hs.98988	ESTs	1.87	0.31	upregulate stage
	429663	M68874	Hs.211587	phosphatase A2, group IVA (cytosolic,	0.61	1.02	upregulate stage
	429824	AA286363	Hs.121520	Human BAC clone GS1-99H8	2.03	0.39	upregulate stage
	429966	BE081342	Hs.226799	HSPC039 protein	7.85	0.08	upregulate stage

	429970	AK000072	Hs.227059	chloride channel, calcium activated, fam	1	0.61	upregulate stage
	430042	AB023170	Hs.227850	KIAA0953 protein	2.5	0.17	upregulate stage
	430168	AW968343	Hs.300896	ESTs, Highly similar to AF128113 1 promi	1.98	0.4	upregulate stage
5	430308	BE540865	Hs.238990	cyclin-dependent kinase inhibitor 1B (p2	6.7	0.09	upregulate stage
	430399	AI916284	Hs.199671	ESTs	8.09	0.08	upregulate stage
	430763	AA485468	Hs.105658	ESTs	3.18	0.24	upregulate stage
	431474	AL133990	Hs.190642	ESTs	0.37	0.51	upregulate stage
	431567	N51357	Hs.260855	Homo sapiens mRNA; cDNA DKFZp761G2311 (f	1.74	0.39	upregulate stage
10	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	3.55	0.15	upregulate stage
	431683	AK001749	Hs.267604	hypothetical protein FLJ10450	8.55	0.08	upregulate stage
	431709	AF220185	Hs.267923	uncharacterized hypothalamus protein HT0	7.95	0.1	upregulate stage
	431846	BE019924	Hs.271580	uroplakin 1B	1.33	0.5	upregulate stage
	431912	AI660552	Hs.154903	ESTs, Weakly similar to A56154 Abl subst	4.15	0.12	upregulate stage
15	432350	NM_005865	Hs.274407	protease, serine, 16 (thymus)	3.7	0.13	upregulate stage
	432520	AI075978	Hs.188007	ESTs	2.05	0.22	upregulate stage
	432524	AI458020	Hs.293287	ESTs	5.15	0.14	upregulate stage
	432540	AI821517	Hs.105866	ESTs	5.5	0.11	upregulate stage
	432623	AA557351	Hs.152448	ESTs, Moderately similar to PUR6_HUMAN M	8.43	0.09	upregulate stage
20	432632	AW973801	Hs.134656	ESTs	2.45	0.16	upregulate stage
	432820	AI554067	Hs.152477	ESTs	8.29	0.09	upregulate stage
	432945	AL043683	Hs.271357	ESTs, Weakly similar to unnamed protein	3.22	0.23	upregulate stage
	433027	AF191018	Hs.279923	putative nucleotide binding protein, est	2.15	0.39	upregulate stage
	433037	NM_014158	Hs.279938	HSPC067 protein	5.1	0.11	upregulate stage
25	433156	R59206	Hs.17519	Homo sapiens cDNA: FLJ22539 fis, clone H	7.9	0.1	upregulate stage
	433171	AA579425		gb:n137c08.s1 NCL_CGAP_Pr2 Homo sapiens	3.54	0.14	upregulate stage
	433311	AA588149		gb:nv16h12.s1 NCL_CGAP_Pr22 Homo sapiens	6.6	0.08	upregulate stage
	433383	AF034837	Hs.192731	double-stranded RNA specific adenosine d	2.45	0.21	upregulate stage
	433409	AI278802	Hs.25661	ESTs	4.75	0.1	upregulate stage
30	433650	AA603472	Hs.28456	ESTs	1.6	0.18	upregulate stage
	433675	AW977663	Hs.110771	Homo sapiens cDNA: FLJ21904 fis, clone H	3.88	0.17	upregulate stage
	434328	BE564937	Hs.15984	pp21 homolog	3	0.15	upregulate stage
	434476	AW858520	Hs.271825	ESTs	4.6	0.1	upregulate stage
	434683	AW298724	Hs.202639	ESTs	2.1	0.19	upregulate stage
35	434726	AF062719	Hs.139053	ESTs	1.76	0.34	upregulate stage
	435124	AA725362	Hs.120456	ESTs	7.7	0.09	upregulate stage
	435563	AF210317	Hs.95497	solute carrier family 2 (facilitated glu	5.8	0.09	upregulate stage
	435899	W89093	Hs.189914	ESTs	1.32	0.42	upregulate stage
	436026	AI349764	Hs.217081	ESTs	1	0.22	upregulate stage
40	436154	AA764950	Hs.119898	ESTs	8.4	0.05	upregulate stage
	436293	AI601188	Hs.120910	ESTs	2.42	0.2	upregulate stage
	436361	AA825814	Hs.149065	ESTs	6.95	0.09	upregulate stage
	436455	AI027959	Hs.132300	ESTs	3.25	0.15	upregulate stage
	436577	W84774	Hs.17643	ESTs	6.3	0.06	upregulate stage
45	436684	AW976319	Hs.94806	KIAA1062 protein	4.75	0.12	upregulate stage
	437036	AI571514	Hs.133022	ESTs	1.4	0.13	upregulate stage
	437146	AA730977		gb:nw55f05.s1 NCL_CGAP_Ew1 Homo sapiens	1	0.37	upregulate stage
	437262	BE250537	Hs.174838	Homo sapiens cDNA FLJ14192 fis, clone NT	3.25	0.17	upregulate stage
	437277	AA748016	Hs.123370	ESTs	6.75	0.09	upregulate stage
50	437882	AI243203	Hs.131572	ESTs	8.12	0.09	upregulate stage
	438392	AA806395	Hs.123205	ESTs	1	0.34	upregulate stage
	438416	N76398	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	8.1	0.1	upregulate stage
	438739	AA815391		gb:at61c02.s1 Soares_tastis_NHT Homo sap	4.69	0.12	upregulate stage
55	439211	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	6.65	0.11	upregulate stage
	439394	AA149250	Hs.56105	ESTs, Weakly similar to WDNM RAT WDNM1 P	3.19	0.11	upregulate stage
	439544	W26354	Hs.28891	hypothetical protein FLJ11360	2.3	0.34	upregulate stage
	439569	AW602166	Hs.222399	CEP1 protein	0.73	0.51	upregulate stage
	439586	AA922936	Hs.110039	ESTs	4.3	0.1	upregulate stage
	439706	AW872527	Hs.59761	ESTs	1	0.14	upregulate stage
60	439897	NM_015310	Hs.6763	KIAA0942 protein	8.4	0.08	upregulate stage
	439898	AW505514	Hs.209561	ESTs, Weakly similar to C05E11.1 gene pr	7.35	0.1	upregulate stage
	439949	AW979197	Hs.292073	ESTs	8.55	0.08	upregulate stage
	440035	BE561589	Hs.285122	hypothetical protein FLJ21839	6	0.11	upregulate stage
	440619	AW408586	Hs.91052	ESTs, Moderately similar to ALU5_HUMAN A	7.95	0.07	upregulate stage
65	440635	AW610331		gb:RC4-ST0316-190100-011-c08 ST0316 Homo	5.95	0.11	upregulate stage
	440787	AW292043	Hs.209433	ESTs	5.05	0.12	upregulate stage
	441233	AA972965	Hs.135568	ESTs	1.7	0.12	upregulate stage
	441528	AI003797	Hs.130815	hypothetical protein FLJ21870	7.2	0.09	upregulate stage
	441670	AW874090	Hs.127392	ESTs, Moderately similar to p33ING1 [H.s	2.45	0.19	upregulate stage
70	441683	BE564214	Hs.102946	ESTs	5.9	0.13	upregulate stage
	441847	AI215564	Hs.220972	ESTs	6.95	0.11	upregulate stage
	442145	AI022650	Hs.8117	erbB2-interacting protein ERBIN	3	0.19	upregulate stage
	442299	AW467791	Hs.155561	ESTs	5.05	0.13	upregulate stage
	442315	AA173992	Hs.7956	ESTs	3.97	0.17	upregulate stage
	442528	AF150317	Hs.134217	ESTs	1.4	0.34	upregulate stage
75	442571	C06338	Hs.165464	ESTs	8	0.08	upregulate stage
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	6.7	0.1	upregulate stage
	442652	AI005163	Hs.201378	ESTs, Weakly similar to KIAA0944 protein	7.15	0.11	upregulate stage

5	442947	R40800	Hs.21303	ESTs	8.5	0.08	upregulate stage
	442993	BE018682	Hs.44343	ESTs	1.91	0.34	upregulate stage
	443015	R33261	Hs.6614	ESTs	8.5	0.09	upregulate stage
	443085	AI032660	Hs.164711	ESTs	4	0.13	upregulate stage
	443228	W24781	Hs.293798	ESTs	1.61	0.47	upregulate stage
	443367	AW071349	Hs.215937	ESTs	1.75	0.29	upregulate stage
	443371	AI792888	Hs.145489	ESTs	5.85	0.11	upregulate stage
	443564	AI921685	Hs.199713	ESTs	1.4	0.18	upregulate stage
10	443638	AW028696	Hs.145679	ESTs	3.25	0.15	upregulate stage
	443677	AV646096	Hs.293776	ESTs, Weakly similar to 1207289A reverse	6.45	0.11	upregulate stage
	443861	AW449462	Hs.134743	ESTs	6.72	0.09	upregulate stage
	444097	AW517412	Hs.150757	ESTs	4.25	0.11	upregulate stage
	444171	AB018249	Hs.10458	small inducible cytokine subfamily A (Cy	8.45	0.09	upregulate stage
15	444184	T87841	Hs.282990	Human DNA sequence from clone RP1-28H20	8.1	0.1	upregulate stage
	444385	BE278964	Hs.11085	CGI-111 protein	8.6	0.09	upregulate stage
	444624	AV650476	Hs.282936	ESTs	7.52	0.1	upregulate stage
	444631	AW995395	Hs.84520	ESTs	1.25	0.21	upregulate stage
	444707	AI188613	Hs.143866	ESTs	2.1	0.21	upregulate stage
20	444735	BE019923	Hs.243122	hypothetical protein FLJ13057 similar to	6.8	0.1	upregulate stage
	444779	AI192105	Hs.147170	ESTs	0.94	0.6	upregulate stage
	444823	BE262989	Hs.12045	putative protein	8.09	0.1	upregulate stage
	444858	AI199738	Hs.208275	ESTs, Weakly similar to unnamed protein	4.6	0.09	upregulate stage
	444875	AI200759	Hs.44737	ESTs	6.85	0.11	upregulate stage
25	444888	AI651039	Hs.148559	ESTs	3.15	0.18	upregulate stage
	445076	AI206888	Hs.154131	ESTs	7.81	0.09	upregulate stage
	445182	AW189787	Hs.147474	ESTs	2	0.07	upregulate stage
	445189	AI936450	Hs.147482	ESTs	2.65	0.12	upregulate stage
	445320	AA503887	Hs.167011	Homo sapiens cDNA: FLJ21362 fis, clone C	1.47	0.46	upregulate stage
30	445594	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	6.2	0.07	upregulate stage
	445674	BE410347	Hs.13063	transcription factor CA150	3.8	0.15	upregulate stage
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	5.6	0.1	upregulate stage
	445871	AI702901	Hs.145582	ESTs	2.3	0.33	upregulate stage
	446140	AA356170	Hs.26750	Homo sapiens cDNA: FLJ21908 fis, clone H	2.15	0.18	upregulate stage
35	446553	AB021179	Hs.15299	HMB-A-inducible	2.55	0.18	upregulate stage
	446651	AA393907	Hs.97179	ESTs	8.05	0.07	upregulate stage
	447086	AI421397	Hs.161321	ESTs	6.9	0.1	upregulate stage
	447290	AI476732	Hs.263912	ESTs	2.35	0.18	upregulate stage
	447379	AI554946	Hs.158794	ESTs	6.3	0.09	upregulate stage
40	447390	X95384	Hs.18426	translational inhibitor protein p14.5	7.25	0.08	upregulate stage
	447533	NM_004786	Hs.18792	thioredoxin-like, 32kD	1	0.24	upregulate stage
	447548	N53388	Hs.7222	ESTs	8.6	0.07	upregulate stage
	447731	AA373527	Hs.19385	CGI-58 protein	7.3	0.08	upregulate stage
	447853	AI434204	Hs.164285	ESTs, Weakly similar to Aflg1p [S.cerevis	6.75	0.11	upregulate stage
45	447857	AA081218	Hs.58608	Homo sapiens cDNA FLJ14206 fis, clone NT	2.2	0.24	upregulate stage
	447965	AW292577	Hs.94445	ESTs	3.6	0.13	upregulate stage
	448072	AI459306	Hs.24908	ESTs	5.8	0.11	upregulate stage
	448474	AI792014	Hs.13809	ESTs	2.72	0.28	upregulate stage
	448513	AA344741	Hs.61773	Homo sapiens cDNA FLJ11648 fis, clone HE	4.8	0.12	upregulate stage
50	448601	R61656	Hs.293690	ESTs	2.65	0.2	upregulate stage
	448625	AW970786	Hs.178470	Homo sapiens cDNA: FLJ22662 fis, clone H	1.68	0.44	upregulate stage
	448735	AW473830	Hs.171442	ESTs	2.95	0.19	upregulate stage
	448807	AI571940	Hs.7549	ESTs	2.3	0.14	upregulate stage
	448920	AW408009	Hs.22580	alkylglycerone phosphate synthase	8.6	0.08	upregulate stage
55	449448	D60730	Hs.57471	ESTs	1	0.13	upregulate stage
	449517	AW500106	Hs.23643	serine/threonine protein kinase MASK	6.4	0.11	upregulate stage
	449585	AI655321	Hs.197693	ESTs	1	0.16	upregulate stage
	449619	AI655992	Hs.300647	ESTs	8.35	0.09	upregulate stage
	449659	R60031	Hs.198899	eukaryotic translation initiation factor	6.65	0.11	upregulate stage
60	449689	AF228421	Hs.301039	Human DNA sequence from clone RP1-132F21	8.35	0.06	upregulate stage
	449901	AI674072		gb:wd15h01.x1 Soares_NFL_T_GBC_S1 Homo s	5.8	0.1	upregulate stage
	449964	AW001741	Hs.273193	hypothetical protein FLJ10706	8.7	0.09	upregulate stage
	450170	AI685366	Hs.32775	ESTs	6.77	0.12	upregulate stage
	450193	AI916071	Hs.224623	ESTs	5.73	0.1	upregulate stage
65	450336	AA046814	Hs.288928	Homo sapiens cDNA: FLJ23296 fis, clone H	8.2	0.08	upregulate stage
	450341	N90956	Hs.17230	hypothetical protein FLJ22087	4.2	0.19	upregulate stage
	450353	AI244661	Hs.103296	ESTs	4.71	0.15	upregulate stage
	450737	AW007152	Hs.203330	ESTs	2.14	0.25	upregulate stage
	450795	AW173371	Hs.60435	ESTs	6	0.1	upregulate stage
70	450928	AI744417		gb:tr10h12.x1 NCI_CGAP_Ov23 Homo sapiens	1.75	0.18	upregulate stage
	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	4.3	0.1	upregulate stage
	451230	BE546208	Hs.26090	hypothetical protein FLJ20272	4.75	0.16	upregulate stage
	451593	AF151879	Hs.26706	CGI-121 protein	5.8	0.11	upregulate stage
	451618	AA115539	Hs.26764	KIAA0546 protein	5.8	0.13	upregulate stage
75	451668	Z43948	Hs.26789	hypothetical protein FLJ10320	0.73	0.26	upregulate stage
	451790	AA927403	Hs.43897	ESTs, Weakly similar to P2CA_HUMAN PROTE	3.2	0.25	upregulate stage
	452001	AI827675	Hs.297735	Homo sapiens cDNA: FLJ22094 fis, clone H	3.7	0.13	upregulate stage
	452039	AI922988	Hs.172510	ESTs	1	0.65	upregulate stage

5	452046	AB018345	Hs.27657	KIAA0802 protein	1.13	0.39	upregulate stage
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	3.2	0.15	upregulate stage
	452278	AL037715	Hs.28785	Homo sapiens mRNA; cDNA DKFZp586F0219 (f	8.25	0.07	upregulate stage
	452381	H23329	Hs.290880	ESTs, Weakly similar to ALU1_HUMAN ALU S	1	0.34	upregulate stage
	452420	BE564871	Hs.29463	centrin, EF-hand protein, 3 (CDC31 yeast	4.97	0.13	upregulate stage
	452714	AW770994	Hs.30340	hypothetical protein KIAA1165	7.6	0.09	upregulate stage
	453078	AF053551	Hs.31584	metaxin 2	5.3	0.09	upregulate stage
	453370	AI470523	Hs.182356	ESTs, Moderately similar to translation	3.78	0.13	upregulate stage
10	453765	BE279901	Hs.35091	hypothetical protein FLJ10775	3.95	0.11	upregulate stage
	453972	AW137224	Hs.245869	ESTs	6	0.09	upregulate stage
	454044	AW022393		gb:df37h12.y1 Morton Fetal Cochlea Homo	1.15	0.18	upregulate stage
	454289	AL137554	Hs.49927	Homo sapiens mRNA; cDNA DKFZp434H1720 (f	7.05	0.1	upregulate stage
	454314	AW364844		gb:QV3-DT0044-221299-045-c03 DT0044 Homo	1	0.37	upregulate stage
15	454315	AW373564	Hs.251928	nuclear pore complex interacting protein	2.7	0.13	upregulate stage
	454775	BE160229		gb:QV1-HT0413-090200-062-a12 HT0413 Homo	8.5	0.09	upregulate stage
	454790	AW820852		gb:RC2-ST0301-120200-011-f12 ST0301 Homo	1.15	0.14	upregulate stage
	454792	AW820794	Hs.252406	hypothetical protein FLJ12296 similar to	3.65	0.12	upregulate stage
	455170	AW860972		gb:QV0-CT0387-180300-167-h07 CT0387 Homo	5.7	0.07	upregulate stage
20	455511	BE144752		gb:CM0-HT0180-041099-065-b04 HT0180 Homo	1	0.25	upregulate stage
	4556141	AI751357	Hs.288741	Homo sapiens cDNA: FLJ22255 fis, clone H	8.35	0.09	upregulate stage
	456258	AW976410	Hs.289069	Homo sapiens cDNA: FLJ21016 fis, clone C	4.85	0.14	upregulate stage
	456279	AW006783	Hs.6686	ESTs	7.25	0.1	upregulate stage
	457518	AA825350	Hs.143805	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.84	0.11	upregulate stage
25	457570	AA579426	Hs.190226	ESTs	2.6	0.2	upregulate stage
	457982	AW856093	Hs.183617	ESTs	1	0.25	upregulate stage
	458080	BE142728		gb:MR0-HT0157-021299-004-d08 HT0157 Homo	2.05	0.27	upregulate stage
	458340	AI457102	Hs.121583	Human glucose transporter pseudogene	2.25	0.18	upregulate stage
	458440	AI095468	Hs.135254	ESTs, Weakly similar to thrombospondin 1	2.35	0.13	upregulate stage
30	458771	AW295151	Hs.163612	ESTs	1	0.19	upregulate stage
	459092	AA722012	Hs.255757	ESTs, Weakly similar to KIAA0611 protein	6.95	0.1	upregulate stage

TABLE 1B

35
 Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

40	Pkey	CAT	Accessions
	407774	101538_1	AA084958 AA214034 AA044587 AA130152 AA130116 D81924
	407939	1027688_1	W05608 AW118352 AW196215
	407980	103087_1	AA046309 AI263500 AA046397
45	408224	1048369_1	AW175997 AW176000 AW175999 AW175994 AW176004 AW175989
	408241	1048867_1	AW176546 AW178965 BE141057
	408268	104987_1	AL138247 AA053529 BE173313
	408277	1050131_1	AW177959 AW177960 AW178086 AW178022
	408306	1050863_1	BE141991 AW178855 BE141990 BE141993 BE141994 BE062405 BE062404 AW178850
	409281	111502_1	AA069998 AA075659 AA075660 AA069828
50	409408	1128045_1	AW387837 AW387874 AW387826 AW387758 AW387864 AW809268 AW387754
	409566	114012_1	AA078899 AA078782 AA075788
	409760	115373_1	AA302840 T93016 T92950 AA077551
	409794	1154785_1	AW885691 BE185989 BE185940 AW500322 H10282
	409810	1155339_1	AW500895 AW937549
55	409840	1156071_1	AW502122 AW502125 AW501663 AW501720
	410071	1174764_1	AW582568 AW818656 AW818647 AW818655 AW818637 AW818234
	410128	117773_1	AW904599 AA325920 AW964919 AA081786 T05150
	410269	1189983_1	AW513597 BE080235 BE080168
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	410495	1205826_1	N95428 W24040 AW751366 H81987
	410520	1206965_1	AW752710 BE180336 BE180186
	410534	1207247_1	AW905138 AW753008 R13818 Z43519
	410537	1207336_1	AW753108 AW852909 N36993 AW894327 AW903629
	410560	1208311_1	N29220 AW754225 AW754224
65	410562	1208415_1	AW858528 AW754362 H74000
	410724	1218202_1	AW799269 AW799385 AW799501 AW799386 AW799270 AW799467
	410751	121964_1	AA357918 AA089516 AA357917
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			AW807195 AW807271
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	410973	1228236_1	AW812278 AW812286 AW812274
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	411112	1232692_1	AW818158 AW865743 AW865702 AW865698
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5	411159	1234102_1 AW820178 AW820183 AW819870 AW819937 AW835709 AW820184 AW820157 AW819945 AW820096
	411162	1234161_1 AW819944 AW820182 AW820168 AW819959 AW819953
	411170	1234379_1 AW820503 AW820306 AW820429 BE174741 AW820244 BE174738
	411173	123446_1 R81571 AW962014 AA324277
	411193	1235254_1 AW821484 AW821461 AW821490 AW821525 AW821526 AW821519
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	411339	1239387_1 BE164598 AW837578 AW837582
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	411771	1257335_1 AW993247 AW861464
	411787	1258789_1 AW863568 BE161696 BE161629 BE161824
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	411840	1260678_1 AW866330 AW866410 AW866332 AW866411 AW866327 AW866326 AW866335 AW866334 AW866331 AW866333 AW866328 AW866329
	411860	126168_1 T89420 N87510 AA095932
	411880	1263110_1 AW872477 BE088101 T05990
	411932	1266125_1 AW876548 AW876577 AW876528 AW876623 AW876519 AW876540 AW876569 AW876534 AW876563 AW876545 AW876574
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	412178	1281471_1 AW898526 AW898525 Z19700
	412296	1288043_1 AW936233 AW936272
	412303	1288130_1 AW936336 AW936339
	412305	1288141_1 AW936369 AW936377 AW936355 AW936410 AW936460
45	412312	1288349_1 AW936686 AW936656 AW936608 AW936635 AW936652 AW936679 AW936726 AW936602 AW936733
	412327	1288935_1 AW937355 AW937450 BE162340 BE162397
	412354	1290342_1 AW939148 AW939200 BE161819
	412357	1290611_1 AW939537 AW939584 W92705
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	413141	1350477_1 BE166323 BE067045
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	413294	1359149_1 BE144034 N72932 BE080176
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	413743	1385884_1 BE161004 BE162497 BE161135 BE160999 BE162492
	413782	1389068_1 BE546104 BE165710 BE382801
	413792	1389912_1 BE166924 BE166921 BE166925 BE166915 BE166970 BE166968
	413804	1390710_1 T64682 BE168190 BE168256
	414091	141621_1 T83742 AW672882 AA135378
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	414220	1426940_1 BE298094 BE267860
	414276	1432115_1 BE297862

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	415114	1523035_1	D60468 D60950 D61218 N98936
	415178	1527354_1	D80503 D81739 N95691
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	415364	1535008_1	F06771 H04895 Z42778
	415371	1535066_1	R15239 Z45189 F06836
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75	TABLE 1C		

Pkey: Unique number corresponding to an Eos probe set

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

NL_position: Indicates nucleotide positions of predicted exons.

5				
	Pkey	Ref	Strand	NL_position
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	400495	9714773	Minus	61902-62137
	400528	6981824	Plus	472381-472528,474170-474277,475328-475542,475878-476000
	400577	7960401	Plus	101535-101881
	400608	9887666	Minus	96756-97558
15	400641	8117693	Plus	4786-4992
	400644	8117693	Plus	27682-27840
	400666	8118496	Plus	17982-18115,20297-20456
	400749	7331445	Minus	9162-9283
	400750	8119067	Plus	198991-199168,199316-199548
	400751	7331445	Minus	35395-35533
20	400761	8131609	Minus	114220-115164
	400762	8131616	Plus	7235-7605
	400773	8131629	Minus	44116-44238,48208-48321
	400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,10634-10789,15254-15403,23827-23958
	400844	9188605	Plus	24746-24872,25035-25204
25	400845	9188605	Plus	34428-34612
	400846	9188605	Plus	39310-39474
	400860	9757499	Minus	151830-152104,152649-152744
	400880	9931121	Plus	29235-29336,36363-36580
	400887	9958187	Plus	119239-121542
30	400888	9958187	Minus	199600-199875
	400937	7652890	Minus	89519-89905
	400977	8072510	Plus	73950-74364
	401002	8117251	Minus	77898-78050
	401024	8117489	Plus	60551-60802
35	401045	8117619	Plus	90044-90184,91111-91345
	401048	7232177	Plus	132430-132761
	401049	7232177	Plus	149157-150692
	401086	9957912	Plus	84561-84884
40	401093	8516137	Minus	22335-23166
	401101	8568122	Plus	77081-77226
	401192	9719502	Minus	69559-70101
	401197	9719705	Plus	176341-176452
	401203	9743387	Minus	172961-173056,173868-173928
45	401205	9743388	Plus	167373-167433,167936-168031
	401256	9796573	Minus	45482-45620
	401262	9796963	Plus	35662-35799
	401271	9797373	Minus	61292-61911
	401276	8954274	Minus	15919-16096
50	401279	9800062	Minus	13535-13669
	401342	9908882	Plus	3096-3242
	401365	9796180	Minus	119572-119672
	401395	7327842	Minus	11502-11771,46357-46489,58720-58916
	401420	7452889	Minus	141362-141502
55	401439	8246737	Plus	92993-94026
	401451	6634068	Minus	119926-121272
	401508	7534110	Minus	110779-110983
	401519	6849315	Plus	157315-157950
	401537	7960358	Minus	186786-187029,190607-190779,198218-198348
60	401561	8224660	Minus	10652-10838,19815-20018
	401566	8469090	Minus	96277-96420,96979-97160
	401604	7689963	Minus	119835-120185
	401619	8516761	Minus	141309-143576
	401669	9801805	Plus	25414-26310
	401691	3582311	Plus	162333-162715
65	401694	3540172	Minus	64056-64168
	401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
	401759	9929699	Plus	59811-60665
70	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
	401866	8018106	Plus	73126-73623
	401905	8671966	Plus	153955-154441,156599-156819
	401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
	402001	9501818	Plus	68052-68223
	402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
75	402076	8117410	Plus	128316-128627
	402089	7249154	Plus	101610-101819
	402110	8131678	Minus	173889-174052

	402176	7543687	Minus	10-750
	402230	9966312	Minus	29782-29932
	402245	7690231	Minus	88253-88417
	402296	6598824	Plus	22587-23723
5	402325	7636348	Minus	60558-60738,61677-61803
	402407	3962498	Minus	115812-116187
	402408	9796239	Minus	110326-110491
	402430	9796372	Minus	62382-62552
	402435	9796462	Plus	114593-115588
10	402472	9797116	Plus	53716-54470
	402474	7547175	Minus	53526-53628,55755-55920,57530-57757
	402480	9797375	Plus	59708-59999
	402490	9797648	Plus	149982-150929
	402522	9798493	Plus	20605-20731
15	402530	7630937	Minus	1524-2003
	402546	7637348	Plus	24673-25170
	402553	9863566	Plus	48292-48398,49564-49944
	402604	9909420	Plus	20393-20767
	402716	8969253	Minus	84065-84242
20	402727	9211324	Plus	54596-54777
	402812	6010110	Plus	25026-25091,25844-25920
	402820	6456853	Minus	82274-82443
	402846	9408716	Minus	5726-5850
	402889	9931133	Plus	89392-89498,90358-90571
25	402892	8086844	Minus	194384-194645
	402901	8894222	Minus	175426-175667
	402922	8216969	Minus	19036-19401,19589-19849,19951-20102
	402938	8953442	Plus	22365-22473
	402995	2996643	Minus	5962-6216
30	403005	5791501	Minus	16945-17053,20018-20403
	403020	6984114	Minus	96644-97021,97462-97868
	403029	7768593	Minus	44558-44766
	403047	3540153	Minus	59793-59968
	403073	8954241	Plus	142964-143260
35	403085	8954241	Plus	165035-165334,165420-165713
	403092	8954241	Plus	174720-175016,175104-175406,175508-175813
	403106	7331404	Plus	77162-77350,81338-81511
	403172	7464784	Minus	64007-64275
	403212	7630897	Minus	156037-156210
40	403214	7630945	Minus	76723-77027,79317-79484
	403277	8072597	Minus	27494-27642
	403331	8567936	Plus	169793-169966
	403344	8569726	Plus	70823-70990
	403362	8571772	Plus	64099-64260
45	403381	9438267	Minus	26009-26178
	403426	9719529	Minus	157156-158183
	403485	9966528	Plus	2888-3001,3198-3532,3655-4117
	403567	8101141	Plus	35349-35614
	403588	8101227	Minus	197672-197944
50	403590	8101229	Plus	405-1296
	403615	8567964	Plus	107671-107866
	403687	7387384	Plus	9009-9534
	403754	7229815	Minus	163899-164726
	403776	7770611	Minus	1414-1513,1624-1756
55	403822	9369510	Minus	142803-142922
	403851	7708872	Plus	22733-23007
	403860	7708960	Minus	95755-96045
	403894	7381715	Minus	1442-2224
	403903	7710671	Minus	101165-102597
60	403959	8224399	Minus	175363-177474
	404015	8655948	Minus	587821-588222
	404059	3548785	Plus	104326-106788
	404113	9588571	Minus	13446-13646
	404148	9863703	Plus	78218-78418,79571-79709
65	404152	9884757	Plus	41111-41281,45495-45716,47801-47910
	404156	9886577	Plus	127319-127754
	404229	7159766	Plus	16607-16841
	404232	8218045	Minus	71800-71956
	404268	9711362	Plus	33238-33463
70	404274	9885189	Plus	104127-104318
	404288	2769644	Plus	3512-3691
	404290	2769644	Plus	36651-36813
	404336	9838028	Plus	157951-158129
	404403	7272157	Minus	72053-72238
75	404440	7528051	Plus	80430-81581
	404488	8113286	Minus	64835-64994
	404498	8151654	Plus	13292-13497

5	404507	8151803	Plus	146359-146739
	404516	8151967	Plus	114153-114322
	404538	8247909	Minus	192748-192945
	404594	9958262	Minus	15310-15510
	404639	9796778	Plus	5779-14387
10	404653	9796999	Plus	164997-165230
	404676	9797204	Minus	56167-56342,58056-58189,58891-59048,60452-60628
	404684	9797403	Minus	110881-111020
	404685	9797437	Minus	153217-153315,154043-154124,159185-159353,161290-161420,163544-163669,166127-166207,167654-167734
	404704	9800728	Minus	88841-89018
15	404819	4678240	Plus	16223-16319,16427-16513,16736-16859,16941-17075,17170-17287,17389-17529,18261-18357,18443-18578
	404829	6624702	Minus	4913-5093,7310-7469,9472-9621,9951-10082
	404860	8979555	Plus	65852-66081
	404874	9650523	Minus	96066-96192
	404881	5931510	Minus	36360-36608
20	404894	6850447	Plus	102822-103127
	404939	6862697	Plus	175318-175476
	404977	3738341	Minus	43081-43229
	405033	7107731	Minus	142358-142546
	405059	7656683	Plus	349-822
25	405064	7658416	Plus	81207-81416
	405071	7708797	Minus	11115-11552
	405102	8076881	Minus	120922-121296
	405167	9966316	Plus	43796-43981,48245-48427,54141-54317
	405170	9966524	Plus	37047-37198
30	405177	7139696	Minus	118465-118663
	405186	7229793	Plus	161475-161581,162930-163067
	405258	7329310	Plus	129930-130076
	405281	6139075	Minus	34202-34351,35194-35336,45412-45475,45731-45958,47296-47457,49549-49658,49790-49904,50231-50342,53583-53667,54111-54279
	405308	3638954	Plus	40778-41034,41383-41573
35	405349	2914717	Minus	85552-85806
	405379	6513908	Minus	22332-22473,24333-24439
	405390	6606064	Minus	94007-94177
	405411	3451356	Minus	17503-17778,18021-18290
	405463	7715630	Minus	123097-123260
40	405494	8050952	Minus	70284-70518
	405520	9454643	Plus	60849-60981
	405526	9558556	Minus	132704-133277
	405580	4512267	Plus	169232-169547
	405600	5923640	Plus	26662-27225
45	405654	4895155	Minus	53624-53759
	405720	9797144	Plus	13409-13861
	405725	9838299	Minus	106417-106521
	405735	9931101	Minus	29854-29976
	405738	9943998	Plus	44370-45410
50	405809	5304920	Minus	6655-6883,6887-8859
	405838	5686575	Plus	3460-3717
	405863	7657810	Plus	49410-49520
	405867	6758731	Minus	74553-75173
	405906	7705124	Minus	10835-11059
55	405920	6758795	Plus	120621-120971
	405968	8247789	Plus	14893-15148
	406017	8272661	Minus	46271-46874
	406036	6758919	Plus	17942-18163
	406081	9123861	Minus	38115-38691
60	406137	9166422	Minus	30487-31058
	406187	7289992	Plus	8044-8877
	406243	7417725	Plus	38899-39369
	406270	7534217	Plus	13136-13591
	406320	9211754	Minus	20170-20511
65	406322	9212102	Minus	130230-130418
	406360	9256107	Minus	7513-7673
	406367	9256126	Minus	58313-58489
	406397	9256243	Minus	127317-127454
	406399	9256288	Minus	63448-63554
70	406434	9256651	Minus	17803-17931
	406467	9795551	Plus	182212-182958
	406471	9795566	Plus	87383-87589
	406475	9797684	Plus	125417-125563,128052-128180
	406485	7711305	Plus	125036-125422
	406511	7711412	Plus	177277-177384
	406588	8189273	Minus	135629-135848

TABLE 2A: 485 GENES UP-REGULATED IN BLADDER CANCER

5	Pkey:	Unique Eos probe/est identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Ratio of mRNA expression in bladder tumors compared to normal bladder			
10	Pkey	ExAccn	UnigeneID	Unigene Title	R1
15	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	3.473
	412841	AJ751157	Hs.101395	hypothetical protein MGC11352	2.279
	421066	AU076725	Hs.101408	branched chain aminotransferase 2, mitoc	3.052
	435136	R27299	Hs.10172	ESTs	4.717
	444042	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	0.003
20	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	188.231
	421318	U63973	Hs.103501	rhodopsin kinase	1.381
	421359	AK001589	Hs.103816	hypothetical protein FLJ10727	1.000
	459462	AA481396	Hs.105167	ESTs	1.000
	430134	BE380149	Hs.105223	ESTs, Weakly similar to T33188 hypotheti	1.000
25	433227	AB040923	Hs.106808	kelch (Drosophila)-like 1	1.000
	421742	AW970004	Hs.107528	androgen induced protein	1.514
	417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	2.782
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	20.064
	451686	AA059246	Hs.110293	ESTs	0.033
30	454417	AJ244459	Hs.110826	trinucleotide repeat containing 9	56.751
	458760	AI498631	Hs.111334	ferritin, light polypeptide	2.512
	422119	AI277829	Hs.111862	KIAA0590 gene product	2.634
	422170	AJ791949	Hs.112432	anti-Mullerian hormone	0.055
	441877	AW273802	Hs.11340	hypothetical protein FLJ23047	0.008
35	445958	BE326257	Hs.114536	ESTs	0.002
	434288	AW189075	Hs.116265	fibrillin3	11.401
	435347	AW014873	Hs.116963	ESTs	0.003
	453134	AA032211	Hs.118493	ESTs	262.962
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	5.336
40	436154	AA764950	Hs.119898	ESTs	103.154
	436246	AW450963	Hs.119991	ESTs	0.071
	436293	AJ601188	Hs.120910	ESTs	29.129
	433078	AW015188	Hs.121575	Homo sapiens cDNA FLJ12231 fls, clone MA	274.769
	438181	AW978608	Hs.122121	ESTs, Weakly similar to I38022 hypotheti	0.024
45	449399	AA760881	Hs.122408	ESTs	1.000
	437722	AW292947	Hs.122872	ESTs, Weakly similar to JU0033 hypotheti	4.314
	457465	AW301344	Hs.122908	DNA replication factor	0.264
	409757	NM_001898	Hs.123114	cystatin SN	1.390
	439907	AA853978	Hs.124577	ESTs	0.010
50	437181	AJ306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	0.344
	440304	BE159984	Hs.125395	ESTs	0.025
	423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	0.014
	441495	AW294603	Hs.127039	ESTs	0.198
	435376	AW770956	Hs.127280	ESTs	0.008
55	427685	AJ751124	Hs.127311	ESTs	3.244
	423349	AF010258	Hs.127428	homeo box A9	0.134
	445457	AF168793	Hs.12743	camitine O-octanoyltransferase	7.255
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fls, clone HE	1.000
	441875	AI435973	Hs.128056	ESTs	0.013
60	441940	AW298115	Hs.128152	ESTs	6.075
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	0.137
	429983	W92620	Hs.128656	ESTs	162.590
	445600	AF034803	Hs.12953	PTPRF interacting protein, binding prote	0.959
	437553	AJ829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	9.163
65	459204	AW194601	Hs.13219	ESTs	1.000
	439842	AJ910896	Hs.132413	ESTs	1.000
	443113	AJ040686	Hs.132908	ESTs	0.069
	423853	AB011537	Hs.133466	slit (Drosophila) homolog 1	0.100
	420792	AA280321	Hs.13392	tethering factor SEC34	16.103
70	427719	AJ393122	Hs.134726	ESTs	0.667
	443861	AW449462	Hs.134743	ESTs	5.100
	447578	AA912347	Hs.136585	ESTs, Weakly similar to JC5314 CDC28/cdc	1.691
	445550	AI242754	Hs.137306	ESTs	0.006
	454284	AW297935	Hs.138493	ESTs, Moderately similar to ALU7_HUMAN A	0.003
75	418937	T71508	Hs.13861	ESTs, Weakly similar to T42383 probable	0.042
	424098	AF077374	Hs.139322	small proline-rich protein 3	1.347
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	0.186
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	47.949
	426900	AW163564	Hs.142375	ESTs	0.404
	439337	AA448718	Hs.142505	ESTs	0.012

	427961	AW293165	Hs.143134	ESTs	0.073
	419888	AI243493	Hs.144049	ESTs	11.958
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	77.269
5	445871	AI702901	Hs.145582	ESTs, Weakly similar to FOR4 MOUSE FORMI	183.782
	445911	AI985587	Hs.145645	ESTs, Moderately similar to ALU1_HUMAN A	0.362
	424395	AA165082	Hs.146388	microtubule-associated protein 7	203.038
	424411	NM_005209	Hs.146549	crystallin, beta A2	1.808
	444517	AI939339	Hs.146883	ESTs	0.004
10	445020	AI205655	Hs.147221	ESTs	0.307
	422109	S73265	Hs.1473	gastrin-releasing peptide	1.000
	445352	AI221087	Hs.147761	ESTs	0.015
	444444	AI149332	Hs.14855	ESTs	140.859
	444152	AI125694	Hs.149305	hypothetical protein MGC2603	2.037
15	446248	AI283014	Hs.149638	ESTs	0.018
	433159	AB035898	Hs.150587	kinesin-like protein 2	0.110
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.179
	456840	H03754	Hs.152213	wingless-type MMTV integration site fami	0.005
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	1.111
20	425206	NM_002153	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	257.949
	446082	AI274139	Hs.156452	ESTs	0.779
	444946	AW139205	Hs.156457	hypothetical protein FLJ22408	1.919
	446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonin	0.417
	447073	AW204821	Hs.157726	ESTs	10.349
25	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	1.839
	446673	NM_016361	Hs.15871	LPAP for lysophosphatidic acid phosphata	1.691
	447475	AI380797	Hs.158992	ESTs	44.641
	425776	U25128	Hs.159499	parathyroid hormone receptor 2	0.340
	418343	AA216372	Hs.159501	ESTs	0.023
30	441143	AI027604	Hs.159650	ESTs	0.280
	440917	AA909651	Hs.160025	ESTs	1.000
	418365	AW014345	Hs.161690	ESTs	0.066
	431839	AW020280	Hs.162025	ESTs	0.005
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	0.606
35	438817	AI023799	Hs.163242	ESTs	2.202
	432441	AW292425	Hs.163484	ESTs	2.305
	442577	AA292998	Hs.163900	ESTs	688.038
	435212	AW300100	Hs.164185	ESTs	0.002
	425048	H05468	Hs.164502	ESTs	0.083
40	442083	R50192	Hs.165062	ESTs	3.844
	423536	L22075	Hs.1666	guanine nucleotide binding protein (G pr	0.157
	418678	NM_001327	Hs.167379	cancer/testis antigen	269.487
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	0.208
	456967	AW004056	Hs.168357	T-box 2	160.397
45	447979	AI457197	Hs.170348	ESTs	0.016
	458814	AI498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	1.036
	446312	BE087853	Hs.171802	ESTs, Weakly similar to T08729 RING zinc	1.334
	426783	Z19084	Hs.172210	MUF1 protein	1.654
	423916	AW993496	Hs.17235	Homo sapiens clone TCCCA00176 mRNA sequ	154.064
50	409092	AI735283	Hs.172608	ESTs	0.007
	426853	U32974	Hs.172777	baculoviral IAP repeat-containing 4	0.009
	426968	U07616	Hs.173034	amphiphysin (Stiff-Mann syndrome with br	0.002
	407581	R48402	Hs.173508	P3ECSL	0.866
	427239	BE270447	Hs.174070	ubiquitin carrier protein	15.708
55	427268	X78520	Hs.174139	chloride channel 3	207.938
	436577	W84774	Hs.17643	ESTs	62.333
	420876	AA918425	Hs.177744	ESTs	32.959
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	1.171
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	1.000
60	427747	AW411425	Hs.180655	serine/threonine kinase 12	12.446
	429813	AW139678	Hs.180791	ESTs	0.013
	439806	AA846824	Hs.180908	ESTs	0.561
	427878	C05766	Hs.181022	CGI-07 protein	0.002
	440284	AA912032	Hs.181059	ESTs, Weakly similar to 2108276A ssDNA-b	0.030
65	427922	AK001934	Hs.181112	HSPC126 protein	0.039
	427972	AA864870	Hs.181304	putative gene product	0.004
	428071	AF212848	Hs.182339	els homologous factor	4.321
	428336	AA503115	Hs.183752	microseminoprotein, beta-	145.128
	428450	NM_014791	Hs.184339	KIAA0175 gene product	0.370
70	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	0.632
	438746	AI885815	Hs.184727	ESTs	0.339
	420557	AA960844	Hs.186579	Homo sapiens, clone IMAGE:4081483, mRNA	0.006
	431014	W67730	Hs.187573	ESTs	0.344
	428651	AF196478	Hs.188401	annexin A10	1.459
75	416225	AA577730	Hs.188684	ESTs, Weakly similar to PC4259 ferritin	0.502
	432497	AA551104	Hs.189048	ESTs, Moderately similar to ALUC_HUMAN I	2.499
	431474	AL133990	Hs.190642	ESTs	0.044
	427742	AA411880	Hs.190888	ESTs	0.158

	428058	AI821625	Hs.191602	ESTs	0.006
	431245	AA496933	Hs.191687	ESTs	0.006
	453204	R10799	Hs.191990	ESTs	1.734
5	435608	AA628980	Hs.192371	down syndrome critical region protein DS	115.500
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	0.152
	454032	W31790	Hs.194293	ESTs, Weakly similar to I54374 gene NF2	60.103
	449121	AI915858	Hs.194980	ESTs	0.003
	447827	U73727	Hs.19718	protein tyrosine phosphatase, receptor I	305.974
10	438401	AL046321	Hs.197484	ESTs, Weakly similar to JC4295 ring finger	0.002
	457200	U33749	Hs.197764	thyroid transcription factor 1	0.011
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3)	9.390
	429257	AW163799	Hs.198365	2,3-bisphosphoglycerate mutase	178.436
	429276	AF056085	Hs.198612	G protein-coupled receptor 51	0.729
15	449818	AW594365	Hs.199365	ESTs	1.000
	429345	R11141	Hs.199695	hypothetical protein	7.339
	443564	AI921685	Hs.199713	ESTs	0.001
	449847	AW204447	Hs.199750	organic anion transporter polypeptide-re	1.000
	449351	AW016537	Hs.200760	ESTs	0.005
20	426322	J05058	Hs.2012	transcobalamin I (vitamin B12 binding pr	381.474
	434411	AA632649	Hs.201372	ESTs	0.039
	448045	AJ297436	Hs.20166	prostate stem cell antigen	2.337
	446555	AV659046	Hs.201847	ESTs	0.024
	450411	D61167	Hs.202156	ESTs	0.004
25	442282	AW451086	Hs.202390	ESTs	1.000
	427587	BE348244	Hs.202628	ESTs, Weakly similar to I78885 serine/th	228.705
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	0.133
	426682	AV660038	Hs.2055	UDP glycosyltransferase 1 family, polype	2.070
	426746	J03626	Hs.2057	uridine monophosphate synthetase (orotid	0.528
30	448275	BE514434	Hs.20830	kinesin-like 2	19.718
	459058	H85939	Hs.209605	EST	0.005
	441795	N58115	Hs.21137	AD024 protein	1.000
	451592	AI805416	Hs.213897	ESTs	0.012
	443367	AW071349	Hs.215937	ESTs	0.003
35	415949	H10582	Hs.21691	ESTs	0.072
	444008	BE544855	Hs.220756	ESTs, Weakly similar to SFR4_HUMAN SPIC	213.962
	432548	AW973399	Hs.22133	hypothetical protein FLJ20121	0.250
	427867	NM_005073	Hs.2217	solute carrier family 15 (oligopeptide t	0.010
	453123	AI953718	Hs.221849	ESTs	0.566
40	439569	AW602166	Hs.222399	CEGP1 protein	10.625
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	27.603
	435956	AF269255	Hs.22604	lysosomal apyrase-like protein 1	127.564
	453883	AI638516	Hs.22630	cofactor required for Sp1 transcription	2.216
	431253	R06428	Hs.226351	ESTs	0.023
45	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	0.103
	430034	X60155	Hs.227767	zinc finger protein 41	1.000
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor	0.024
	417997	AA418189	Hs.23017	Homo sapiens cDNA: FLJ22747 fis, clone K	1.635
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	120.167
50	452956	AW003578	Hs.231872	ESTs	1.000
	446009	AI989885	Hs.231926	ESTs	4.000
	430499	AW969408	Hs.231991	ESTs	0.014
	448560	BE613183	Hs.23213	ESTs	285.090
	441508	AW015203	Hs.232237	ESTs	0.261
55	453228	AW628325	Hs.232327	ESTs	1.000
	442167	H18740	Hs.23248	hypothetical protein from EUROIMAGE 2005	0.240
	453321	AI984381	Hs.232521	ESTs	0.609
	449207	AL044222	Hs.23255	nucleoporin 155kD	0.551
	430152	AB001325	Hs.234642	aquaporin 3	1.040
60	439239	AI031540	Hs.235331	ESTs	0.598
	435087	AW975241	Hs.23567	ESTs	0.007
	451276	AW294386	Hs.236533	ESTs, Highly similar to dJ742C19.2 (Hsa	0.012
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	1.280
	431011	AA490631	Hs.23783	ESTs	0.016
65	430307	BE513442	Hs.238944	hypothetical protein FLJ10631	284.526
	444371	BE540274	Hs.239	forkhead box M1	3.691
	424264	D80400	Hs.239388	Human DNA sequence from clone RP1-304B14	0.255
	449722	BE280074	Hs.23960	cyclin B1	0.467
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	13.419
70	430168	AW968343	Hs.24255	DKFZP434I1735 protein	1.192
	452292	AW139588	Hs.244369	ESTs	1.000
	412661	N32860	Hs.24611	ESTs, Weakly similar to I54374 gene NF2	2.500
	456682	AW500321	Hs.246766	Homo sapiens cDNA FLJ12360 fis, clone MA	0.014
75	457343	NM_013936	Hs.247862	olfactory receptor, family 12, subfamily	0.233
	430978	U53583	Hs.248182	olfactory receptor, family 1, subfamily	1.000
	431020	AF097874	Hs.248226	caspase 14, apoptosis-related cysteine p	5.666
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	1.838
	431098	AW501465	Hs.249230	ribonuclease L (2',5'-oligoadenylate	0.004

	454170	AW177225	Hs.250158	ESTs	0.243
	439223	AW238299	Hs.250618	UL16 binding protein 2	0.516
	438081	H49546	Hs.251391	claudin 16	0.080
5	431347	AI133461	Hs.251664	insulin-like growth factor 2 (somatomedi	843.974
	450663	H43540	Hs.25292	ribonuclease H1, large subunit	5.928
	450684	AA872605	Hs.25333	Interleukin 1 receptor, type II	1.000
	413094	H24184	Hs.25413	TOLLIP protein	268.885
	450796	NM_001988	Hs.25482	envoplakin	1.643
10	408827	AW275730	Hs.254825	ESTs	0.008
	444129	AW294292	Hs.256212	ESTs	0.002
	430637	BE160081	Hs.256290	S100 calcium-binding protein A11 (calgiz	3.240
	436138	H53323	Hs.25717	Homo sapiens cDNA: FLJ23454 fis, clone H	0.679
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	280.231
15	453459	BE047032	Hs.257789	ESTs	2.133
	456535	AW135986	Hs.257859	ESTs	98.795
	438424	AI912498	Hs.25895	hypothetical protein FLJ14996	1.882
	451161	AA211329	Hs.26006	hypothetical protein FLJ10559	0.012
	430634	AI860651	Hs.26685	calyphosine	9.561
20	435562	AL046988	Hs.268677	ESTs, Moderately similar to ALU7_HUMAN A	0.957
	417964	R71449	Hs.268760	ESTs	0.004
	445703	AV654845	Hs.27	glycine dehydrogenase (decarboxylating;	1.324
	431846	BE019924	Hs.271580	uropalakin 18	303.679
	453074	AA031813	Hs.271880	ESTs	0.004
25	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	1.828
	435182	AA669386	Hs.272035	ESTs, Weakly similar to gonadotropin ind	0.013
	430791	AA486293	Hs.272068	ESTs, Weakly similar to ALU3_HUMAN ALU S	8.978
	432136	AA157632	Hs.272630	vacuolar proton pump delta polypeptide	0.316
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	0.014
30	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	26.348
	423031	AI278955	Hs.27457	ESTs	53.288
	455612	BE042896	Hs.274848	ESTs	21.013
	452046	AB018345	Hs.27657	KIAA0802 protein	129.013
	436567	AI492860	Hs.276904	ESTs	0.007
35	459006	AW298631	Hs.27721	Wolf-Hirschhorn syndrome candidate 1-lik	0.031
	430157	BE348706	Hs.278543	ESTs	99.244
	452012	AA307703	Hs.279766	kinesin family member 4A	0.408
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	1.721
	458663	AV658444	Hs.280776	tankyrase, TRF1-interacting ankyrin-rela	38.231
40	450020	AI680684	Hs.282219	ESTs	0.003
	435858	AF254260	Hs.283009	tufellin 1	1.516
	430733	AW975920	Hs.283361	ESTs	1.000
	446024	AB040946	Hs.284227	KIAA1513 protein	9.424
	433967	AF113018	Hs.284302	PRO1621 protein	0.008
45	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	0.030
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	1.058
	414595	AA641726	Hs.289015	hypothetical protein MGC4171	273.013
	432097	X51730	Hs.2905	progesterone receptor	0.002
	452345	AA293279	Hs.29173	hypothetical protein FLJ20515	4.010
50	457733	AW974812	Hs.291971	ESTs	1.000
	441398	AA932398	Hs.292036	ESTs, Weakly similar to B34087 hypotheti	1.000
	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	0.006
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	0.003
	433365	AF026944	Hs.293797	ESTs	0.049
55	417151	AA194055	Hs.293858	ESTs	6.593
	424242	AA337476	Hs.293984	hypothetical protein MGC13102	1.656
	432375	BE536069	Hs.2962	S100 calcium-binding protein P	17.094
	422424	AI186431	Hs.296638	prostate differentiation factor	2.646
	432410	X68561	Hs.2982	Sp4 transcription factor	0.007
60	426847	S78723	Hs.298623	5-hydroxytryptamine (serotonin) receptor	0.005
	454054	AI336329	Hs.301519	Homo sapiens cDNA FLJ12536 fis, clone NT	0.488
	452142	AB028947	Hs.301654	KIAA1024 protein	0.009
	449773	R76294	Hs.302383	ESTs	0.001
	438366	AA805760	Hs.303567	ESTs	1.000
65	452724	R84810	Hs.30464	cyclin E2	1.000
	429343	AK000785	Hs.307036	Homo sapiens, Similar to epsin 3, clone	0.494
	446466	H38026	Hs.308	arrestin 3, retinal (X-arrestin)	0.022
	430694	AA810624	Hs.30936	ESTs, Weakly similar to H2BH_HUMAN HISTO	16.744
	432789	D26381	Hs.3104	KIAA0042 gene product	0.302
70	432666	AW204069	Hs.312716	ESTs, Weakly similar to unnamed protein	0.001
	453028	AB006532	Hs.31442	RecQ protein-like 4	13.392
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	2.766
	427122	AW057736	Hs.323910	HER2 receptor tyrosine kinase (c-erb-b2,	553.782
	453216	AL137566	Hs.32405	Homo sapiens mRNA; cDNA DKFZp568G0321 (f	84.115
75	443247	BE614387	Hs.333893	c-Myc target JPO1	79.385
	439632	AW410714	Hs.334437	hypothetical protein MGC4248	337.474
	431448	AL137517	Hs.334473	hypothetical protein DKFZp564O1278	0.842
	411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HE	402.500

	433958	AW043909	Hs.334707	aminoacylase 1	191.179
	432842	AW674093	Hs.334822	hypothetical protein MGC4485	313.462
	457292	AI921270	Hs.334882	hypothetical protein FLJ14251	21.744
	451359	H85334	Hs.336623	ESTs	0.038
5	440249	AI246590	Hs.337275	ESTs	0.432
	434487	AF143867	Hs.337588	ESTs, Moderately similar to S65657 alpha	1.102
	447437	U07225	Hs.339	purinergic receptor P2Y, G-protein coupl	0.483
	447519	U46258	Hs.339655	ESTs	1.032
	434192	AW387314	Hs.34371	ESTs	0.003
10	453765	BE279901	Hs.35091	hypothetical protein FLJ10775	0.056
	441020	W79283	Hs.35982	ESTs	75.141
	453884	AA355925	Hs.36232	KIAA0186 gene product	0.138
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	0.008
15	453945	NM_005171	Hs.36908	activating transcription factor 1	0.044
	447289	AW247017	Hs.36978	melanoma antigen, family A, 3	0.002
	407626	U39198	Hs.37169	potassium inwardly-rectifying channel, s	0.009
	423620	N71320	Hs.39938	ESTs	1.000
	436027	AI864053	Hs.39972	ESTs, Weakly similar to I38588 reverse t	0.042
20	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wil	1.810
	443133	AI033878	Hs.41379	ESTs	0.534
	434534	H90477	Hs.41407	ESTs	0.013
	452934	AA581322	Hs.4213	hypothetical protein MGC16207	3.679
	434952	T10269	Hs.4285	Homo sapiens cDNA: FLJ22505 fis, clone H	2.885
25	432237	AK001926	Hs.44143	polybromo 1	0.010
	420900	AL045633	Hs.44269	ESTs	10.436
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK (human,	3.393
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	386.256
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	0.922
30	408947	AL080093	Hs.49117	Homo sapiens mRNA; cDNA DKFZp564N1662 (f	0.003
	435647	AI853240	Hs.49823	ESTs	175.910
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	2.584
	436291	BE568452	Hs.5101	protein regulator of cytokinesis 1	0.610
	455506	AA703584	Hs.5105	hypothetical protein FLJ10569	0.008
35	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	1.089
	409287	AL080213	Hs.52792	Homo sapiens mRNA; cDNA DKFZp586I1823 (f	16.910
	435047	AA454985	Hs.54973	cadherin-like protein VR20	0.612
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	5.938
	439452	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	1.000
40	439482	W70045	Hs.58089	ESTs	0.118
	439606	W79123	Hs.58561	G protein-coupled receptor 87	0.095
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	0.055
	452240	AI591147	Hs.61232	ESTs	0.221
	452316	AA298484	Hs.61265	ESTs, Moderately similar to G786_HUMAN P	2.595
45	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	3.677
	434876	AF160477	Hs.61460	Ig superfamily receptor LNIR	7.587
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	0.046
	438779	NM_003787	Hs.6414	nucleolar protein 4	0.030
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	12.016
50	440126	AA975145	Hs.66194	ESTs	0.008
	451291	R39288	Hs.6702	ESTs	0.012
	439953	AW247529	Hs.6793	platelet-activating factor acetylhydrola	1.653
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	8.628
	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 g	140.908
55	418107	R41726	Hs.7284	ESTs	0.146
	436326	BE085236	Hs.75313	aldo-keto reductase family 1, member B1	0.649
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	0.237
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	2.242
	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	0.202
60	414682	AL021154	Hs.76884	inhibitor of DNA binding 3, dominant neg	2.318
	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	1.622
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	245.564
	451575	AA767622	Hs.78893	KIAA0244 protein	1.000
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	4.552
65	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	5.128
	458921	AI682088	Hs.79375	holocarboxylase synthetase (biotin-[prop	0.246
	409235	AA188827	Hs.7988	ESTs, Weakly similar to I38022 hypotheti	7.249
	440371	BE268550	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA,	0.792
	452732	BE300078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA,	360.782
70	417003	AL038170	Hs.80756	betaine-homocysteine methyltransferase	60.590
	407584	W25945	Hs.8173	hypothetical protein FLJ10803	9.988
	417312	AW888411	Hs.81915	leukemia-associated phosphoprotein p18 (402.705
	417389	BE260954	Hs.82045	midkine (neurite growth-promoting factor	10.806
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	1.051
75	438315	R56795	Hs.82419	ESTs	0.226
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	26.260
	417933	X02308	Hs.82962	thymidylate synthetase	221.050
	418067	AI127958	Hs.83393	cystatin E/M	2.396

	438086	AA336519	Hs.83623	nuclear receptor subfamily 1, group I, m	1.000
	418205	L21715	Hs.83760	troponin I, skeletal, fast	0.159
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	0.490
5	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	3.527
	413529	U11874	Hs.846	interleukin 8 receptor, beta	0.077
	458027	L49054	Hs.85195	myeloid leukemia factor 1	0.008
	418543	NM_005329	Hs.85962	hyaluronan synthase 3	1.813
	418583	AA604379	Hs.86211	hypothetical protein	125.769
10	441801	AW242799	Hs.86366	ESTs	55.026
	414792	BE314949	Hs.87128	hypothetical protein FLJ23309	8.139
	407246	S70348	Hs.87149	integrin, beta 3 (platelet glycoprotein	0.020
	433417	AA587773	Hs.8859	Homo sapiens, Similar to RUKEN cDNA 5830	313.141
	445060	AA830811	Hs.88808	ESTs	1.000
15	453450	AW797627	Hs.89474	ADP-ribosylation factor 6	137.718
	419227	BE537383	Hs.89739	cholinergic receptor, nicotinic, beta po	0.006
	401464	AF039241	Hs.9028	histone deacetylase 5	6.846
	443162	T49951	Hs.9029	DKFZP434G032 protein	14.057
	431024	AA713666	Hs.90462	Homo sapiens, clone IMAGE:4132043, mRNA,	3.507
20	419559	Y07828	Hs.91096	ring finger protein	0.025
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	684.577
	443426	AF088158	Hs.9329	chromosome 20 open reading frame 1	0.363
	424457	AI249036	Hs.94292	hypothetical protein FLJ23311	175.667
	410348	AW182663	Hs.95469	ESTs	0.011
25	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (lg),	428.231
	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	0.005
	443767	BE662136	Hs.9736	proteasome (prosome, macropain) 26S subu	1.168
	426902	AI126334	Hs.97408	ESTs	37.457
	444874	AI218496	Hs.97515	BRCA1-Interacting protein 1; BRCA1-assoc	0.067
30	427356	AW023482	Hs.97849	ESTs	1.000
	430000	AW205931	Hs.99598	hypothetical protein MGC5338	0.812
	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	0.342
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	19.785
35	421934	AA300625		gb:EST13476 Testis tumor Homo sapiens cD	103.769
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	0.258
	424040	AA334400		gb:EST38610 Embryo, 9 week Homo sapiens	0.011
	433108	AB002446		gb:Homo sapiens mRNA from chromosome 5q2	0.023
	458829	AI557388		gb:PT2.1_6_G03.r.tumor2 Homo sapiens cDN	1.000
	459169	AI905517		gb:RC-BT091-210199-105 BT091 Homo sapien	0.773
40	400300	X03363		HER2 receptor tyrosine kinase (c-erb-b2,	468.462
	440012	AA861072		gb:ak32e05.s1 Soares_testis_NHT Homo sap	0.002
	412799	AI267606		gb:aq91h03.x1 Stanley Frontal SB pool 1	0.010
	412964	BE019688		gb:bb28g08.x1 NIH_MGC_5 Homo sapiens cDN	0.003
	406992	S82472		gb:beta-pol=DNA polymerase beta (exon a	0.005
45	414969	C16195		gb:C16195 Clontech human aorta polyA mRN	0.023
	413158	BE068098		gb:CM1-BT0368-061299-060-c09 BT0368 Homo	0.007
	453823	AL137967		gb:DKFZp761D2315_r1 761 (synonym: hamy2)	0.994
	453846	AL157586		gb:DKFZp761H0216_r1 761 (synonym: hamy2)	0.004
	407055	X89211		gb:H.sapiens DNA for endogenous retrovir	0.037
50	415204	T27434		gb:hbc2294 Human pancreatic islet Homo s	76.500
	434572	AF147340		gb:Homo sapiens full length insert cDNA	0.030
	438990	AF085890		gb:Homo sapiens full length insert cDNA	1.000
	439780	AL109688		gb:Homo sapiens mRNA full length insert	0.256
	413671	Z43712		gb:HSC1JA121 normalized infant brain cDN	0.009
55	406974	M57293		gb:Human parathyroid hormone-related pep	0.004
	455797	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	2.616
	455807	BE141140		gb:MR0-HT0075-021299-006-d07 HT0075 Homo	0.413
	432189	AA527941		gb:bnh30c04.s1 NCL_CGAP_Pr3 Homo sapiens	0.015
	443309	AI821874		gb:nl58f10.x5 NCL_CGAP_Pr3 Homo sapiens	0.007
60	437240	AA747537		gb:rx85c05.s1 NCL_CGAP_GCB1 Homo sapiens	0.006
	455189	AW864176		gb:PM0-SN0014-260400-002-b08 SN0014 Homo	0.059
	444163	AI126098		gb:qc54g07.x1 Soares_placenta_8to9weeks_	394.282
	455170	AW860972		gb:QV0-CT0387-180300-167-h07 CT0387 Homo	0.757
	454789	BE156314		gb:QV0-HT0387-150200-114-d02 HT0387 Homo	1.000
65	433005	AW939074		gb:QV1-DT0069-010200-057-c12 DT0069 Homo	0.013
	455380	BE160188		gb:QV1-HT0413-010200-059-g05 HT0413 Homo	0.249
	455650	BE064655		gb:RC1-BT0313-301299-012-c09 BT0313 Homo	1.000
	436383	BE065178		gb:RC1-BT0314-020200-012-h01 BT0314 Homo	1.000
	413100	BE065208		gb:RC1-BT0314-310300-015-b09 BT0314 Homo	271.372
70	428436	BE080180		gb:RC4-BT0629-120200-011-b10 BT0629 Homo	0.002
	455831	BE144956		gb:RC6-HT0187-201099-031-c04 HT0187 Homo	0.011
	434414	AI798376		gb:tr34b07.x1 NCL_CGAP_Ov23 Homo sapiens	293.654
	414221	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCL_CGAP_Su	0.807
	409488	AW402825		gb:UI-HF-BKO-aaq-d-08-0-UI.r1 NIH_MGC_36	0.965
75	437938	AI950087		gb:xwq05c02.x1 NCL_CGAP_Kid12 Homo sapien	2.952
	451385	AA017656		gb:ze39h01.r1 Soares retina N2b4HR Homo	7.341
	449325	AA001162		gb:ze48b06.r1 Soares retina N2b4HR Homo	0.004
	413316	W91931		gb:zh47c01.r1 Soares_fetal_liver_spleen_	0.004

	401016	0.342
	401335	0.256
	401555	1.000
5	401760	301.372
	401781	247.141
	401961	1.722
	402239	5.180
	402305	0.917
10	402424	551.141
	402777	153.231
	402778	0.006
	402837	0.367
	402948	154.103
	402952	17.038
15	403142	0.196
	403297	12.744
	403637	0.304
	403657	0.032
20	404136	0.008
	404249	0.065
	404875	1.105
	404917	69.590
	404983	1.000
	405238	1.000
25	405364	294.141
	405531	1.747
	405601	145.551
	405621	0.224
30	405932	1.968
	406117	0.333
	406354	1.000
	406548	0.002
	406599	0.010
35	459702 AI204995	0.449

TABLE 2B

Pkey: Unique Eos probeset Identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
45	409488	1134791_1 AW402825 BE544338
	412799	132817_1 AI267606 AA121045 AA126521
	412964	1339278_1 BE019688 BE144460
	413100	1349119_1 BE065208 BE065224 BE065168 BE065313
	413158	1351251_1 BE068098 BE068119 BE068083 BE068088 BE068120 BE068155 BE068111
	413316	1360169_1 W91931 W94979 BE081744
50	413671	1382504_1 Z43712 BE156729 BE156538 BE156731 BE156673 BE156539 BE156674 BE156430 BE156672 BE156675 BE156432 BE156541
	414221	142696_1 AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367
	414969	1510393_1 BE011368 BE011362 BE011215 BE011365 BE011363
	415204	1529407_1 C16195 C16230 C16211 C16164 C16251
55	421934	209339_1 T27434 Z25288 F00323 D82802 R85077
	424040	234659_1 AA300625 R16859 R16860 AW898335 W24337
	428436	291472_1 AA334400 AA334257 AW966124
	431322	331543_1 BE080180 AW827313 AW231970 AA995028 AA428584 AW872716 AW892508 AW854593 AA578441 AW975234 AA664937 AA984131 AA528743
60	432189	342819_1 AA552874 AA564758 AW063245 AI267534 AW070190 AW893483 AA770330 AA906928 AA906582 AA758746 AA551717 AW063311 AA429538
	433005	357346_1 AW970622 AA503009 AA502998 AA502989 AA502805 T92188
	433108	35898_1 AA527941 AI810608 AI620190 AA635266
	434414	38585_1 AW939074 AW939073 BE160476 AW939938 AW939206 AW940012 AW939076 AA573577 AW750479 AA574383 AW970057
65	434572	38911_1 AB002446 T03146
	436383	41888_1 AI798376 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231
	437240	435139_1 AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174
	437938	44573_2 T61139 AA149776 AA698829 AW879188 AW813567 AW813538 AI267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705
70		AA157730 AA157715 AA053524 AW849581 AW854566 C05254 AW882836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824
		AI829309 AW991957 N66951 AA527374 H66215 AA045584 AI694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817662
		AW817705 AW817703 AW817659 BE081531 H59570
75		AF147340 T51948 T52029
		BE065178 AJ227879
		AA747537 BE089068 BE089070
		AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875
		AI820501 AI820532 W87891 T65904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493
		AA927794 AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI699062
		AA282915 AW102898 AI872193 AI763273 AW173588 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539842
		AA642789 AA856975 AW505512 AI961530 AW629970 BE612881 AW276997 AW513501 AW512843 AA044209 AW856538 AA180009 AA337499
		AW961101 AA251669 AA251874 AI819225 AW205882 AI83338 AI858509 AW276905 AI633005 AA972584 AA908741 AW072629 AW513996

		AA293273 AA969759 N75628 N22388 HB4729 H60052 T92487 AJ022058 AA780419 AA551005 W80701 AW613456 AJ373032 AI564269 F00531 HB3488 W37181 W78802 R66056 AJ002839 R67840 AA300207 AW959581 T63226 F04005
5	438990	46760_1 AF085890 H29949 H29856
	439780	47673_1 AL109688 R23665 R26578
	440012	483290_1 AA861072 H02819 R25946
	443309	56604_1 AI821874 AI821868 AA630932 AA653897 AA650103 AI821131 AI821124
	444163	593658_1 AI126098 AI184746 AI148521
	449325	80480_1 AA001162 AA018950 AA017505 R84446
10	451385	85787_1 AA017656 AA017374 AA019761
	453823	982526_1 AL137967 BE064160 BE064186
	453846	983043_1 AL157586 AL157590
	454789	1234742_1 BE156314 BE156316 AW820750
	455170	1256906_1 AW860972 AW862598 AW862599 AW860988 AW860983 AW860898 AW860925 AW860922 AW860986 AW860984 AW860989
	455189	1259271_1 AW864176 AW864133 AW864185 AW864137
15	455380	1287679_1 BE160188 AW935785 BE160401 BE160319 BE160313 BE160395
	455650	1348720_1 BE064655 BE153953
	455797	1366826_1 BE091833 BE091874 BE091871
	455807	1370914_1 BE141140 BE141139 BE141105 BE141143 BE141127 BE141202 BE141108
20	455831	1373969_1 BE144966 BE144957 BE144958
	458829	773443_1 AI557388 BE158936
	459169	920641_1 AI905517 AI905455 AI905452

TABLE 2C

25	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
30	NL_position:	Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	NL_position
35	401016	8117441	Plus	126234-126359,128050-128236
	401335	9884881	Plus	15736-16352
	401555	8099284	Minus	162520-162657
	401760	9929699	Plus	83126-83250,85320-85540,94719-95287
	401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
40	401961	4581193	Minus	124054-124209
	402239	7690131	Plus	38175-38304,42133-42266
	402305	7328724	Plus	40832-41362
	402424	9796344	Minus	64925-65073
	402777	9588235	Plus	126786-126948
	402778	9588235	Plus	128560-128702
45	402837	9369121	Minus	2013-2186,9570-9758,11138-11309,19429-19677,21210-21455,23368-23562,24342-24527,29132-29320
	402948	9368458	Minus	143456-143626,143808-143935
	402952	9408724	Minus	119452-119619
	403142	9444521	Plus	89286-90131
50	403297	8096824	Minus	16584-17264
	403637	8671936	Minus	142647-142771,145531-145762
	403657	8843996	Minus	158223-158370
	404136	6981900	Minus	42538-46428
	404249	8655533	Plus	64270-64633
55	404875	9801324	Plus	96588-96732,97722-97831
	404917	7341851	Plus	49330-49498
	404983	4432779	Minus	51178-51374,52000-52173
	405238	7249119	Minus	51728-51836
	405364	2281075	Minus	48325-48491,49136-49252
	405531	9665194	Plus	35602-35803
60	405601	5815493	Minus	147835-147935,149220-149299
	405621	5523811	Plus	59362-59607
	405932	7767812	Minus	123525-123713
	406117	9142932	Plus	54304-54584
65	406354	9256049	Minus	2095-2377
	406548	7711514	Minus	25138-26762
	406599	8248616	Plus	10933-11086

Table 3A: Preferred therapeutic targets for bladder cancer

5	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	90th percentile of bladder tumor Als divided by the 90th percentile of normal bladder sample Als			
10	R2:	90th percentile of bladder tumor Als divided by the 90th percentile of normal body sample Als			
15	Pkey	ExAccn	UnigeneID	Unigene Title	R1 R2
	421948	L42583	Hs.334309	keratin 6A	14.20 1.20
	439926	AW014875	Hs.137007	ESTs	11.31 21.34
	413324	V00571	Hs.75294	corticotropin releasing hormone	9.15 45.75
	421110	AJ250717	Hs.1355	cathepsin E	9.07 45.35
20	417308	H60720	Hs.81892	KIAA0101 gene product	8.50 1.99
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	8.39 1.28
	418406	X73501	Hs.84905	cytokeratin 20	8.10 40.50
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	7.98 1.38
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	7.67 2.12
25	408243	Y00787	Hs.624	interleukin 8	7.56 4.85
	417715	AW969587	Hs.86366	ESTs	7.45 4.70
	417720	AA205625	Hs.208067	ESTs	7.34 9.18
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	7.30 26.07
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	7.12 35.60
30	413753	U17760	Hs.75517	laminin, beta 3 (nicotin (125kD), kalinin	6.95 4.96
	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	6.42 0.89
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	6.08 3.49
	407242	M18728		gb:Human nonspecific crossreacting anti	5.96 0.96
	405033			C1002652*gi544327 sp Q04799 FMO5_RABIT	5.84 16.22
35	448230	BE613348	Hs.211579	melanoma cell adhesion molecule	5.82 2.28
	406685	M18728		gb:Human nonspecific crossreacting anti	5.80 0.89
	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	5.77 28.85
	415511	AI732617	Hs.182362	ESTs	5.65 28.25
	426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase doma	5.60 6.51
40	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	5.59 2.33
	428651	AF196478	Hs.188401	annexin A10	5.55 27.75
	400843			NM_003105*:Homo sapiens sortilin-related	5.51 4.92
	402230			Target Exon	5.36 21.44
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	5.33 2.80
45	415065	BE267931	Hs.78996	proliferating cell nuclear antigen	5.17 1.98
	428450	NM_014791	Hs.184339	KIAA0175 gene product	4.90 2.63
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	4.77 2.35
	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	4.77 3.71
	418663	AK001100	Hs.41690	desmocollin 3	4.74 1.48
50	414683	S78296	Hs.76888	hypothetical protein MGC12702	4.74 2.92
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	4.68 1.61
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	4.65 11.63
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	4.63 2.06
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.55 3.35
55	401780			NM_005557*:Homo sapiens keratin 16 (foca	4.49 1.62
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	4.43 2.39
	401093			C12000586*gi5330167 dbj BAAB8477.1 (A	4.40 12.94
	417933	X02308	Hs.82962	thymidylate synthetase	4.35 2.29
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	4.32 2.82
60	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (raklines	4.24 8.15
	401781			Target Exon	4.15 1.31
	425234	AW152225	Hs.165909	ESTs, Weakly similar to 138022 hypotheti	4.14 7.39
	432842	AW674093	Hs.334822	hypothetical protein MGC4485	4.12 2.51
	408380	AF123050	Hs.44532	diubiquitin	4.11 3.26
65	449722	BE280074	Hs.23960	cyclin B1	4.09 3.72
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	4.07 2.50
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	4.00 7.14
	404977			Insulin-like growth factor 2 (somatomedi	3.89 5.17
	400409	AF153341		Homo sapiens winged helix/forkhead trans	3.88 7.29
70	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	3.87 1.61
	444371	BE540274	Hs.239	forkhead box M1	3.87 2.75
	443171	BE281128	Hs.9030	TONDU	3.83 9.48
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E. coli Re	3.82 2.98
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	3.77 3.83
75	407137	T97307		gbye53h05.s1 Soares fetal liver spleen	3.73 4.91
	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	3.68 7.08
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.68 2.29
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.67 3.06
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	3.67 1.18
	421508	NM_004833	Hs.105115	absent in melanoma 2	3.67 3.65
	443162	T49951	Hs.9029	DKFZP434G032 protein	3.66 3.21

	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.66	3.57
	417771	AA804698	Hs.82547	retinoic acid receptor responder (lazar	3.62	2.73
	441495	AW294603	Hs.127039	ESTs	3.60	2.71
5	422282	AF019225	Hs.114309	apolipoprotein L	3.57	3.92
	417079	U85590	Hs.81134	interleukin 1 receptor antagonist	3.55	0.80
	417275	X63578	Hs.295449	parvalbumin	3.54	4.60
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	3.52	2.59
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.50	3.61
10	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	3.50	17.50
	404875			NM_022819:Homo sapiens phospholipase A2	3.46	3.24
	420005	AW271106	Hs.133294	ESTs	3.40	2.22
	409757	NM_001898	Hs.123114	cystatin SN	3.39	2.93
	427719	AJ393122	Hs.134726	ESTs	3.31	2.51
15	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	3.28	0.42
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	3.28	2.62
	406081			Target Exon	3.25	13.54
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.25	2.46
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	3.23	2.88
20	429983	W92620	Hs.260855	ESTs	3.20	2.84
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	3.18	1.54
	426451	AI908165	Hs.169946	GATA-binding protein 3 (T-cell receptor	3.17	5.44
	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncog	3.13	15.65
	415752	BE314524	Hs.78776	putative transmembrane protein	3.11	2.46
25	408633	AW963372	Hs.46677	PRO2000 protein	3.11	3.30
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	3.09	1.52
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	3.08	2.22
	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	3.05	12.49
	437931	AI249468	Hs.124434	ESTs	3.01	3.70
30	421451	AA291377	Hs.50831	ESTs	2.99	14.95
	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	2.97	2.10
	402239			Target Exon	2.97	3.37
	429345	R11141	Hs.199695	hypothetical protein	2.96	2.61
35	435904	AF261655	Hs.8910	1,2-alpha-mannosidase IC	2.93	2.13
	423961	D13666	Hs.136348	periostin (OSF-2os)	2.93	1.44
	420923	AF097021	Hs.273321	differentially expressed in hematopoieti	2.92	0.95
	436608	AA628980		down syndrome critical region protein DS	2.92	4.86
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	2.88	2.93
	439223	AW238299	Hs.250618	UL16 binding protein 2	2.88	2.15
40	401747			Homo sapiens keratin 17 (KRT17)	2.88	3.44
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	2.86	14.30
	444444	AI149332	Hs.14855	ESTs	2.85	2.68
	421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C	2.84	2.46
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	2.78	2.26
45	417389	BE280964	Hs.82045	midkine (neurite growth-promoting factor	2.77	2.34
	442994	AI026718	Hs.16954	ESTs	2.75	2.82
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	2.74	2.44
	434487	AF143867	Hs.337588	ESTs, Moderately similar to S65657 alpha	2.72	3.37
	417003	AL038170	Hs.80756	betaine-homocysteine methyltransferase	2.69	2.70
50	404440			NM_021048:Homo sapiens melanoma antigen,	2.69	13.45
	400844			NM_003105:Homo sapiens soritin-related	2.69	13.45
	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	2.69	1.36
	431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	2.69	12.08
	403381			ENSP00000231844:Ecotropic virus integra	2.68	13.40
55	411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HE	2.68	2.43
	425206	NM_002153	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	2.67	2.68
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	2.67	1.79
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	2.65	0.73
	413281	AA861271	Hs.222024	transcription factor BMAL2	2.65	2.23
60	446082	AI274139	Hs.156452	ESTs	2.65	2.65
	422424	AI186431	Hs.296538	prostate differentiation factor	2.64	2.68
	407839	AA045144	Hs.161566	ESTs	2.64	1.08
	432441	AW292425	Hs.163484	ESTs	2.64	6.14
	417312	AW888411	Hs.250811	leukemia-associated phosphoprotein p18 (2.64	1.31
65	430157	BE348706	Hs.278543	ESTs	2.63	2.58
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	2.61	1.93
	418686	Z36830	Hs.87268	annexin A8	2.60	1.62
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	2.59	2.87
70	429276	AF056085	Hs.198612	G protein-coupled receptor 51	2.57	3.89
	439738	BE246502	Hs.9598	sema domain, Immunoglobulin domain (Ig),	2.57	2.49
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	2.56	1.43
	414812	X72755	Hs.77357	monokine induced by gamma interferon	2.54	3.10
	451668	Z43948	Hs.326444	cartilage acidic protein 1	2.51	3.60
75	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.50	2.91
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	2.49	1.78
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	2.49	1.80
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	2.49	3.46
	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	2.48	2.36

	418941	AA452970	Hs.239527	E18-55kDa-associated protein 5	2.46	2.33
	414807	AI738816	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	2.44	2.49
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	2.43	1.42
5	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	2.41	2.05
	449019	AI949095	Hs.57776	ESTs, Weakly similar to T22341 hypotheti	2.40	1.90
	417366	BE185289	Hs.1076	small proline-rich protein 1B (cornifin)	2.40	0.49
	420370	Y13645	Hs.97234	uropakln 2	2.39	3.81
	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	2.38	1.45
10	406399			NM_003122*:Homo sapiens serine protease	2.36	4.20
	435563	AF210317	Hs.95497	solute carrier family 2 (facilitated glu	2.31	4.05
	442117	AW684964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	2.31	1.17
	436246	AW450963	Hs.119991	ESTs	2.30	11.50
	433078	AW015188	Hs.121575	Homo sapiens cDNA FLJ12231 fis, clone MA	2.30	2.40
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	2.29	1.89
15	411263	BE297802	Hs.89360	kinesin-like 6 (mitotic centromere-assoc	2.28	2.14
	432829	W60377	Hs.57772	ESTs	2.28	4.85
	415025	AW207091	Hs.72307	ESTs	2.28	11.40
	436293	AI601188	Hs.120910	ESTs	2.27	3.80
	415989	AI267700		ESTs	2.27	11.35
20	418067	AI127958	Hs.83393	cystatin EM	2.25	1.54
	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	2.25	2.45
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	2.25	1.55
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	2.22	11.10
	434247	BE614387	Hs.333893	c-Myc target JPO1	2.21	1.32
25	424364	AW383226	Hs.201189	ESTs, Weakly similar to G01763 atrophin-	2.21	1.52
	405932			C15000305:gi3806122[gb]AAC69198.1] (AF0	2.20	1.55
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.19	1.99
	423271	W47225	Hs.126256	interleukin 1, beta	2.19	2.01
	420305			C19000735*:gi4508027[ref]NP_003414.1] z	2.19	2.54
30	421064	AI245432	Hs.101382	tumor necrosis factor, alpha-induced pro	2.19	2.16
	427747	AW411425	Hs.180655	serine/threonine kinase 12	2.18	1.80
	437181	AI306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	2.17	10.85
	431890	X17033	Hs.271986	Integrin, alpha 2 (CD49B, alpha 2 subuni	2.17	2.14
	433437	U20536	Hs.3280	caspase 6, apoptosis-related cysteine pr	2.16	1.37
35	407581	R48402	Hs.173508	P3EC5L	2.15	1.95
	400845			NM_003105*:Homo sapiens sortilin-related	2.15	2.23
	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	2.14	1.70
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	2.13	1.83
40	448045	AJ297436	Hs.20166	prostate stem cell antigen	2.13	3.49
	453459	BE047032	Hs.257789	ESTs	2.13	2.30
	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	2.12	10.60
	436251	BE515065	Hs.295585	nucleolar protein (KKE/D repeat)	2.11	1.89
	445911	AI985987	Hs.145645	ESTs, Moderately similar to ALU1_HUMAN A	2.11	2.57
45	420876	AA918425	Hs.177744	ESTs	2.09	2.30
	438817	AI023799	Hs.163242	ESTs	2.09	10.45
	434293	NM_004445	Hs.3796	EphB6	2.08	2.42
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	2.08	2.10
	418216	AA662240	Hs.283099	AF15q14 protein	2.08	4.62
50	437915	AI637993	Hs.202312	Homo sapiens clone N11 Ntera2D1 teratoca	2.08	10.40
	409420	Z15008	Hs.54451	laminin, gamma 2 (niclin (100kD), kalini	2.05	5.39
	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	2.05	1.20
	400773			NM_003105*:Homo sapiens sortilin-related	2.05	1.78
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.04	2.06
55	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.04	1.70
	444476	AF020038	Hs.11223	isocitrate dehydrogenase 1 (NADP), solub	2.03	2.26
	447437	U07225	Hs.339	purinergic receptor P2Y, G-protein coupl	2.02	1.73
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	2.02	2.93
	407601	AC002300	Hs.37129	sodium channel, nonvoltage-gated 1, beta	2.02	1.55
60	441801	AW242799	Hs.86366	ESTs	2.01	10.05
	439780	AL109588		gb:Homo sapiens mRNA full length insert	2.00	10.00
	452732	BE300078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA,	2.00	1.53
	434876	AF160477	Hs.61460	Ig superfamily receptor LNIR	2.00	1.91
	430152	AB001325	Hs.234642	aquaporin 3	1.99	1.74
65	453134	AA032211	Hs.118493	ESTs	1.99	3.16
	412719	AW016610	Hs.816	ESTs	1.99	0.34
	442577	AA292998	Hs.163900	ESTs	1.99	3.09
	409402	AF208234	Hs.695	cystatin B (stefin B)	1.98	1.50
	414774	X02419	Hs.77274	plasminogen activator, urokinase	1.97	1.84
70	439318	AW837046	Hs.6527	G protein-coupled receptor 56	1.95	1.42
	447334	AA515032	Hs.91109	ESTs	1.95	2.53
	432015	AL157504	Hs.159115	Homo sapiens mRNA; cDNA DKFZp586O0724 (I	1.94	9.70
	429002	AW248439	Hs.2340	junction plakoglobin	1.94	1.57
	410553	AW016824	Hs.255527	hypothetical protein MGC14128	1.94	2.02
75	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	1.93	0.56
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	1.92	1.01
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	1.92	1.47
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	1.92	1.59

5	414918	AI219207	Hs.72222	hypothetical protein FLJ13459	1.92	2.77
	424522	AL134847	Hs.149957	ribosomal protein S6 kinase, 90kD, polyp	1.92	1.21
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.92	1.72
	428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	1.91	1.41
	414595	AA641726	Hs.289015	hypothetical protein MGC4171	1.90	1.61
10	400846			sortilin-related receptor, L(DLR class)	1.90	1.93
	417409	BE272506	Hs.82109	syndecan 1	1.89	1.75
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	1.88	1.16
	418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	1.88	3.09
	419092	J05581	Hs.89603	mucin 1, transmembrane	1.88	1.18
15	446673	NM_016361	Hs.15871	LPAP for lysophosphatidic acid phosphata	1.87	2.01
	431347	AI133461	Hs.251664	Insulin-like growth factor 2 (somatomedi	1.86	1.87
	430168	AW968343	Hs.24255	DKFZP4341735 protein	1.86	2.11
	412115	AK001763	Hs.73239	hypothetical protein FLJ10901	1.86	1.77
	402901			NM_025206: Homo sapiens hypothetical pro	1.85	2.35
20	449027	AJ271216	Hs.22880	dipeptidylpeptidase III	1.85	1.59
	410418	D31382	Hs.63325	transmembrane protease, serine 4	1.84	1.90
	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	1.84	1.03
	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	1.84	1.54
	432210	AI567421	Hs.273330	Homo sapiens, clone IMAGE:3544662, mRNA,	1.83	1.74
25	452934	AA581322	Hs.4213	hypothetical protein MGC16207	1.82	1.84
	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	1.82	1.83
	427239	BE270447	Hs.174070	ubiquitin carrier protein	1.82	1.74
	402424			NM_024901: Homo sapiens hypothetical prot	1.81	1.61
	418068	AW971155	Hs.293902	ESTs, Weakly similar to ISHUS protein d	1.81	3.67
30	431846	BE019924	Hs.271580	uroplakin 1B	1.80	4.11
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	1.80	9.00
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,	1.80	1.02
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	1.80	2.26
	451541	BE279383	Hs.26557	plakophilin 3	1.79	1.16
35	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	1.79	5.59
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	1.79	8.95
	425852	AK001504	Hs.159551	death receptor 6, TNF superfamily member	1.79	2.08
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 [H.s.	1.77	2.96
	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	1.76	1.43
40	439606	W79123	Hs.58561	G protein-coupled receptor 87	1.76	8.80
	424098	AF077374	Hs.139322	small proline-rich protein 3	1.76	0.57
	430890	X54232	Hs.2699	glypican 1	1.73	1.39
	452862	AW378065	Hs.8687	ESTs	1.73	1.99
	427335	AA448542	Hs.251677	G antigen 7B	1.73	8.65
45	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	1.72	2.07
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	1.72	1.65
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	1.72	1.03
	453883	AI638516	Hs.347524	cofactor required for Sp1 transcriptiona	1.71	1.66
	448993	AI471630	Hs.8127	KIAA0144 gene product	1.71	1.52
50	422406	AF025441	Hs.116206	Opa-interacting protein 5	1.71	5.52
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	1.71	8.55
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	1.71	8.55
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	1.71	8.55
	424735	U31875	Hs.272499	short-chain alcohol dehydrogenase family	1.71	13.98
55	447532	AK000614	Hs.18791	hypothetical protein FLJ20507	1.70	1.84
	414053	BE391635	Hs.75725	transgelin 2	1.69	1.51
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	1.69	8.45
	426050	AF017307	Hs.166096	E74-like factor 3 (ets domain transcript	1.69	1.60
	448262	AW880830	Hs.186273	ESTs	1.67	2.07
60	452316	AA298484	Hs.61265	ESTs, Moderately similar to G786_HUMAN P	1.66	0.70
	452240	AI591147	Hs.61232	ESTs	1.66	1.23
	417151	AA194055	Hs.293858	ESTs	1.65	2.08
	452461	N78223	Hs.108106	transcription factor	1.65	8.25
	418462	BE001596	Hs.85266	Integrin, beta 4	1.65	1.78
65	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	1.64	1.59
	438746	AI885815	Hs.184727	Human melanoma-associated antigen p97 (m	1.64	1.13
	423161	AL049227	Hs.124776	downstream of cadherin 6 (by 3.3kb)	1.63	1.81
	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso	1.62	1.51
	402777			C1002652: gij544327[spjQ04795]FMO5_RABIT	1.62	2.33
70	436569	BE439539	Hs.279837	glutathione S-transferase M2 (muscle)	1.62	2.18
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	1.62	1.27
	413385	M34455	Hs.840	indoleamine-pyrole 2,3 dioxygenase	1.61	2.05
	410407	X66839	Hs.63287	carbonic anhydrase IX	1.60	1.78
	450635	AW403954	Hs.25237	mesenchymal stem cell protein DSCD75	1.60	1.63
75	437016	AU076916	Hs.5398	guanine monophosphate synthetase	1.59	1.50
	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	1.58	1.92
	422247	U18244	Hs.113602	solute carrier family 1 (high affinity a	1.57	1.79
	408908	BE296227	Hs.250822	serine/threonine kinase 15	1.56	7.80
	433159	AB035898	Hs.150587	kinesin-like protein 2	1.56	7.80
	443211	AI128388	Hs.143655	ESTs	1.56	7.80
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	1.55	1.44

	426900	AW163564	Hs.142375	ESTs	1.54	1.93
	421066	AU076725	Hs.101408	branched chain aminotransferase 2, mito	1.54	1.71
	413804	T64682		gb:yc48b02.r1 Stratagene liver (937224)	1.53	1.55
5	418641	BE243136	Hs.86947	a disintegrin and metalloproteinase doma	1.53	1.59
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), acli	1.52	7.60
	414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibito	1.49	0.52
	418543	NM_005329	Hs.85952	hyaluronan synthase 3	1.48	1.54
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	1.48	1.39
10	402260			NM_001436*:Homo sapiens fibrillarin (FBL	1.47	1.48
	424264	D80400	Hs.239388	Human DNA sequence from clone RP1-304B14	1.47	7.35
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.47	1.37
	422164	NM_014312	Hs.112377	cortic al thymocyte receptor (X. laevis	1.46	1.80
	444163	AI126098		gb:qc54g07.x1 Soares_placenta_8to9weeks_	1.45	1.58
15	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	1.45	1.58
	445182	AW189787		ESTs	1.43	7.15
	408930	AA146721	Hs.334686	hypothetical protein FLJ21588	1.43	1.53
	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	1.43	1.34
	406467			Target Exon	1.42	7.10
20	424244	AV647184	Hs.143601	hypothetical protein hCLA-iso	1.42	1.32
	422094	AF129535	Hs.272027	F-box only protein 5	1.41	4.55
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	1.39	10.36
	401760			Target Exon	1.37	1.16
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	1.36	1.39
25	424420	BE614743	Hs.146688	prostaglandin E synthase	1.33	1.49
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	1.31	1.44
	422119	AI277829	Hs.111862	KIAA0590 gene product	1.31	1.22
	418729	AB028449	Hs.87889	helicase-mol	1.30	0.84
	418399	AF131781	Hs.84753	hypothetical protein FLJ12442	1.30	1.32
30	453028	AB006532	Hs.31442	RecQ protein-like 4	1.29	1.42
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (1.29	0.61
	453321	AI984381	Hs.232521	ESTs	1.27	6.35
	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	1.26	6.30
	425726	AF085808	Hs.159330	uropodkin 3	1.26	2.26
35	406906	Z25424		gb:H.sapiens protein-serine/threonine ki	1.26	1.11
	429413	NM_014058	Hs.201877	DESC1 protein	1.25	1.01
	418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	1.23	1.17
	418140	AA534908	Hs.2860	POU domain, class 5, transcription facto	1.22	1.59
	417433	BE270266	Hs.82128	ST4 oncofetal trophoblast glycoprotein	1.20	1.38
40	422397	AJ223366	Hs.116051	Homo sapiens cDNA: FLJ22495 fis, clone H	1.19	1.23
	403903			C5001632*:gij10645308[gb]AAG21430.1 AC00	1.19	1.98
	425721	AC002115	Hs.159309	uropodkin 1A	1.17	2.30
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	1.17	5.85
	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	1.17	1.39
45	443859	NM_013409	Hs.9914	folistatin	1.17	1.17
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	1.13	2.83
	422330	D30783	Hs.115263	epiregulin	1.13	5.65
	420281	AI623693	Hs.323494	Predicted cation efflux pump	1.11	5.55
	424717	H03754	Hs.152213	wingless-type MMTV Integration site fami	1.08	5.40
50	440304	BE159984	Hs.125395	ESTs	1.06	5.30
	422170	AI791949	Hs.112432	anti-Mullerian hormone	1.06	1.55
	417599	AA204688	Hs.62954	ESTs	1.05	1.02
	411874	AA096106	Hs.20403	ESTs	1.04	7.20
	449961	AW265634	Hs.133100	ESTs	1.03	0.65
55	418506	AA084248	Hs.85339	G protein-coupled receptor 39	1.03	0.92
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	1.02	5.10
	453216	AL137566	Hs.32405	Homo sapiens mRNA; cDNA DKFZp586G0321 (f	1.02	0.60
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	1.00	0.05
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	1.00	0.25
60	453365	AA035211	Hs.17404	SOX7 SRY (sex determining region Y)-box	1.00	0.25
	439239	AI031540	Hs.235331	ESTs	1.00	0.27
	450684	AA872605	Hs.25333	interleukin 1 receptor, type II	1.00	0.45
	425650	NM_001944	Hs.1925	desmoglein 3 (pamphigus vulgaris antigen	1.00	0.72
	404403			Target Exon	1.00	1.00
65	406974	M57293		gb:Human parathyroid hormone-related pep	1.00	1.00
	410348	AW182663	Hs.95469	ESTs	1.00	1.00
	412661	N32860	Hs.24611	ESTs, Weakly similar to I54374 gene NF2	1.00	1.00
	419121	AA374372	Hs.89826	parathyroid hormone-like hormone	1.00	1.00
	426320	W47595	Hs.169300	transforming growth factor, beta 2	1.00	1.00
70	426958	U07616	Hs.173034	amphiphysin (Stiff-Mann syndrome with br	1.00	1.00
	432097	X51730	Hs.2905	progesterone receptor	1.00	1.00
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	1.00	1.00
	453389	BE273648	Hs.32963	cadherin 6, type 2, K-cadherin (fetal ki	1.00	1.00
	419078	M93119	Hs.89584	insulinoma-associated 1	1.00	1.25
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfami	1.00	1.35
75	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1.00	1.75
	451844	T61430		gb:yc06a03.s1 Stratagene lung (937210) H	1.00	1.80
	415178	D80503	Hs.322850	ESTs	1.00	2.20

5	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leuc	1.00	2.25
	425048	H05468	Hs.164502	ESTs	1.00	2.25
	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	1.00	2.60
	449448	D60730	Hs.57471	ESTs	1.00	2.70
	417791	AW965339	Hs.111471	ESTs	1.00	2.95
10	421373	AA808229	Hs.167771	ESTs	1.00	3.00
	427356	AW023482	Hs.97849	ESTs	1.00	3.15
	421070	AA283185	Hs.19327	ESTs	1.00	3.25
	415542	R13474	Hs.290263	ESTs, Weakly similar to I38022 hypotheti	1.00	3.35
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	1.00	3.55
15	402075			ENSP00000251056*:Plasma membrane calcium	1.00	3.95
	419559	Y07828	Hs.91096	ring finger protein	1.00	4.00
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	1.00	4.00
	418738	AW388633	Hs.6582	solute carrier family 7, (cationic amino	1.00	4.35
	412723	AA648459	Hs.335951	hypothetical protein AF301222	1.00	4.40
20	404877			NM_005365:Homo sapiens melanoma antigen,	1.00	4.45
	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	1.00	4.45
	403047			NM_005656*:Homo sapiens transmembrane pr	1.00	4.50
	406434			NM_030579*:Homo sapiens cytochrome b5 ou	1.00	4.65
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	1.00	4.65
25	433365	AF026944	Hs.293797	ESTs	1.00	10.05
	427665	AI791495	Hs.180142	calmodulin-like skin protein (CLSP)	0.99	0.60
	429504	X99133	Hs.204238	lipocatin 2 (oncogene 24p3)	0.99	1.00
	431474	AL133990	Hs.190642	CEGP1 protein	0.94	9.14
	411880	AW872477		gb:hm3003.x1 NCI_CGAP_Thy4 Homo sapiens	0.93	21.15
30	414221	AW450979		gb:UL-H-BI3-ala-a-12-0-UL.s1 NCI_CGAP_Su	0.91	2.60
	444649	AW207523	Hs.197628	ESTs	0.89	11.15
	456034	AW450979		gb:UL-H-BI3-ala-a-12-0-UL.s1 NCI_CGAP_Su	0.89	5.13
	414521	D28124	Hs.76307	neuroblastoma, suppression of tumorigeni	0.84	0.85
	439569	AW602166	Hs.222399	CEGP1 protein	0.84	2.42
35	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	0.81	6.75
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	0.80	0.57
	457292	AI921270	Hs.281462	hypothetical protein FLJ14251	0.77	1.40
	431089	BE041395		ESTs, Weakly similar to unknown protein	0.76	14.88
	459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	0.74	11.03
40	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	0.56	0.80
	406964	M21305		gb:Human alpha satellite and satellite 3	0.53	11.16
	416225	AA577730	Hs.188684	ESTs, Weakly similar to PC4259 ferritin	0.48	3.01
	400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	0.40	0.70
	421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	0.40	0.61

TABLE 3B

45	Pkey:	Unique Eos probeset identifier number				
	CAT number:	Gene cluster number				
50	Accession:	Genbank accession numbers				
55	Pkey	CAT Number	Accession			
	411880	1263110_1	AW872477 BE088101 T05990			
60	413804	1390710_1	T64682 BE168190 BE168256			
	414221	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367			
65	415989	156454_1	BE011368 BE011362 BE011215 BE011365 BE011363			
	431089	327825_1	AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172238 AW953397 AA355086			
70	431322	331543_1	BE041395 AA491825 AA621946 AA715980 AA666102			
	432222	343347_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188			
75	435608	42361_3	AI204995 AW827539 AW969908 AW440776 AA528756			
	439780	47673_1	AA628980 AI126603 BE504035			
80	444163	593658_1	AL109688 R23665 R26578			
	445182	632151_1	AI126098 AI184746 AI148521			
85	451844	888230_1	AW189787 AI215430 AW268499 AW205930 AI392907 BE093017 BE093019 BE093010			
	456034	142696_1	T61430 AI820546 AI821336			
90			AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367			
			BE011368 BE011362 BE011215 BE011365 BE011363			

TABLE 3C

70	Pkey:	Unique number corresponding to an Eos probeset				
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.				
75	Strand:	Indicates DNA strand from which exons were predicted.				
	Nt_position:	Indicates nucleotide positions of predicted exons.				
80						
85	Pkey	Ref	Strand	Nt_position		
	400773	8131629	Minus	44116-44238,48208-48321		

5	400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,10634-10789,15254-15403,23827-23958
	400844	9188605	Plus	24746-24872,25035-25204
	400845	9188605	Plus	34428-34612
	400846	9188605	Plus	39310-39474
	401093	8516137	Minus	22335-23166
10	401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
	401760	9929699	Plus	83126-83250,85320-85540,94719-95287
	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
	401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
	402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
15	402230	9966312	Minus	29782-29932
	402239	7690131	Plus	38175-38304,42133-42266
	402260	3399665	Minus	113765-113910,115653-115765,116808-116940
	402305	7328724	Plus	40832-41362
	402424	9796344	Minus	64925-65073
20	402777	9588235	Plus	126786-126948
	402901	8894222	Minus	175426-175667
	403047	3540153	Minus	59793-59968
	403381	9438267	Minus	26009-26178
	403903	7710671	Minus	101165-102597
25	404403	7272157	Minus	72053-72238
	404440	7528051	Plus	80430-81581
	404875	9801324	Plus	96588-96732,97722-97831
	404877	1519284	Plus	1095-2107
	404977	3738341	Minus	43081-43229
30	405033	7107731	Minus	142358-142546
	405932	7767812	Minus	123525-123713
	406081	9123861	Minus	38115-38691
	406399	9256288	Minus	63448-63554
	406434	9256651	Minus	17803-17931
	406467	9795551	Plus	182212-182958

TABLE 4A: Preferred diagnostics for bladder cancer

5	Pkey:	Unique Eos probeset identifier number					
	ExAccn:	Exemplar Accession number, Genbank accession number					
	UnigenelD:	Unigene number					
	Unigene Title:	Unigene gene title					
	R1:	80th percentile of muscle-invasive bladder tumor (stage T2-T4) Als divided by the 80th percentile of exophytic non-invasive carcinoma (stage Ta) Als					
10	R2:	90th percentile of bladder tumor Als minus background divided by 90th percentile of normal body sample Als minus background, where background equals the 15th percentile of all sample Als					
	R3:	90th percentile of bladder tumor Als divided by the 90th percentile of normal body sample Als					
	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2	R3
15	423961	D13666	Hs.136348	periostin (OSF-2os)	11.22	1.40	1.44
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	8.40	1.31	1.38
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothe	7.88	2.06	2.44
	408243	Y00787	Hs.624	interleukin 8	7.54	2.86	4.85
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	6.14	1.18	1.18
20	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	5.32	1.34	1.36
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	5.27	0.61	0.57
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	5.17	7.47	35.60
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	4.30	1.75	1.54
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	4.29	1.35	1.60
25	413324	V00571	Hs.75294	corticotropin releasing hormone	4.20	6.27	45.75
	412429	AV650262	Hs.75765	GRO2 oncogene	4.00	0.94	0.93
	406636	L12054		gb:Homo sapiens (clone WR4.12VL) anti-th	3.66	1.25	1.25
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.58	2.07	2.26
	406687	M31126		matrix metalloproteinase 11 (stromelysin	3.41	4.37	3.37
30	422550	BE297626	Hs.296049	microfibrillar-associated protein 4	3.09	0.39	0.40
	410867	X63556	Hs.750	fibrillin 1 (Marfan syndrome)	2.96	0.44	0.45
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	2.90	1.94	3.46
	414812	X72755	Hs.77367	monokine induced by gamma interferon	2.80	1.67	3.10
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	2.77	5.62	26.07
35	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.71	2.26	2.91
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytoltactin)	2.40	0.47	0.37
	417849	AW291587	Hs.82733	nidogen 2	2.34	0.88	0.86
	400419	AF084545		Target	2.33	1.54	2.12
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antag	2.10	1.01	1.01
40	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	1.99	3.19	17.50
	414774	X02419	Hs.77274	plasminogen activator, urokinase	1.94	2.49	1.84
	409420	Z15008	Hs.54451	laminin, gamma 2 (niclin (100kD), kalini	1.94	2.02	5.39
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	1.84	1.99	8.55
	414476	AA301887	Hs.76224	EGF-containing fibulin-like extracellula	1.76	0.33	0.31
45	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	1.76	1.13	1.16
	421958	AA357185	Hs.109918	ras homolog gene family, member H	1.75	1.33	1.27
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	1.58	2.42	1.39
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	1.57	2.02	8.55
	421493	BE300341	Hs.104925	ectodermal-neural cortex (with BTB-like	1.55	1.57	1.55
50	407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	1.41	0.79	0.67
	429344	R94038	Hs.199538	Inhibin, beta C	1.36	1.39	1.34
	402727			NM_025065:Homo sapiens hypothetical prot	1.34	1.34	1.56
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	1.31	1.63	2.22
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	1.27	2.00	1.67
55	424206	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc	1.25	0.16	0.30
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	1.23	1.70	4.34
	424479	AF064238	Hs.149098	smoothelin	1.19	0.27	0.47
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	1.17	1.59	2.93
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	1.16	0.82	0.80
60	421634	AA437414	Hs.106283	hypothetical protein FLJ10262	1.16	1.05	1.05
	439569	AW602166	Hs.222399	CEGP1 protein	1.15	2.01	2.42
	431346	AA371059	Hs.251636	ubiquitin specific protease 3	1.10	1.64	1.52
	448901	AK001021	Hs.22505	hypothetical protein FLJ10159	1.10	0.31	0.31
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	1.03	1.51	1.42
65	422424	AJ186431	Hs.296538	prostate differentiation factor	1.02	2.77	2.68
	458781	AJ444821	Hs.63085	ESTs, Weakly similar to MPP3_HUMAN MAGUK	1.00	1.64	5.45
	445413	AA151342	Hs.12677	CGI-147 protein	1.00	1.51	5.20
	432350	NM_005865	Hs.274407	protease, serine, 16 (thymus)	1.00	1.55	4.30
	403106			C8000084* g 10432393 emb CAC10283.1 (A	1.00	1.48	4.24
70	402075			ENSP00000251056* Plasma membrane calcium	1.00	1.67	3.95
	404860			C1003394* g 12314272 emb CAC00591.1 (A	1.00	1.40	3.90
	434037	AF116601		WW domain-containing oxidoreductase	1.00	1.58	3.70
	405738			CX000390* g 6014646 gb AAAF01438.1 AF187	1.00	1.35	2.95
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	1.00	1.45	1.60
75	439898	AW505514	Hs.209561	KIAA1715 protein	1.00	1.28	1.59
	452567	D87120	Hs.29882	predicted osteoblast protein	1.00	1.10	1.31
	401271			C9000559* g 12314195 emb CAB99338.1 (A	1.00	2.12	1.00
	411339	BE164598	Hs.274251	hypothetical protein FLJ20375; KIAA1797	1.00	2.05	1.00

	403005		C21000027*:gij1817556[dbj]BAA13672.1] (D	1.00	1.89	1.00
	431146	Z83850	Human DNA sequence from PAC 82J11 and co	1.00	1.89	1.00
	434939	AF161422	Hs.305567 Homo sapiens HSPC304 mRNA, partial cds	1.00	1.86	1.00
	431753	X76029	Hs.2841 neuromedin U	1.00	1.82	1.00
5	419121	AA374372	Hs.89626 parathyroid hormone-like hormone	1.00	1.69	1.00
	435505	AF200492	Hs.211238 interleukin-1 homolog 1	1.00	1.67	1.00
	452401	NM_007115	Hs.29352 tumor necrosis factor, alpha-induced pro	1.00	1.67	1.00
	406397		C16001447*:gij12053709[emb]CAC20419.1] (1.00	1.66	1.00
	404488		NM_030958*:Homo sapiens organic anion tr	1.00	1.56	1.00
10	441206	BE552314	Hs.131823 ESTs, Weakly similar to TERA HUMAN [H.sa	1.00	1.49	1.00
	407853	AA336797	Hs.40499 dickkopf (Xenopus laevis) homolog 1	1.00	1.47	1.00
	446119	D29527	Hs.290931 ESTs	1.00	1.47	1.00
	406471		Target Exon	1.00	1.44	1.00
	402110		C18000178:gij11990779[emb]CAC19649.1] (A	1.00	1.42	1.00
15	407911	AF104922	Hs.41565 growth differentiation factor 8	1.00	1.40	1.00
	404829		C1002937*:gij7499208[pir]T20993 hypothe	1.00	1.37	1.00
	421925	S80310	Hs.109620 acidic epididymal glycoprotein-like 1	1.00	1.26	1.00
	406076	AL390179	Hs.13755 Homo sapiens mRNA; cDNA DKFZp547P134 (fr	1.00	1.19	1.00
20	458622	AA972412	Hs.13755 f-box and WD-40 domain protein 2	1.00	1.09	1.00
	416018	AW138239	Hs.78977 proprotein convertase subtilisin/kexin 1	1.00	1.04	1.00
	409357	M73628	Hs.54415 casein, kappa	1.00	1.03	1.00
	436684	AW976319	Hs.94806 ATP-binding cassette, sub-family A (ABC1	1.00	0.84	0.84
	436178	BE152396	Hs.21590 hypothetical protein DKFZp564O0523	1.00	0.91	0.80
25	402522		C1000568*:gij12697965[dbj]BAB21801.1] (A	1.00	0.80	0.67
	405735		ENSP00000252164*:KIAA1578 protein (Fragm	1.00	0.86	0.56
	401905		ENSP00000252232*:Sterol regulatory eleme	1.00	0.65	0.52
	404152		C6000931*:gij9558454[dbj]BAB03398.1] (AB	1.00	0.58	0.51
	418693	AI750878	Hs.87409 thrombospondin 1	1.00	0.85	0.51
30	451375	AI792066	Hs.283902 Homo sapiens BAC clone RP11-481J13 from	1.00	0.46	0.38
	430132	AA204686	Hs.234149 hypothetical protein FLJ20647	1.00	0.84	0.33
	456983	AI081687	Hs.11355 thymopoietin	1.00	0.61	0.29
	439681	AW384815	Hs.149208 KIAA1555 protein	1.00	0.60	0.28
	409038	T97490	Hs.50002 small inducible cytokine subfamily A (Cy	1.00	0.39	0.19
35	409196	NM_001874	Hs.334873 carboxypeptidase M	1.00	0.43	0.13
	410023	AB017169	Hs.57929 slit (Drosophila) homolog 3	1.00	0.30	0.12
	420674	NM_000055	Hs.1327 butyrylcholinesterase	1.00	0.30	0.08
	415165	AW887604	Hs.78065 complement component 7	1.00	0.08	0.06
	425545	N98529	Hs.158295 Homo sapiens, clone MGC:12401, mRNA, com	1.00	0.10	0.01
40	448256	BE614149	Hs.20814 CGI-27 protein	0.96	1.32	1.55
	417389	BE260964	Hs.82045 midkine (neurite growth-promoting factor	0.95	3.15	2.34
	403214		NM_016232*:Homo sapiens interleukin 1 re	0.94	1.63	2.51
	414799	AI752416	Hs.77326 insulin-like growth factor binding prote	0.92	1.87	1.60
	406665	U22961	Hs.184411 albumin	0.92	1.09	1.03
45	401519		C15000476*:gij12737279[ra]XP_012163.1]	0.88	1.46	3.44
	417501	AL041219	Hs.82222 sema domain, immunoglobulin domain (Ig),	0.87	0.41	0.50
	409632	W74001	Hs.55279 serine (or cysteine) proteinase inhibito	0.85	1.38	1.43
	405494		C2001837*:gij12697903[dbj]BAB21770.1] (A	0.83	1.46	4.65
	444171	AB018249	Hs.10458 small inducible cytokine subfamily A (Cy	0.80	0.91	0.91
50	439706	AW872527	Hs.59761 ESTs, Weakly similar to DAPI_HUMAN DEATH	0.79	0.58	0.43
	436396	AI683487	Hs.152213 wingless-type MMTV integration site fami	0.77	1.47	2.37
	426716	NM_006379	Hs.171921 sema domain, immunoglobulin domain (Ig),	0.75	1.13	1.18
	431347	AI133461	Hs.251664 insulin-like growth factor 2 (somatomedi	0.68	2.61	1.87
	413753	U17760	Hs.75517 laminin, beta 3 (nicein (125kD), kalinin	0.68	2.70	4.96
55	426322	J05058	Hs.2012 transcobalamin I (vitamin B12 binding pr	0.67	1.50	1.36
	426514	BE616633	Hs.170195 bone morphogenetic protein 7 (osteogenic	0.56	2.05	2.46
	422282	AF019225	Hs.114309 apolipoprotein L	0.55	3.91	3.92
	409757	NM_001898	Hs.123114 cystatin SN	0.53	2.72	2.93
	427450	AB014526	Hs.178121 KIAA0526 gene product	0.52	1.34	1.97
60	414555	N98569	Hs.76422 phospholipase A2, group IIA (platelets,	0.50	1.04	1.05
	423774	L39064	Hs.1702 interleukin 9 receptor	0.49	2.81	6.46
	404977		Insulin-like growth factor 2 (somatomedi	0.28	5.78	5.17
	428336	AA503115	Hs.183752 microseminoprotein, beta-	0.21	1.47	1.56
	451668	Z43948	Hs.326444 cartilage acidic protein 1	0.18	4.05	3.60
65	428651	AF196478	Hs.188401 annexin A10	0.17	5.14	27.75
	421110	AJ250717	Hs.1355 cathepsin E	0.12	5.49	45.35

TABLE 4B

70 Key: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

75 Key CAT Number Accession
 431146 32854_1 Z83850 AA459717 AW965384 AA333635
 434037 37918_1 AF116601 AI110691 AF063566

TABLE 4C

5	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
	NL_position:	Indicates nucleotide positions of predicted exons.		
10	Pkey	Ref	Strand	NL_position
	401271	9797373	Minus	61292-61911
15	401519	6649315	Plus	157315-157950
	401905	8671966	Plus	153965-154441,156599-156819
20	402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
	402110	8131678	Minus	173889-174062
25	402522	9798493	Plus	20605-20731
	402727	9211324	Plus	54596-54777
30	403005	5791501	Minus	16945-17053,20018-20403
	403106	7331404	Plus	77162-77350,81338-81511
	403214	7630945	Minus	76723-77027,79317-79484
	404152	9884757	Plus	41111-41281,45495-45716,47801-47910
	404488	8113286	Minus	64835-64994
	404829	6624702	Minus	4913-5093,7310-7469,9472-9621,9951-10082
	404860	8979555	Plus	65852-66081
	404977	3738341	Minus	43081-43229
	405494	8050952	Minus	70284-70518
	405735	9931101	Minus	29854-29976
	405738	9943998	Plus	44370-45410
	406076	9123123	Plus	89972-90319
	406397	9256243	Minus	127317-127454
	406471	9795566	Plus	87383-87589

TABLE 5A: Genes upregulated in bladder cancer

	Pkey:	Unique Eos probaset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
5	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1	90th percentile of bladder tumor Als divided by the 90th percentile of normal body sample Als			
10	Pkey	ExAccn	UnigeneID	Unigene Title	R1
	459702	AI204995		gb:an03c03x1 Stratagene schizo brain S1	11.03
	437915	AI637993	Hs.202312	Homo sapiens clone N11 Ntera2D1 teratoca	10.40
	404917			Target Exon	9.65
	401066			C11000517*:gil7293105[gblAA48490.1] (AE	9.00
15	447475	AI380797	Hs.158992	ESTs	8.92
	427335	AA448542	Hs.251677	G antigen 7B	8.65
	450061	AI797034	Hs.346238	ESTs	8.35
	401335			Target Exon	7.95
20	424264	D80400	Hs.239388	Human DNA sequence from clone RP1-304B14	7.35
	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	7.20
	436608	AA628980		down syndrome critical region protein DS	4.86
	451950	AW292317	Hs.213307	ESTs	4.45
	406542			C19000728*:gil12585552[sp]Q9Y2Q1[Z257_HU	3.73
25	437931	AI249468	Hs.124434	ESTs	3.70
	443133	AI033878	Hs.41379	ESTs	3.60
	434487	AF143867	Hs.337588	ESTs, Moderately similar to S65657 alpha	3.37
	402239			Target Exon	3.37
	443162	T49951	Hs.9029	DKFZP434G032 protein	3.21
30	403383			Target Exon	3.13
	438315	R56795	Hs.82419	ESTs	3.04
	452827	AI571835	Hs.55468	ESTs	3.01
	416225	AA577730	Hs.188684	ESTs, Weakly similar to PC4259 fertilin	3.01
	402948			NM_025206:Homo sapiens hypothetical prot	2.91
35	429983	W92620	Hs.260855	ESTs	2.84
	429238	NM_002849	Hs.198288	protein tyrosine phosphatase, receptor t	2.78
	444371	BE540274	Hs.239	forkhead box M1	2.75
	417003	AL038170	Hs.80756	betaine-homocysteine methyltransferase	2.70
	414906	AA157911	Hs.72200	ESTs	2.70
40	425206	NM_002153	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	2.68
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	2.62
	429345	R11141	Hs.199695	hypothetical protein	2.61
	414221	AW450979		gb:U1-H-B13-ala-a-12-0-U1.s1 NCI_CGAP_Su	2.60
	402305			C19000735*:gil4508027[ref]NP_003414.1] z	2.54
45	432842	AW674093	Hs.334822	hypothetical protein MGC4485	2.51
	427719	AI393122	Hs.134726	ESTs	2.51
	455797	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	2.50
	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15(N	2.49
	456967	AW004056	Hs.168357	T-box 2	2.49
50	406387			Target Exon	2.48
	417997	AA418189	Hs.23017	Homo sapiens cDNA: FLJ22747 fis, clone K	2.48
	415752	BE314524	Hs.78776	putative transmembrane protein	2.46
	411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HE	2.43
	434293	NM_004445	Hs.3796	EphB6	2.42
55	433078	AW015188	Hs.121575	Homo sapiens cDNA FLJ12231 fis, clone MA	2.40
	425997	AK000086	Hs.165948	hypothetical protein FLJ20079	2.38
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	2.35
	452012	AA307703	Hs.279766	kinesin family member 4A	2.34
	445600	AF034803	Hs.12953	PTPRF Interacting protein, binding prote	2.33
60	418941	AA452970	Hs.239527	E1B-55kDa-associated protein 5	2.33
	454609	AW810204		gb:MR4-ST0125-021199-017-008 ST0125 Homo	2.28
	444476	AF020038	Hs.11223	isocitrate dehydrogenase 1 (NADP), solub	2.26
	420005	AW271106	Hs.133294	ESTs	2.22
	439826	NM_014965	Hs.6705	KIAA1042 protein	2.22
65	405531			Target Exon	2.21
	436569	BE439539	Hs.279837	glutathione S-transferase M2 (muscle)	2.18
	404394			ENSP00000241075:TRRAP PROTEIN.	2.17
	427479	BE410092	Hs.178471	KIAA0798 gene product	2.17
	435904	AF261655	Hs.8910	1,2-alpha-mannosidase IC	2.13
70	431620	AA126109	Hs.264981	2'-5'-oligoadenylate synthetase 2 (69-71	2.12
	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	2.10
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	2.10
	451385	AA017656		gb:za39h01.r1 Soares retina N2b4HR Homo	2.09
	403477			C3002160*:gil7662420[ref]NP_055738.1] KI	2.09
	417151	AA194055	Hs.293858	ESTs	2.08
75	448262	AW880830	Hs.186273	ESTs	2.07
	415192	D17793	Hs.78183	aldo-keto reductase family 1, member C3	2.04
	402994			NM_002463*:Homo sapiens myxovirus (influ	2.04

	426053	U68105	Hs.172182	poly(A)-binding protein, cytoplasmic 1	2.02
	423271	W47225	Hs.126256	interleukin 1, beta	2.01
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	1.99
	407581	R48402	Hs.173508	P3ECSE	1.95
5	410197	NM_005518	Hs.59889	3-hydroxy-3-methylglutaryl-Coenzyme A sy	1.95
	427122	AW057736	Hs.323910	HER2 receptor tyrosine kinase (c-erb-b2,	1.93
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	1.93
	436251	BE515055	Hs.296585	nucleolar protein (KKE/D repeat)	1.89
	401961			NM_021626:Homo sapiens serine carboxypep	1.86
10	434042	AI589941	Hs.8254	Homo sapiens, Similar to tumor different	1.85
	447532	AK000614	Hs.18791	hypothetical protein FLJ20607	1.84
	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	1.83
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	1.80
	422164	NM_014312	Hs.112377	cortic al thymocyte receptor (X. laevis	1.80
15	422247	U18244	Hs.113602	solute carrier family 1 (high affinity a	1.79
	410407	X66839	Hs.63287	carbonic anhydrase IX	1.78
	412115	AK001763	Hs.73239	hypothetical protein FLJ10901	1.77
	414809	AI434699	Hs.77356	transferrin receptor (p90, CD71)	1.75
	432210	AI567421	Hs.273330	Homo sapiens, clone IMAGE:3544662, mRNA,	1.74
20	427239	BE270447	Hs.174070	ubiquitin carrier protein	1.74
	459198	AI086347	Hs.151138	ESTs	1.74
	421066	AU076725	Hs.101408	branched chain aminotransferase 2, mitoc	1.71
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	1.70
	450663	H43540	Hs.25292	ribonuclease H1, large subunit	1.70
25	417324	AW265494		ESTs	1.67
	453883	AI638516	Hs.347524	cofactor required for Sp1 transcriptiona	1.66
	428000	R35145	Hs.291904	accessory proteins BAP31/BAP29	1.65
	450635	AW403954	Hs.25237	mesenchymal stem cell protein DSCD75	1.63
30	423397	NM_001838	Hs.1652	chemokine (C-C motif) receptor 7	1.62
	415440	D83782	Hs.78442	SREBP CLEAVAGE-ACTIVATING PROTEIN	1.62
	428028	U52112	Hs.182018	interleukin-1 receptor-associated kinase	1.62
	426783	Z19084	Hs.172210	MUF1 protein	1.62
	445937	AI452943	Hs.321231	UDP-Gal:beta-GlcNAc beta 1,4-galactosylt	1.61
	445462	AA378776	Hs.288549	hypothetical protein MGC3077	1.60
35	400965			C11002190*gi12737279 ref XP_012163.1	1.59
	432269	NM_002447	Hs.2942	macrophage stimulating 1 receptor (c-met	1.59
	429578	AI969028	Hs.99389	ESTs	1.59
	449027	AJ271216	Hs.22880	dipeptidylpeptidase III	1.59
40	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	1.59
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	1.59
	429002	AW248439	Hs.2340	junction plakoglobin	1.57
	442410	AW996503	Hs.197680	ESTs	1.56
	407601	AC002300	Hs.37129	sodium channel, nonvoltage-gated 1, beta	1.55
45	418543	NM_005329	Hs.85962	hyaluronan synthase 3	1.54
	424611	NM_001421	Hs.151139	E74-like factor 4 (ets domain transcript	1.54
	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	1.54
	408930	AA146721	Hs.334686	hypothetical protein FLJ21588	1.53
	448993	AI471630	Hs.8127	KIAA0144 gene product	1.52
50	414053	BE391635	Hs.75725	transgelin 2	1.51
	433562	W07162	Hs.150826	CATX-8 protein	1.50
	432562	BE531048	Hs.278422	DKFZP586G1122 protein	1.50
	402260			NM_001436*:Homo sapiens fibrillarin (FBL	1.48
	426127	L36983	Hs.167013	dynamitin 2	1.48
55	427557	NM_002659	Hs.179657	plasminogen activator, urokinase recepto	1.48
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	1.47
	418960	NM_004494	Hs.89525	hepatoma-derived growth factor (high-mob	1.46
	428293	BE250944	Hs.183556	solute carrier family 1 (neutral amino a	1.46
	432344	AI476474	Hs.248156	ESTs	1.46
60	453449	W16752	Hs.32981	sema domain, immunoglobulin domain (Ig),	1.46
	450690	AA296696	Hs.333418	FXRD domain-containing ion transport reg	1.46
	441940	AW298115	Hs.128152	ESTs	1.45
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	1.44
	439318	AW837046	Hs.6527	G protein-coupled receptor 56	1.42
65	422565	BE259035	Hs.118400	slinged (Drosophila)-like (sea urchin fas	1.41
	428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	1.41
	445417	AK001058	Hs.12680	Homo sapiens cDNA FLJ10196 fis, clone HE	1.39
	441565	AW953575	Hs.303125	p53-Induced protein PIGPC1	1.37
	439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	1.35
70	418399	AF131781	Hs.84753	hypothetical protein FLJ12442	1.32
	432636	AA340864	Hs.278562	claudin 7	1.32
	439053	BE244588	Hs.6456	chaperonin containing TCP1, subunit 2 (b	1.32
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	1.31
	453914	NM_000507	Hs.574	fructose-1,6-bisphosphatase 1	1.28
75	430056	X97548	Hs.228059	KRAB-associated protein 1	1.24
	451524	AK001466	Hs.26516	hypothetical protein FLJ10604	1.23
	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	1.20
	439863	BE547830	Hs.9408	paired immunoglobulin-like receptor beta	1.19

451541	BE279383	Hs.26557	plakophilin 3	1.16
406906	Z25424		gb:H.sapiens protein-serine/threonine ki	1.11
429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	1.00
414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	0.86
431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor {	0.61

TABLE 58

10 Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
414221	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368 BE011382 BE011215 BE011365 BE011363
417324	166714_1	AW265494 AA455904 AA195677 AW265432 AW991605 AA456370
436608	42361_3	AA628980 AI126603 BE504035
451385	86787_1	AA017656 AA017374 AA019761
454609	1226517_1	AW810204 AW810555 AW810196 AW810619 AW810507
455797	1366826_1	BE091833 BE091874 BE091871

TABLE 5C

25 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400955	7770576	Minus	173043-173564
401066	8217436	Plus	71448-71574
401335	9884881	Plus	15736-16352
401961	4581193	Minus	124054-124209
402239	7690131	Plus	38175-38304,42133-42266
402260	3399665	Minus	113765-113910,115653-115765,116808-116940
402305	7328724	Plus	40832-41362
402948	9368458	Minus	143456-143626,143808-143935
402994	2996643	Minus	4727-4969
403383	9438267	Minus	119837-121197
403477	9958251	Plus	111834-112008
404394	3135305	Minus	37121-37205,37491-37762,41053-41140,41322-41593,41773-41919
404917	7341851	Plus	49330-49498
405531	9665194	Plus	35602-35803
406387	9256180	Plus	116229-116371,117512-117651
406542	7711499	Plus	117335-118473

TABLE 6A: Genes upregulated in bladder cancer

5	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1	90th percentile of bladder tumor AIs divided by the 90th percentile of normal urothelium biopsy AIs			
10	R2	90th percentile of bladder tumor AIs divided by the 90th percentile of normal urothelium biopsy and normal bladder AIs			
	Pkey	ExAccn	UnigeneID	Unigene Title	R1 R2
	439926	AW014875	Hs.137007	ESTs	11.31 11.31
	413324	V00571	Hs.75294	corticotropin releasing hormone	9.15 9.15
	421110	AJ250717	Hs.1355	cathepsin E	9.07 9.07
15	417308	H60720	Hs.81892	KIAA0101 gene product	8.50 8.50
	418406	X73501	Hs.84905	cytokeratin 20	8.10 8.10
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	7.98 7.98
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	7.67 7.67
	408243	Y00787	Hs.624	interleukin 8	7.56 7.56
20	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	7.17 5.17
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	7.17 8.24
	414183	AW957446	Hs.301711	ESTs	7.14 4.62
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	7.12 7.12
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolog	6.90 3.38
25	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIb, r	6.85 4.98
	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	6.42 6.42
	438091	AW373062	Hs.75184	nuclear receptor subfamily 1, group I, m	6.32 6.32
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprotein	6.09 3.67
	414219	W20010	Hs.75823	ALL1-fused gene from chromosome 1q	5.93 4.68
30	405033			C1002652*gi544327 sp Q04799 FMO5_RABIT	5.84 5.84
	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalytic	5.79 5.68
	428336	AA503115	Hs.183752	microseminoprotein, beta-	5.78 4.57
	449230	BE613348	Hs.215179	melanoma cell adhesion molecule	5.69 5.82
	423673	BE003054	Hs.1696	matrix metalloproteinase 12 (macrophage	5.69 7.30
35	415511	AJ732617	Hs.182362	ESTs	5.65 5.65
	426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase domain	5.60 5.60
	421948	L42583	Hs.334309	keratin 6A	5.59 14.20
	428651	AF196478	Hs.188401	annexin A10	5.55 5.55
	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	5.38 5.59
40	406687	M31126		matrix metalloproteinase 11 (stromelysin	5.36 5.34
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	5.35 5.35
	408246	N55669	Hs.333823	mitochondrial ribosomal protein L13	5.20 3.50
	427678	BE267756	Hs.180312	mitochondrial ribosomal protein S16	5.13 4.10
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	4.97 3.71
45	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	4.90 4.90
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	4.90 4.77
	417720	AA205625	Hs.208067	ESTs	4.84 7.34
	423979	AF229181	Hs.136644	CS box-containing WD protein	4.81 4.81
	420981	L40904	Hs.100724	peroxisome proliferative activated recep	4.81 4.43
50	433470	AW960564		transmembrane 4 superfamily member 1	4.72 4.72
	429138	AB020657	Hs.197298	NS1-binding protein	4.71 4.71
	408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	4.71 4.71
	452714	AW770994	Hs.30340	hypothetical protein KIAA1165	4.69 4.69
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	4.68 4.68
55	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	4.65 4.65
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	4.64 4.64
	427490	Z95152	Hs.178695	mitogen-activated protein kinase 13	4.63 5.12
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	4.61 4.61
	416030	BE207573	Hs.83321	neuromedin B	4.60 4.60
60	401192			Target Exon	4.60 4.29
	426761	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586I2022 (I	4.59 3.51
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	4.58 5.33
	446618	AJ076459	Hs.15978	KIAA1272 protein	4.58 4.58
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.55 4.55
65	415701	NM_003878	Hs.78619	gamma-glutamyl hydrolase (conjugase, fol	4.52 4.70
	446742	AA232119	Hs.16085	putative G-protein coupled receptor	4.49 4.11
	419433	AA814807	Hs.7395	hypothetical protein FLJ23182	4.48 4.48
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	4.47 4.47
	427528	AJ077143	Hs.179565	minichromosome maintenance deficient (S.	4.45 4.45
70	444371	BE540274	Hs.239	forkhead box M1	4.44 3.87
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	4.43 3.63
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	4.43 4.43
	401093			C12000586*gi6330167 dbj BA88477.1 (A	4.40 4.40
	447644	AW861622	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	4.39 4.39
75	417933	X02308	Hs.82962	thymidylate synthetase	4.38 4.35
	409461	AA382169	Hs.54483	N-myc (and STAT) interactor	4.36 3.68
	401451			NM_004496*:Homo sapiens hepatocyte nucle	4.35 4.35
	450746	D82673	Hs.278589	general transcription factor II, I	4.35 3.36

5	414683	S78296	Hs.76888	hypothetical protein MGC12702	4.34	4.74
	434203	BE262677	Hs.283558	hypothetical protein PRO1855	4.31	4.31
	417615	BE548541	Hs.82314	hypoxanthine phosphoribosyltransferase 1	4.30	4.30
	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	4.30	4.30
	440086	NM_005402	Hs.288757	v-rat simian leukemia viral oncogene hom	4.29	4.29
10	417715	AW695687	Hs.86366	ESTs	4.27	7.45
	409757	NM_001898	Hs.123114	cystatin SN	4.24	3.39
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	4.24	4.24
	432842	AW674093	Hs.334822	hypothetical protein MGC4485	4.21	4.12
	446847	T51454	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	4.20	4.20
15	436856	AI469355	Hs.127310	ESTs	4.19	4.19
	428450	NM_014791	Hs.184339	KIAA0175 gene product	4.16	4.90
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	4.14	4.14
	409231	AA446544	Hs.692	GA733-2 antigen; epithelial glycoprotein	4.14	5.99
	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	4.12	4.12
20	446849	AU076617	Hs.16251	cleavage and polyadenylation specific fa	4.12	3.43
	400843			NM_003105*:Homo sapiens sortilin-related	4.11	5.51
	449722	BE280074	Hs.239560	cyclin B1	4.09	4.09
	405506			Target Exon	4.09	3.75
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	4.07	4.07
25	426997	BE620738	Hs.173125	peptidylprolyl isomerase F (cyclophilin	4.05	4.80
	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	4.03	7.64
	437150	R51407	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	4.02	4.02
	413794	AF234532	Hs.61638	myosin X	4.02	4.02
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	4.02	4.72
30	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	4.01	3.99
	416391	AI878927	Hs.79284	mesoderm specific transcript (mouse) hom	4.01	4.01
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	4.00	4.00
	400277			Eos Control	4.00	3.47
	415791	H09366	Hs.78853	uracil-DNA glycosylase	3.99	3.37
35	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	3.98	4.77
	427557	NM_002659	Hs.179657	plasminogen activator, urokinase recepto	3.98	3.95
	413753	U17760	Hs.75517	laminin, beta 3 (nlcn (125kD), kalinin	3.96	6.95
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	3.92	5.04
	400409	AF153341		Homo sapiens winged helix/forkhead trans	3.91	3.88
40	408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	3.90	3.90
	411678	AI907114	Hs.71465	squalene epoxidase	3.89	3.89
	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	3.87	3.87
	428428	AL037544	Hs.184298	cyclin-dependent kinase 7 (homolog of Xe	3.87	3.87
	442932	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	3.85	4.50
45	429083	Y09397	Hs.227817	BCL2-related protein A1	3.85	3.85
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	3.82	3.77
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E. coli Re	3.82	3.82
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	3.81	3.81
	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	3.81	3.62
50	430259	BE550182	Hs.127826	RatGEF-like protein 3, mouse homolog	3.80	3.80
	447973	AB011169	Hs.20141	similar to S. cerevisiae SSM4	3.77	3.77
	404875			NM_022819*:Homo sapiens phospholipase A2	3.77	3.46
	411299	BE409857	Hs.69499	hypothetical protein	3.76	3.76
	418827	BE327311	Hs.47166	HT021	3.76	3.76
55	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	3.75	3.75
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.73	3.73
	433376	AJ249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	3.71	3.71
	400294	N95796	Hs.278695	Homo sapiens protein mRNA, complete cds	3.70	3.45
	409518	BE384836	Hs.3454	KIAA1821 protein	3.69	3.69
60	430024	AI808780	Hs.227730	integrin, alpha 6	3.69	3.69
	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	3.68	3.68
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.68	3.66
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.67	3.67
	413670	AB000115	Hs.75470	hypothetical protein, expressed in osteo	3.67	3.41
65	424840	D79987	Hs.153479	extra spindle poles, S. cerevisiae, homo	3.67	3.88
	434263	N34895	Hs.44648	ESTs	3.65	3.65
	438280	AW015534	Hs.217493	annexin A2	3.63	3.36
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.63	3.68
	408989	AW361666	Hs.49500	KIAA0746 protein	3.61	3.66
70	416640	BE262478	Hs.79404	neuron-specific protein	3.60	4.22
	416926	H03109	Hs.108920	HT018 protein	3.59	3.59
	414368	W70171	Hs.75939	uridine monophosphate kinase	3.59	3.53
	402727			NM_025065:Homo sapiens hypothetical prot	3.58	3.58
	419381	AB023420	Hs.90093	heat shock 70kD protein 4	3.56	3.77
75	416114	AI695549	Hs.183868	glucuronidase, beta	3.55	3.55
	424941	AA128376	Hs.153884	ATP binding protein associated with cell	3.55	3.55
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	3.54	4.63
	429238	NM_002849	Hs.198288	protein tyrosine phosphatase, receptor t	3.53	3.92
	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	3.51	5.77
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	3.50	3.50
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.50	3.50

	415220	AA431880	Hs.181174	ESTs, Weakly similar to T19201 hypotheti	3.50	3.50
	428371	AB012193	Hs.183874	cullin 4A	3.46	3.46
	418663	AK001100	Hs.41690	desmocollin 3	3.45	4.74
5	404977			Insulin-like growth factor 2 (somatomedi	3.45	3.89
	422663	AW500087	Hs.119014	zinc finger protein 175	3.44	3.44
	434061	AW024973	Hs.283675	NP0009 protein	3.41	5.64
	418113	AJ272141	Hs.83484	SRY (sex determining region Y)-box 4	3.41	4.32
	431689	AA305688	Hs.287695	UDP-GalbetaGlcNAc beta 1,3-galactosyltr	3.40	3.40
10	411943	BE502436	Hs.7962	ESTs, Weakly similar to S44608 C02F5.6 p	3.39	4.27
	420005	AW271106	Hs.133294	ESTs	3.38	3.40
	453450	AW797627	Hs.347459	ADP-ribosylation factor 6	3.38	3.87
	410315	AJ638871	Hs.17625	Homo sapiens cDNA: FLJ22524 fis, clone H	3.36	3.36
	428839	AJ767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	3.35	3.35
	437469	AW753112	Hs.15514	hypothetical protein MGC3260	3.35	3.35
15	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	3.34	3.34
	428157	AJ738719	Hs.198427	hexokinase 2	3.33	3.73
	450293	N36754	Hs.171118	hypothetical protein FLJ00026	3.33	3.33
	400750			Target Exon	3.33	3.33
20	450139	AK001838	Hs.296323	serum/glucocorticoid regulated kinase	3.33	3.33
	412636	NM_004415		desmoplakin (DPI, DPII)	3.30	4.81
	447578	AA912347	Hs.136585	ESTs, Weakly similar to JC5314 CDC28cdc	3.27	3.38
	430315	NM_004293	Hs.239147	guanine deaminase	3.26	4.30
	421594	R45689	Hs.21889	Homo sapiens cDNA FLJ12978 fis, clone NT	3.26	3.41
25	443030	R68048	Hs.9238	hypothetical protein FLJ23516	3.19	3.34
	436911	AA142984	Hs.5344	adaptor-related protein complex 1, gamma	3.17	3.40
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	3.06	3.52
	443171	BE281128	Hs.9030	TONDU	3.05	3.83
	429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, clone	3.01	3.53
30	408380	AF123050	Hs.44532	diubiquitin	2.99	4.11
	421508	NM_004833	Hs.105115	absent in melanoma 2	2.99	3.67
	439750	AL359053	Hs.57654	Homo sapiens mRNA full length insert cDN	2.97	4.55
	452046	AB018345	Hs.27657	KIAA0802 protein	2.95	3.39
	451940	AJ735759	Hs.52620	integrin, beta 8	2.93	3.58
35	407722	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin B6) kinas	2.90	3.68
	422282	AF019225	Hs.114309	apolipoprotein L	2.89	3.57
	402230			Target Exon	2.88	5.36
	406685	M18728		gb:Human nonspecific crossreacting antig	2.80	5.80
40	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	2.79	3.89
	447957	NM_014821	Hs.20126	KIAA0317 gene product	2.75	3.45
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	2.75	3.46
	417275	X63578	Hs.295449	parvalbumin	2.73	3.54
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	2.72	8.39
	401781			Target Exon	2.62	4.15
45	407242	M18728		gb:human nonspecific crossreacting antig	2.54	5.96
	428423	AU076517	Hs.184276	solute carrier family 9 (sodium/hydrogen	2.52	4.27
	430200	BE613337	Hs.234896	geminin	2.52	4.19
	451035	AU076785	Hs.430	plastin 1 (I isoform)	2.51	4.15
	443162	T49951	Hs.9029	DKFZP434G032 protein	2.48	3.66
50	441495	AW294603	Hs.127039	ESTs	2.45	3.60
	449245	AW411209	Hs.23363	hypothetical protein FLJ10983	2.45	3.52
	401780			NM_005557*:Homo sapiens keratin 16 (foca	2.22	4.49
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	2.20	3.55
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias	2.15	6.08
55	439394	AA149250	Hs.56105	ESTs	2.05	3.95
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	1.79	3.88

TABLE 6B

60	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers
65	Pkey	CAT Number
	412636	13165_1
70	Accession	NM_004415 AL031058 M77830 BE149760 AW752599 AW848723 AW376697 AW376817 AW376699 AW848371 AW376782 AW848789
		AW361413 AW849074 AW997139 AW799304 AW799309 BE077020 BE077017 BE185187 AW997196 BE156621 BE179915 BE006561
		BE143155 AW890985 BE002107 AW103521 AA857316 AW383133 BE011378 AW170253 BE185750 AW886475 BE160433 J05211 BE082576
		BE082584 BE004047 AW607238 AW377700 AW377699 BE082526 BE082505 BE082507 BE082514 AW178000 AW177933 AJ905935
		AW747877 AW748114 BE148516 AW265328 AW847678 AW847688 AW365151 AW365148 AW365153 AW365156 AW365175 AW365157
		AW365154 AW068840 BE005272 AW365145 BE001925 BE182166 BE144243 BE001923 AJ951766 AJ434518 BE184920 BE184933 AJ284090
		BE184941 AW804674 BE184924 C04715 W39488 AW995515 BE184948 BE159545 AW606553 AA099891 AA131128 AA337270 AA340777
		AW384371 AA852212 R58704 AW386566 AW364859 AA025851 AA025852 AA455100 AA719958 AW352220 AW996245 BE165351 BE073467
		AA377127 AW890264 AW609750 AW391912 AW849690 T87267 AW853812 AA852213 W74149 BE009090 AA056401 H91011 AW368529
		AW390272 C18467 AW674920 N57176 AA026480 AW576767 H93284 AA026863 AW177787 AA026654 AW177786 BE092134 BE092137
75		BE092136 AW177784 AJ022862 BE091653 AW376811 AW848592 AA040018 BE185331 BE182164 AA368564 AW951576 T29918 AA131077
		W95048 W25458 AW205789 H90899 N29754 W32490 R20904 BE167181 BE167165 N84767 H27408 H30146 AJ190690 C03378 AJ554403
		AJ205263 AA128470 AJ392926 AF139055 AW370813 AW370827 AW798417 AW798780 AW798883 AW798569 R33557 AA149190 C03029

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AW177783 AA088866 AW370829 AA247685 BE002273 AI760816 AI439101 AW879451 AI700963 AA451923 AI340326 AI590975 T48793
 AI568096 AI142882 AA039975 AI470146 AA946936 BE067737 BE067786 W19287 AA644381 AA702424 AI417612 AI306554 AI686869
 AI568892 AW190555 AI571075 AI220573 AA056527 AI471874 AI304772 AW517828 AI915596 AI627383 AI270345 AW021347 AW166807
 AW105614 AI346078 AA552300 W95070 AI494069 AI911702 AA149191 AA026864 AI830049 AI887258 AW780435 AI910434 AI819984
 AI858282 AI078449 AI025932 AI860584 AI635878 AA026047 AA703232 D12062 AW192085 AA658154 AW514597 AW591892 T87181
 AA782066 AW243815 AW150038 AW268383 AW004633 AI927207 AA782109 AW473233 AI804485 AW169216 AI572669 AA602182
 AW015480 AW771865 AI270027 AA951816 AA283207 AI076962 AI498487 AI348053 AI783914 H44405 AW799118 AA128330 AA515500
 AA918281 W02156 AI905927 AA022701 W38382 R20795 T77861 AW860878
 AW960564 AA092457 T55890 D56120 T92525 AI815987 BE182608 BE182595 AW080238 M90657 AA347236 AW961686 AW176445
 AA304671 AW583735 T61714 AA316968 AI446615 AA343532 AA083489 AA488005 W52095 W39480 N57402 D82638 W25540 W52847
 D82729 D58990 BE619182 AA315188 AA308636 AA112474 W76162 AA088544 H52265 AA301631 H80982 AA113786 BE620997 AW651691
 AA343799 BE613669 BE547180 BE546656 F11933 AA376800 AW239185 AA376086 BE544387 BE619041 AA452515 AA001806 AA190873
 AA180483 AA169546 F00242 AI940609 AI940602 AI189753 T97653 T66110 AW062896 AW062910 AW062902 AI051622 AI828930 AA102452
 AI685095 AI819390 AA557597 AA383220 AI804422 AI633575 AW338147 AW603423 AW606800 AW750567 AW510672 AI250777 AA083510
 AW629109 AW513200 AA921353 AI677934 AI148698 AI955858 AA173825 AA453027 AI027865 AW375542 AA454099 AA733014 AI591384
 R79300 R80023 AA843108 AA626058 AA844898 AW375550 AA889018 AI474275 AW205937 AI052270 AW388117 AW388111 AA699452
 AI242230 N47476 H38178 AA366621 AA113196 AA130023 H39740 T61629 AI885973 AW083671 AA179730 AA305757 AI285455 N83956
 AA216013 AA336155 AW999959 T97525 AA345349 T91762 AA771981 AI285092 AI591386 BE392486 BE385852 AA682601 AI682884
 AA345840 T85477 AA292649 AA932079 AA098791 D82607 T48574 AW752038 C06300
 AW373062 T55662 AI299190 BE174210 AW579001 H01811 W40186 R67100 AI923886 AW952164 AA628440 AW898607 AW898616
 AA709126 AW898628 AW898544 AA947932 AW898625 AW898622 AI276125 AI185720 AW510698 AA987230 T52522 BE467708 AW243400
 AW043642 AI288245 AI186932 D52654 D55017 D52715 D52477 D53933 D54679 AI298739 AI146984 AI922204 N98343 BE174213 AA845571
 AI813854 AI214518 AI635262 AI139455 AI707807 AI698085 AW884528 AI024768 AI004723 AW087420 AI565133 N94964 AI268939
 AW513280 AI061126 AI435818 AI859106 AI360506 AI024767 AA513019 AA757598 X56196 AA902959 AI334784 AI860794 AA010207
 AW890091 AW513771 AI951391 AI337671 T52499 AA890205 AI640908 H75966 AA463487 AA358688 AI961767 AI865295 AA780994
 AI985913 BE174196 AA029094 AW592159 T55581 N79072 AI611201 AA910812 AI220713 AW149306 AI758412 AA045713 R79750 N76096

TABLE 6C

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Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
 sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

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Pkey	Ref	Strand	Nt_position
400750	8119067	Plus	198991-199168, 199316-199548
400843	9188605	Plus	5863-5970, 7653-7784, 8892-9023, 9673-9807, 10634-10789, 15254-15403, 23827-23958
401093	8516137	Minus	22335-23166
401192	9719502	Minus	69559-70101
401451	6634068	Minus	119926-121272
401780	7249190	Minus	28397-28617, 28920-29045, 29135-29296, 29411-29567, 29705-29787, 30224-30573
401781	7249190	Minus	83215-83435, 83531-83656, 83740-83901, 84237-84393, 84955-85037, 86290-86814
402230	9966312	Minus	29782-29932
402727	9211324	Plus	54596-54777
404875	9801324	Plus	96588-96732, 97722-97831
404977	3738341	Minus	43081-43229
405033	7107731	Minus	142358-142546
405506	6466489	Plus	80014-80401, 80593-81125

TABLE 7A: Genes downregulated in bladder cancer

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1 90th percentile of normal urothelium biopsy Als divided by 75th percentile of bladder tumor Als
 R2 90th percentile of normal urothelium biopsy and normal bladder Als divided by the 90th percentile bladder tumor Als

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
403010			C21000152:gi 6226483 sp Q52118 YMO3_ERWS	4.86	2.49
426796	S78234	Hs.172405	cell division cycle 27	4.28	2.48
416225	AA577730	Hs.188684	ESTs, Weakly similar to PC4259 ferritin	4.04	2.07
459006	AW298631	Hs.27721	Wolf-Hirschhorn syndrome candidate 1-lik	3.82	2.66
404917			Target Exon	3.78	2.00
426488	X03350	Hs.4	alcohol dehydrogenase 1B (class I), beta	2.64	1.79
419543	AA244170		gb:nc05h02.s1 NCL CGAP_Pr1 Homo sapiens	2.63	3.42
453180	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	2.32	3.24
428957	NM_003881	Hs.194679	WNT1 Inducible signaling pathway protein	2.20	3.80
451529	AI917901	Hs.208641	ESTs	2.18	3.69
417076	AW973454	Hs.238442	ESTs, Moderately similar to ALU7_HUMAN A	2.03	3.03
425438	T62216	Hs.270840	ESTs	2.00	5.17
450515	AW304226		biphenyl hydrolase-like (serine hydrolas	1.89	2.46
432873	AW837268	Hs.279639	Homo sapiens mRNA; cDNA DKFZp586M2022 (f	1.70	2.79
452123	AI267615	Hs.38022	ESTs	1.69	2.46
424378	W28020	Hs.167988	neural cell adhesion molecule 1	1.65	4.67
437601	AA761546	Hs.248844	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.50	3.34
402096			ENSP00000217725*-Laminin alpha-1 chain p	1.48	3.02
439563	AI018768	Hs.12482	glyceronephosphate O-acyltransferase	1.47	3.22
412810	M21574	Hs.74615	platelet-derived growth factor receptor,	1.46	2.30
458651	AW612481	Hs.104105	ESTs	1.39	2.89
414033	AL079707	Hs.207443	hypothetical protein MGC10848	1.35	2.80
433572	AL046859	Hs.3407	protein kinase (cAMP-dependent, catalyti	1.35	3.49
413305	NM_000426	Hs.323511	Homo sapiens cDNA: FLJ23176 fis, clone L	1.34	2.93
420412	AW976674	Hs.125103	ESTs	1.32	5.13
421406	AF179897	Hs.104105	Meis (mouse) homolog 2	1.31	4.07
417446	AL118671	Hs.82163	monoamine oxidase B	1.27	2.86
452886	AI478250	Hs.13751	ESTs	1.26	1.95
446808	AA703226	Hs.16193	Homo sapiens mRNA; cDNA DKFZp586B211 (fr	1.25	3.44
443105	X95753	Hs.9004	chondroitin sulfate proteoglycan 4 (mela	1.24	2.07
421348	M94048	Hs.103724	peripheral myelin protein 22	1.24	2.63
433070	N75346	Hs.306121	CDC20 (cell division cycle 20, S. cerevi	1.23	2.80
420059	AF161488	Hs.94769	RAB23, member RAS oncogene family	1.22	3.43
408491	AI080663	Hs.7882	ESTs	1.20	6.01
447384	AI377221	Hs.40528	ESTs	1.00	7.92
421998	R74441	Hs.117176	poly(A)-binding protein, nuclear 1	1.00	7.38
409619	AK001015	Hs.55220	BCL2-associated athanogene 2	1.00	6.40
444795	AI193356	Hs.160316	ESTs	1.00	5.53
408495	W68796	Hs.237731	ESTs	1.00	5.05
417124	BE122762	Hs.25338	ESTs	1.00	4.73
443998	AI620661	Hs.296276	ESTs	1.00	4.39
406303			C16000922:gi 7499103 pir T20903 hypothe	1.00	4.37
422994	AW891802	Hs.296276	ESTs	1.00	4.37
422195	AB007903	Hs.113082	KIAA0443 gene product	1.00	4.35
452877	AI250789	Hs.32478	ESTs	1.00	3.90
452487	AW207659	Hs.6630	Homo sapiens cDNA FLJ13329 fis, clone OV	1.00	3.90
417159	R01761		gb:ye81f10.s1 Soares fetal liver spleen	1.00	3.82
445607	AA488107	Hs.30156	ESTs, Weakly similar to unnamed protein	1.00	3.62
406274			Target Exon	1.00	3.59
410611	AW954134	Hs.20924	KIAA1628 protein	1.00	3.06
426495	NM_001151	Hs.2043	solute carrier family 25 (mitochondrial	1.00	2.89
422292	AI815733	Hs.114360	transforming growth factor beta-stimulat	1.00	2.61
413040	AA193338	Hs.12321	sodium calcium exchanger	1.00	2.51
429623	NM_005308	Hs.211569	G protein-coupled receptor kinase 5	1.00	2.05
456607	AI660190	Hs.108070	cyclin-dependent kinase inhibitor 1C (p5	1.00	2.01
429143	AA333327	Hs.197335	plasma glutamate carboxypeptidase	0.97	2.45
400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	0.90	2.47
442498	U54617	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	0.88	5.08
414449	AA557660	Hs.76152	decorin	0.88	3.13
412014	AI620650	Hs.43761	ESTs, Weakly similar to A46010 X-linked	0.78	1.88
425100	AF051850	Hs.154567	supervillin	0.70	3.90
432094	AI658580	Hs.61426	Homo sapiens mesenchymal stem cell prote	0.68	3.41
427818	AW511222	Hs.193765	ESTs	0.63	3.75

TABLE 7B

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number
Accession: Genbank accession numbers

5 Pkey CAT Number Accession
417159 1653899_1 R01761 R01760 N49787
419543 185745_1 AA244170 AJ018087 AA244355
450515 837110_1 AW304226 AW008420 AA349212 H15015 AA317021 A1829484 H25661 H81744 A1906147 AA837938 AW167766 AW603578 AW842359
10 BE439926 AA902417 AW235409 AA010062 AW069319 A1280242 AW672925 H06848 H05608 R51905 R45023 AW675471 H28475 A1085597
A1197815 A1825355 N99134 A1075956 A1470122 AA449985 AW662633 AA860423 AA913342 T23825 A1394207 A1310319 T32467 A1589870
A1682293 A1810633 BE223045 H14620 AA626645 AA876023 T33571 AA953982 A1138631 H15016 A1304356 AA983631 A1350990 A1143993
A1708171 AA526961 H26247 W38485 AA847598 H81745 AW855486 BE299605 A1079409 A1278050 A1223168 A1860904 AW025415 A1339003
AA393692 A1354302 A1492838 N80194 A1015651 N34543 BE295397 A1085154 W24135

15 TABLE 7C

20 Pkey: Unique number corresponding to an Eos probaset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

25 Pkey Ref Strand Nt_position
402096 8117697 Minus 24993-25186
403010 3132346 Plus 78385-79052
404917 7341851 Plus 49330-49498
406274 7543787 Plus 932-1123
30 406303 8575868 Plus 173622-173786

TABLE 8A: Genes predictive of bladder cancer progression

5	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1	80th percentile of Ta or T1 tumor AIs from patients who upstaged divided by 80th percentile of Ta or T1 tumor AIs from patients who did not upstage			
10	R2	median of Ta or T1 tumor AIs from patients who upstaged divided by the median of Ta or T1 tumor AIs from patients who did not upstage			
	Pkey	ExAccn	UnigeneID	Unigene Title	R1 R2
	413324	V00571	Hs.75294	corticotropin releasing hormone	8.30 4.18
	437802	AI475995	Hs.122910	ESTs	7.51 2.50
15	444444	AI149332	Hs.14855	ESTs	2.58 1.38
	445033	AV652402	Hs.72901	mucin 13, epithelial transmembrane	2.26 1.13
	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	3.27 5.33
	449618	AI076459	Hs.15978	KIAA1272 protein	2.70 3.33
	407242	M18728		gb:Human nonspecific crossreacting anti	3.58 1.90
20	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	3.32 1.00
	423441	R68649	Hs.278359	absent in melanoma 1 like	2.44 2.40
	405033			C1002652*gi544327[sp]Q04799[FM05_RABIT	1.75 3.48
	423024	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	3.72 1.28
	425118	AU076611	Hs.154572	methylene tetrahydrofolate dehydrogenase	2.40 2.78
25	437928	NM_005476	Hs.5920	UDP-N-acetylglucosamine-2-epimerase/N-ac	2.20 1.53
	446584	U53445	Hs.15432	downregulated in ovarian cancer 1	1.38 2.33
	436608	AA628980		down syndrome critical region protein DS	3.32 4.53
	404440			NM_021048:Homo sapiens melanoma antigen,	2.64 1.00
	435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	2.06 1.09
30	424098	AF077374	Hs.139322	small proline-rich protein 3	2.47 3.64
	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	2.09 0.91
	428036	AW068302		Homo sapiens mRNA for caldesmon, 3' UTR	2.71 4.58
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	3.18 2.33
	448479	H96115	Hs.21293	UDP-N-acetylglucosamine pyrophosphorylas	2.61 1.81
35	412059	AA317962	Hs.249721	ESTs, Moderately similar to PC4259 ferri	1.90 2.02
	401241	AB028989		mitogen-activated protein kinase 8 inter	1.26 2.55
	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	2.12 1.23
	415989	AI267700		ESTs	1.60 1.00
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	1.73 1.50
40	452140	AB007928	Hs.28169	KIAA0459 protein	2.44 2.95
	443162	T49951	Hs.9029	DKFZP434G032 protein	2.98 1.00
	435904	AF261655	Hs.8910	1,2-alpha-mannosidase IC	2.56 1.20
	407379	AA332127	Hs.325804	transcription factor 17	2.10 1.72
	442712	BE465168	Hs.131011	ESTs	2.54 2.72
45	411678	AI907114	Hs.71465	squalene epoxidase	1.12 3.11
	406791	AI220684	Hs.347939	hemoglobin, alpha 2	1.69 1.38
	431805	NM_014053	Hs.270594	FLVCR protein	1.92 2.05
	438414	AA806794	Hs.131511	ESTs	1.04 2.15
	413924	AL119964	Hs.75616	seladin-1	1.69 2.05
50	437679	NM_014214	Hs.5753	inositol(myo)-1(or 4)-monophosphatase 2	2.27 2.26
	445911	AI985987	Hs.145645	ESTs, Moderately similar to ALU1_HUMAN A	1.42 2.74
	408349	BE546947	Hs.44276	homeo box C10	1.60 2.05
	422545	X02761	Hs.287820	fibronectin 1	1.77 3.02
	406643	N77976	Hs.347939	hemoglobin, alpha 2	1.57 1.35
55	407228	M25079	Hs.155376	hemoglobin, beta	1.81 1.50
	449644	AW960707	Hs.148324	ESTs	1.90 3.19
	402305			C19000735*gi4508027[ref]NP_003414.1 z	2.25 1.49
	427683	BE545490	Hs.15053	Homo sapiens HCMOGT-1 mRNA for sperm ant	1.08 2.25
	441690	R81733	Hs.33106	ESTs	1.80 2.65
60	434487	AF143887	Hs.337588	ESTs, Moderately similar to S65657 alpha	2.13 1.63
	403362			NM_001615*:Homo sapiens actin, gamma 2,	2.33 2.22
	445496	AB007860	Hs.12802	development and differentiation enhancin	1.12 2.60
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I39022 hypothe	1.83 3.05
	402366	AV648601		apolipoprotein B (including Ag(x) antige	1.32 2.05
65	427254	AL121523	Hs.97774	ESTs	2.44 1.00
	414533	AA149060	Hs.296100	ESTs	1.70 2.06
	430157	BE348706	Hs.278543	ESTs	2.54 3.00
	413433	NM_003199	Hs.326198	transcription factor 4	2.26 1.41
	410532	T53088	Hs.155376	hemoglobin, beta	1.52 1.56
70	405779			NM_005367:Homo sapiens melanoma antigen,	2.42 1.22
	450455	AL117424	Hs.25035	chloride intracellular channel 4	2.48 2.13
	414081	AW969976	Hs.279009	maltrix Gla protein	1.81 1.53
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	1.65 2.08
	415062	H45100	Hs.49753	uveal autoantigen with coiled coil domai	1.62 3.75
75	406317			C2002658*gi5625694[gb]AAF19354.1 AF185	1.68 2.11
	453259	R93125	Hs.124187	ESTs	1.08 2.25
	445937	AI452943	Hs.321231	UDP-Gal-beta-GlcNAc beta 1,4- galactosylt	1.76 1.01
	434370	AF130988	Hs.58346	ectodysplasin 1, anhidrotic receptor	1.12 2.08
	418058	AW161552	Hs.83381	guanine nucleotide binding protein 11	2.02 2.40

	432331	W37862	Hs.274368	MSTP032 protein	4.36	2.18
	451736	AW080356	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	1.51	3.45
	413109	AW389845	Hs.110855	ESTs	4.34	5.98
5	413643	AA130987	Hs.188727	ESTs	1.30	2.42
	433217	AB040914	Hs.278628	KIAA1481 protein	1.70	2.49
	435232	NM_001262	Hs.4854	cyclin-dependent kinase inhibitor 2C (p1	1.79	1.66
	438006	BE148799	Hs.127951	hypothetical protein FLJ14503	1.76	2.04
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi]	2.32	2.45
10	433656	AW974941	Hs.292385	ESTs, Weakly similar to I78885 serine/th	1.14	2.50
	415714	NM_002290	Hs.78672	laminin, alpha 4	2.52	1.13
	450282	AA007655	Hs.93523	ESTs	1.40	2.58
	442855	AI074465	Hs.133469	ESTs	1.54	2.20
	432917	NM_014125	Hs.241517	PRO0327 protein	2.24	3.03
15	429041	AJ132820	Hs.194768	a disintegrin and metalloproteinase doma	1.61	2.60
	442807	AL049274	Hs.8736	Homo sapiens mRNA; cDNA DKFZp564H203 (fr	1.73	1.19
	427719	AI393122	Hs.134726	ESTs	1.46	2.00
	408778	AI500519	Hs.63382	hypothetical protein PRO2714	1.46	2.58
	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	1.40	2.03
20	424425	AB031480	Hs.146824	SPR1 protein	1.60	1.11
	445391	T92576	Hs.191168	ESTs	1.69	2.40
	446899	NM_005397	Hs.16426	podocytin-like	1.22	2.42
	420996	AK001927	Hs.100895	hypothetical protein FLJ10462	2.68	2.98
	424909	S78187	Hs.153752	cell division cycle 25B	2.18	1.33
25	413593	AA205248		gbzq78c12.r1 Stralagene hNT neuron (937	1.69	2.00
	408734	AW264996	Hs.254299	ESTs	2.06	2.94
	413860	AJ660842	Hs.110915	interleukin 22 receptor	1.24	2.20
	437053	AA351109	Hs.5437	Tax1 (human T-cell leukemia virus type I	1.78	2.60
	418044	AJ640532	Hs.119830	ESTs, Weakly similar to ALUF_HUMAN !!!!!	1.54	2.53
30	441971	W27060	Hs.265855	ESTs	1.62	2.13
	450401	AW959281	Hs.8184	ESTs	1.42	2.30
	440157	AA868350	Hs.343536	ESTs	1.38	2.60
	457587	AA992841	Hs.27263	KIAA1458 protein	1.47	2.42
	440707	BE256751	Hs.22667	Homo sapiens cDNA: FLJ22073 fis, clone H	1.18	2.10
35	402241			Target Exon	2.58	2.52
	413428	AA430155	Hs.151343	KIAA1524 protein	1.22	2.45
	416735	R11275	Hs.194485	ESTs	1.14	2.14
	421582	AJ910275		trefoil factor 1 (breast cancer, estroge	1.25	1.03
40	431031	AA830335	Hs.105273	ESTs	2.35	2.95
	433336	AF017986	Hs.31386	secreted frizzled-related protein 2	3.72	1.00
	420786	AW296466	Hs.43628	deleted in lymphocytic leukemia, 2	1.23	2.60
	401335			Target Exon	1.18	1.68
	417670	R07785		gb:Y15c06.r1 Soares fetal liver spleen	1.55	2.00
45	406314			C14001020.gij12597441[gb]AAG60049.1[AF31	1.60	3.08
	458981	AW968318	Hs.285996	hypothetical protein FLJ23375	1.70	2.50
	417509	AA203414	Hs.42009	ESTs	1.82	2.05
	452732	BE300078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA,	1.34	1.37
	418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	1.37	1.02
50	457871	AI168278		ESTs	1.20	2.19
	444163	AJ126098		gb:qc54g07.x1 Soares_placenta_8to9weeks_	1.43	1.22
	413276	Z24725	Hs.75260	mitogen inducible 2	1.78	2.28
	421097	AJ280112	Hs.125232	Homo sapiens cDNA FLJ13266 fis, clone OV	2.55	2.60
55	417151	AA194055	Hs.293858	ESTs	1.68	1.67
	453566	AA425414	Hs.33287	nuclear factor I/B	2.06	2.40
	440859	AW070865	Hs.346390	ESTs	1.12	1.70
	420629	AW204343	Hs.156823	ESTs, Weakly similar to T30868 RhoA-bind	1.21	2.38
	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	1.58	2.15
60	434831	AA248060	Hs.273397	KIAA0710 gene product	1.69	1.78
	412055	AA099907	Hs.271806	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.35	2.65
	445468	AW450439		ESTs	1.52	2.50
	444550	BE250716	Hs.87614	ESTs	1.30	2.28
65	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	1.50	3.02
	430233	AW367902	Hs.236443	Homo sapiens mRNA; cDNA DKFZp564N1063 (f	1.24	2.95
	413444	BE141019		gb:MR0-HT0067-201099-002-b10 HT0067 Homo	1.68	2.80
	433844	AA610175	Hs.179647	Homo sapiens cDNA FLJ12195 fis, clone MA	1.49	2.01
	427055	AJ301740	Hs.173381	dihydropyrimidinase-like 2	1.11	2.58
70	454244	R51604	Hs.300842	KIAA1608 protein	1.00	2.02
	429503	AA394183	Hs.26873	ESTs	2.58	4.08
	422940	BE077458		gb:RC1-BT0606-090500-015-b04 BT0606 Homo	3.48	2.46
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	3.13	1.48
	437312	AA809350	Hs.246180	ESTs	1.10	2.05
75	449426	T92251	Hs.198882	ESTs	1.22	2.08
	447620	AW290951	Hs.224955	ESTs	1.80	2.18
	444700	NM_003645	Hs.11729	fatty-acid-Coenzyme A ligase, very long-	1.72	2.81
	436258	AW867491	Hs.107125	plasmalemma vesicle associated protein	1.99	1.80
	415712	AW249188	Hs.169577	Homo sapiens cDNA FLJ14743 fis, clone NT	1.66	2.98
	432877	AW974111	Hs.292477	ESTs	1.63	2.79
	412085	AW891667		gb:CM3-NT0089-110500-179-h09 NT0089 Homo	1.40	2.08

5	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	1.96	3.58
	409714	AW367812	Hs.199961	ESTs, Weakly similar to ALU7_HUMAN ALU S	1.24	2.10
	423013	AW875443	Hs.22209	secreted modular calcium-binding protein	1.49	2.09
	422663	AW500087	Hs.119014	zinc finger protein 175	1.01	2.78
	439737	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN	1.54	2.57
10	413196	AA127386		gb:zn90d09.r1 Stratagene lung carcinoma	1.04	2.18
	439349	AI660898	Hs.195602	ESTs	2.03	2.43
	443005	AI027184	Hs.200918	ESTs	1.42	2.10
	424762	AL119442	Hs.183684	eukaryotic translation initiation factor	2.58	3.43
	427373	AB007972	Hs.130760	myosin phosphatase, target subunit 2	2.08	1.70
15	413916	N49813	Hs.75615	apolipoprotein C-II	0.70	0.42
	418332	R34976	Hs.78293	ESTs	2.74	2.43
	426552	BE297660	Hs.170328	moesin	1.28	1.52
	456583	AF179897	Hs.104105	Meis (mouse) homolog 2	1.42	2.02
	447214	AI367288	Hs.273621	Homo sapiens cDNA: FLJ21350 fis, clone C	1.14	2.10
20	449254	W26908	Hs.172762	ESTs	2.04	2.50
	443651	W22152	Hs.282929	ESTs	2.94	3.08
	421021	AA808018	Hs.109302	ESTs	1.41	2.04
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	1.61	1.21
	432027	AI096678	Hs.272353	KIAA0957 protein	1.70	2.76
25	452688	AA721140	Hs.49930	ESTs, Weakly similar to putative p150 [H	1.80	2.95
	417042	C75563	Hs.113029	ribosomal protein S25	2.22	3.20
	443574	U83993	Hs.321709	purinergic receptor P2X, ligand-gated io	1.21	2.51
	429372	AA451859	Hs.99253	ESTs	1.28	2.43
	424290	AA338396		gb:EST43386 Fetal brain I Homo sapiens c	1.82	2.03
30	428518	AW969656		gb:EST381733 MAGE resequences, MAGK Homo	1.72	2.52
	456649	BE065051		gb:RC1-BT0313-110500-017-c04 BT0313 Homo	1.65	3.03
	414665	AA160873	Hs.332053	serum amyloid A1	1.36	1.08
	418298	AA256014	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	1.04	2.03
	429655	U48959	Hs.211582	myosin, light polypeptide kinase	4.94	4.34
35	433924	AA618304	Hs.258785	ESTs	1.44	2.40
	452683	AI089575	Hs.9071	progesterone membrane binding protein	1.48	2.48
	439437	AI207788	Hs.343628	sialyltransferase 4B (beta-galactosidase	1.36	2.33
	432314	AA533447	Hs.312989	ESTs	0.96	2.78
	400881			NM_025080:Homo sapiens hypothetical prot	1.70	3.15
40	426477	AA379464		gb:EST92386 Skin tumor I Homo sapiens cD	2.01	2.37
	454741	BE154396		gb:CM2-HT0342-091299-050-b05 HT0342 Homo	2.12	3.44
	423977	AA333232		gb:EST37283 Embryo, 8 week I Homo sapien	1.38	2.13
	450396	AU077002	Hs.24950	regulator of G-protein signalling 5	2.13	3.28
	431842	NM_005764	Hs.271473	epithelial protein up-regulated in carci	1.90	2.23
45	415157	D63257		gb:HUM514B08B Clontech human placenta po	1.29	2.90
	418236	AW994005	Hs.337534	ESTs	1.74	2.37
	454390	AB020713	Hs.56966	KIAA0906 protein	1.47	1.38
	436143	AA705245	Hs.192189	ESTs	1.46	2.45
	436251	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)	1.43	2.07
50	450735	AI732321		SRY (sex determining region Y)-box 4	1.36	2.02
	420136	AW801090	Hs.195851	actin, alpha 2, smooth muscle, aorta	2.70	1.68
	447100	AI361801	Hs.167130	hypothetical protein	1.66	2.03
	453577	AL043049		gb:DKFZp434A1523_r1 434 (synonym: htes3)	1.41	2.75
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,	1.59	1.38
55	412632	AL120379	Hs.74294	aldehyde dehydrogenase 7 family, member	1.81	2.51
	423291	NM_004129	Hs.126590	guanylate cyclase 1, soluble, beta 2	1.54	2.83
	456172	R99050		gb:yq65c02.r1 Soares fetal liver spleen	1.46	2.68
	452123	AI267615	Hs.38022	ESTs	1.24	1.93
	433900	AA721668	Hs.257761	ESTs	1.78	2.66
60	408436	R31954	Hs.7885	phosphatidylinositol binding clathrin as	1.21	2.35
	417123	BE326521	Hs.159450	ESTs	1.46	2.09
	436023	T81819	Hs.302251	ESTs	2.68	2.70
	454150	AA131893	Hs.154088	hypothetical protein FLJ22756	1.40	2.50
	444094	AI695764	Hs.202394	ESTs	1.28	4.03
65	429176	AW975021	Hs.193800	ESTs	1.08	2.53
	422259	AA307584		gb:EST178498 Colon carcinoma (HCC) cell	1.80	3.03
	451164	AA015912	Hs.60659	ESTs, Weakly similar to T46471 hypotheti	1.47	1.17
	417501	AL041219	Hs.82222	sama domain, immunoglobulin domain (Ig),	2.92	2.70
	455642	BE063965		gb:QV3-BT0296-140200-085-h01 BT0296 Homo	1.70	2.70
70	443387	BE139135	Hs.254629	ESTs	1.48	2.32
	420995	AA282495	Hs.89014	ESTs	1.45	1.51
	407329	AA576061	Hs.269834	ESTs, Weakly similar to ALUD_HUMAN !!!!	1.13	2.38
	438797	C16161	Hs.283040	hypothetical protein PRO2543	0.99	2.75
	443357	AW016773		low molecular mass ubiquitinone-binding pr	1.60	2.08
75	412656	AF006011	Hs.74375	dishevelled 1 (homologous to Drosophila	1.32	1.13
	427377	AU077029	Hs.177543	antigen identified by monoclonal antibod	1.24	0.79
	412200	R08110	Hs.187462	ESTs, Weakly similar to I38022 hypotheti	1.35	1.54
	432586	AA568548		ESTs	1.50	2.25
	411590	T96183		gb:ye09f07.s1 Stratagene lung (937210) H	1.22	2.53
	422572	X12784	Hs.119129	collagen, type IV, alpha 1	2.27	2.20
	420256	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula	1.59	2.11

	419900	AI469960	Hs.170698	ESTs	1.30	2.68
	410805	AW804742	Hs.84264	acidic protein rich in leucines	1.16	2.28
	452560	BE077084	Hs.99969	ESTs	1.44	2.58
5	448429	D17408	Hs.21223	calponin 1, basic, smooth muscle	4.02	1.00
	424436	AW818428	Hs.4953	golgi autoantigen, golgin subfamily a, 3	1.10	2.00
	447400	AK000322	Hs.18457	hypothetical protein FLJ20315	1.45	1.28
	422522	AI023428	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	1.82	2.10
	443696	AW607444	Hs.134622	ESTs	1.98	2.01
10	436094	AI798701	Hs.222222	ESTs	1.34	2.40
	420168	AF217508	Hs.95594	serine carboxypeptidase vitellogenic-lik	1.58	2.45
	430325	AF004562	Hs.239356	syntaxin binding protein 1	1.34	2.43
	439022	AA356599	Hs.173904	ESTs	2.76	2.40
	420563	AA278327	Hs.136237	ESTs, Moderately similar to Y140_HUMAN H	1.78	2.65
15	429494	AA769365	Hs.126058	ESTs	1.50	2.40
	420689	H79979	Hs.88678	ESTs	1.26	2.28
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	1.72	1.29
	439943	AW083789	Hs.124620	ESTs	1.45	2.84
	442300	AI765908	Hs.129166	ESTs	1.24	2.35
20	449614	AI989490	Hs.197703	ESTs	1.12	2.22
	444363	AI142827	Hs.143656	ESTs	1.32	2.08
	424479	AF064238	Hs.149098	smoothelin	1.59	1.10
	437321	AA768966	Hs.292026	ESTs, Weakly similar to 2109260A B cell	1.28	2.07
	431926	AW972724		gb:EST384816 MAGE resequences, MAGL Homo	1.52	2.63
25	433640	AW390125	Hs.240443	Homo sapiens cDNA: FLJ23538 fis, clone L	1.69	1.30
	415901	H08396	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1.71	2.19
	437199	AL110175	Hs.306337	Homo sapiens mRNA; cDNA DKFZp564H0616 (f	1.48	2.50
	457450	AW294163	Hs.146127	ESTs	1.07	2.60
	456678	AF141305	Hs.173736	ancient ubiquitous protein 1	1.44	2.35
30	451079	AI827988	Hs.240728	ESTs, Moderately similar to PC4259 ferri	0.95	3.00
	405944			Target Exon	1.48	2.45
	408877	AA479033	Hs.130315	ESTs, Weakly similar to A47582 B-cell gr	1.38	2.20
	446682	AW205632	Hs.211198	ESTs	1.38	3.00
	431380	AW610282	Hs.291003	ESTs	1.43	2.64
35	442027	AI652926	Hs.128395	ESTs	1.18	2.43
	423578	AW960454	Hs.222830	ESTs	1.56	2.18
	441495	AW294603	Hs.127039	ESTs	2.80	1.73
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	1.36	1.18
	443949	AW827419	Hs.235070	ESTs	1.30	2.28
40	440495	AA887212	Hs.14161	hypothetical protein DKFZp434I1930	1.74	2.78
	449948	R19156	Hs.20798	ESTs	1.12	2.23
	439564	W77911	Hs.110006	ESTs	1.34	2.85
	423225	AA852604	Hs.125359	Thy-1 cell surface antigen	1.24	1.09
	436139	AA765786	Hs.120936	ESTs	1.30	2.10
45	456968	AI174861	Hs.190623	ESTs	1.14	2.15
	437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	1.21	2.18
	411652	AW855393		gb:CM3-CT0275-191099-024-f10 CT0275 Homo	1.85	1.94
	420732	AA789133	Hs.88650	ESTs	1.66	2.71
	409291	AW373472		gb:RC3-BT0523-181299-011-d12 BT0523 Homo	1.56	2.30
50	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	1.56	1.39
	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	1.58	1.24
	450946	AA374569	Hs.127698	ESTs, Moderately similar to 2109260A B c	1.02	2.25
	428423	AU076517	Hs.184276	solute carrier family 9 (sodium/hydrogen	1.70	2.39
	415361	F06724		gb:HSC11G021 normalized infant brain cDN	1.34	2.40
55	406490			C5001926:gi7511572 pir T42245 probable	1.28	2.40
	410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	1.52	2.00
	440010	AA534930	Hs.127236	hypothetical protein FLJ12879	1.12	2.20
	429508	AW369520	Hs.33944	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.33	2.28
60	426340	Z97989	Hs.169370	FYN oncogene related to SRC, FGR, YES	1.88	2.18
	416889	AW250318	Hs.80395	mal, T-cell differentiation protein	1.65	1.16
	451870	AI820991	Hs.8377	ESTs	1.24	2.03
	444091	AV647924	Hs.282376	ESTs	1.05	2.13
	410793	AW581906	Hs.66392	Intersectin 1 (SH3 domain protein)	2.00	3.13
	452222	AW806287	Hs.21432	SEX gene	1.25	1.10
65	433010	AW970018		gb:EST382097 MAGE resequences, MAGK Homo	1.36	2.41
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	1.14	2.03
	438855	AW946276	Hs.6441	Homo sapiens mRNA; cDNA DKFZp586J021 (fr	2.24	1.77
	448718	AA220235	Hs.153959	hypothetical protein MGC15436	1.52	2.65
	402685			Target Exon	2.04	2.46
70	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	1.66	2.05
	422068	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	1.89	4.98
	451225	AI433694	Hs.293608	ESTs	1.79	2.70
	441078	AI453268	Hs.323409	Homo sapiens cDNA FLJ14113 fis, clone MA	1.44	2.58
	409406	H83092	Hs.49605	ESTs	1.38	2.05
75	422297	AW961290		p30 DBC protein	1.20	2.73
	408711	AW378061	Hs.63335	ESTs, Moderately similar to A46010 X-fin	1.20	2.08
	426696	AW363332	Hs.171844	Homo sapiens cDNA: FLJ22296 fis, clone H	1.35	2.68
	417324	AW265494		ESTs	1.68	1.25

5	408283	BE141579		gb:QV2-HT0083-071299-018-b05 HT0083 Homo	1.25	2.65
	415166	NM_003652	Hs.78068	carboxypeptidase Z	1.34	1.09
	406300			Target Exon	1.61	2.47
	411880	AW872477		gb:jhm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	3.60	4.03
	422287	F16365	Hs.114346	cytochrome c oxidase subunit VIIa polype	2.16	1.44
10	422567	AF111178	Hs.118407	glypican 6	1.57	2.03
	436855	AA732624	Hs.165852	ESTs	1.08	2.75
	403536			Target Exon	0.93	2.13
	447733	AF157482	Hs.19400	MAD2 (mitotic arrest deficient, yeast, h	1.18	1.07
	417117	N46778		gb:yy52b02.r1 Soares_multiple_sclerosis_	1.70	2.85
15	411690	AA669253	Hs.136075	RNA, U2 small nuclear	2.12	2.78
	443243	AI452496	Hs.132056	ESTs	1.15	2.63
	423074	AL109963		FSH primary response (LRPR1, rat) homolo	1.37	1.43
	408916	AW295232	Hs.429	ATP synthase, H transporting, mitochondr	1.63	2.23
	449799	AI143466	Hs.125060	ESTs	1.40	2.08
20	415378	T16964		gb:NIB2079-5R Normalized infant brain, B	1.88	1.85
	431089	BE041395		ESTs, Weakly similar to unknown protein	1.57	2.57
	434959	AW974949	Hs.186564	ESTs, Weakly similar to I38022 hypothi	1.30	2.30
	416311	D80529		gb:HUM081H05B Human fetal brain (TFujiwa	1.58	4.35
	444614	R44284	Hs.2730	heterogeneous nuclear ribonucleoprotein	1.88	2.98
25	456206	NM_006895	Hs.81182	histamine N-methyltransferase	1.24	2.08
	410583	AW770280	Hs.36258	ESTs, Moderately similar to JC5238 galac	1.56	4.33
	430410	AF099144	Hs.334455	trypsin beta 1	1.91	1.58
	408139	AA451966		RAB9-like protein	1.42	2.14
	432621	AI298501	Hs.12807	ESTs, Weakly similar to T46428 hypothi	2.08	1.94
30	441584	AW148329	Hs.175208	ESTs	1.12	2.05
	445940	D60438	Hs.34779	ESTs	1.86	2.70
	453022	AA031499	Hs.118489	ESTs	2.02	1.75
	444008	BE544855	Hs.236572	ESTs, Weakly similar to SFR4_HUMAN SPLIC	1.54	1.29
	442994	AI026718	Hs.16954	ESTs	3.60	3.78
35	402085			C18000504*:gij2627436[gb]AAB86683.1] (AF	1.36	2.53
	411918	AW876354		gb:PM4-PT0019-141299-009-F08 PT0019 Homo	2.00	2.63
	455508	AW976165		gb:EST388274 MAGE resequences, MAGN Homo	1.70	3.04
	426106	AI678765	Hs.21812	ESTs	1.49	2.11
	425131	BE252230	Hs.99163	ESTs	2.04	2.65
40	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	1.17	2.55
	420447	AA687306	Hs.88448	ESTs	1.66	2.58
	428055	AA420564	Hs.101760	ESTs	1.08	2.15
	422110	AI376736	Hs.111779	secreted protein, acidic, cysteine-rich	1.76	1.82
	438581	AW977766	Hs.292133	ESTs, Moderately similar to I78885 serin	1.08	2.10
45	403280			C10001011*:gij4758212[ref]NP_004411.1] d	0.97	2.48
	408175	W29089	Hs.19066	hypothetical protein DKFZp667O2416	1.42	1.41
	432390	AA936177	Hs.274460	olfactory receptor, family 5, subfamily	1.26	2.05
	443441	AW291196	Hs.92195	ESTs	1.52	2.13
	418925	AA159850	Hs.93765	lipoma HMGIC fusion partner	1.72	2.80
50	445256	AI856635	Hs.144763	ESTs	1.97	3.33
	456381	AA236606		gb:zr99b10.r1 NCI_CGAP_GCB1 Homo sapiens	1.16	1.95
	422433	AA310560	Hs.153746	hypothetical protein FLJ22490	1.06	2.20
	432529	AI989507	Hs.162245	ESTs	1.36	2.25
	424951	AW964082		gb:EST376155 MAGE resequences, MAGH Homo	2.22	2.58
55	420785	H89633	Hs.191346	ESTs	1.26	2.15
	411347	AW838126		gb:QV2-LT0051-240300-097-f01 LT0051 Homo	1.38	2.38
	438742	AW204126	Hs.196543	ESTs	1.10	2.30
	414900	AW452420	Hs.248678	ESTs	2.01	3.08
	443284	AI369813	Hs.64783	ESTs, Weakly similar to T42705 hypothi	0.66	0.43
60	402049			Target Exon	2.28	2.00
	429400	AW604940	Hs.201668	transcription factor 20 (AR1)	1.16	2.00
	423916	AW993496	Hs.17235	Homo sapiens clone TCCCA00176 mRNA sequ	1.59	1.05
	432495	AW973537	Hs.186734	ESTs, Weakly similar to I61746 pheromona	1.50	2.05
	414840	R27319	Hs.23823	hair/enhancer-of-split related with YRP	1.89	2.09
65	428711	R46414	Hs.56828	trinucleotide repeat containing 5	1.77	1.83
	448609	AW139420	Hs.7972	KIAA0871 protein	1.14	2.26
	443859	NM_013409	Hs.9914	folistatin	1.17	1.05
	411141	AW819661		gb:RC5-ST0293-140200-013-G04 ST0293 Homo	1.44	2.40
	440116	AI798851	Hs.266959	hemoglobin, gamma G	1.18	2.08
70	417944	AU077196	Hs.82985	collagen, type V, alpha 2	2.10	1.37
	429640	U83508	Hs.2463	angiotensin 1	1.92	2.98
	410064	X53416	Hs.195464	filamin A, alpha (actin-binding protein-	1.51	1.29
	458218	AI435179	Hs.126820	ESTs	1.49	1.15
	443114	AI033377	Hs.153298	ESTs	1.38	2.05
75	427788	AA412397	Hs.116858	ESTs	1.45	1.85
	435913	W95006	Hs.269559	ESTs, Weakly similar to S65657 alpha-1C-	1.63	3.90
	457949	W89171	Hs.71741	ESTs, Highly similar to I38945 melanoma	1.01	2.00
	419203	AA488719	Hs.190151	ESTs	1.94	2.45
	412510	AI056689	Hs.133538	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.91	2.20
	413885	BE177442		gb:RC1-HT0595-200400-012-f01 HT0595 Homo	1.48	2.80
	426239	AA669515	Hs.214226	ESTs	1.36	2.50

	408866	AW292096	Hs.255036	ESTs	1.93	2.92
	412857	AI703484	Hs.128052	ESTs	1.72	1.60
	427340	BE167242	Hs.47099	hypothetical protein FLJ21212	1.46	2.13
5	412902	BE030818		gb:QV0-BN0147-290400-214-c01 BN0147 Homo	0.90	2.05
	451141	AW7772713	Hs.247186	ESTs	2.38	3.95
	412626	AA114945	Hs.151839	ESTs	1.75	2.15
	405667			Target Exon	2.62	3.79
	417777	AI823763	Hs.7055	ESTs, Weakly similar to I78885 serine/th	1.24	2.08
10	401400			Target Exon	1.16	1.90
	426796	S78234	Hs.172405	cell division cycle 27	2.14	1.63
	435046	AA662772	Hs.174330	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.14	2.28
	448401	AI498509	Hs.346254	ESTs	2.50	2.83
	450832	AW970602	Hs.105421	ESTs	0.55	0.39
15	441057	AL043897	Hs.126483	ESTs	1.08	2.13
	438725	AA815163	Hs.127307	ESTs	1.31	2.65
	450062	AW001043	Hs.200854	ESTs	1.30	2.48
	441214	AI820648	Hs.129136	ESTs	1.43	1.71
	431723	AW058350	Hs.15762	Homo sapiens mRNA; cDNA DKFZp564B2062 (I	1.22	2.30
20	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	1.35	1.49
	423622	BE154847		gb:PM1-HT0345-121199-001-d05 HT0345 Homo	1.57	2.30
	450835	BE262773	Hs.25584	hypothetical protein FLJ10767	1.40	1.12
	444014	AI095718	Hs.135015	ESTs	2.30	1.78
	431603	AA807955	Hs.325984	EST	1.26	2.03
25	408697	AW419069	Hs.209670	ESTs	1.35	2.60
	444312	R44007		ESTs	1.95	2.07
	404286			C6001909:gi704441 dbj BAA18909.1 (D298	2.29	2.22
	438813	M27346		gb:Homo sapiens (clone HGP09/HGP32) T c	1.03	2.43
30	445534	AL038823	Hs.12840	Homo sapiens germline mRNA sequence	1.00	2.16
	426046	AA833655	Hs.206868	Homo sapiens cDNA FLJ14056 fis, clone HE	1.59	2.73
	451907	AI822065	Hs.50749	ESTs, Moderately similar to ALU7_HUMAN A	1.74	2.65
	418796	AA228351	Hs.34060	ESTs	1.28	2.12
	422431	AI769410	Hs.221461	ESTs	1.80	3.58
	417557	AA225622	Hs.293589	ESTs	1.32	2.14
35	455313	AW894409	Hs.125472	ESTs, Moderately similar to KIAA0877 pro	1.48	2.57
	415479	F10042	Hs.4840	ESTs	1.83	2.01
	450433	AW444538	Hs.231863	ESTs	1.31	2.58
	410581	AA018982	Hs.125036	tumor endothelial marker 7 precursor	1.54	1.62
	455407	AW936813		gb:PM2-DT0023-050400-003-b10 DT0023 Homo	1.32	2.15
40	417552	R00916	Hs.166510	ESTs	1.50	2.63
	428290	AI932995	Hs.183475	Homo sapiens clone 25061 mRNA sequence	1.94	2.70
	432391	AI732374	Hs.339827	Human DNA sequence from clone RP5-881L22	0.96	2.38
	456283	U68162	Hs.84171	myeloproliferative leukemia virus oncoge	1.22	2.13
	438535	L09078		gb:Homo sapiens mRNA fragment	2.14	1.95
45	416564	AW795793	Hs.2575	Homo sapiens cDNA FLJ12257 fis, clone MA	2.28	1.93
	435200	AA670310	Hs.145903	ESTs	1.16	2.13
	457635	AV660976	Hs.3569	hypothetical protein	1.37	3.10
	449330	BE185536	Hs.301183	molecule possessing ankyrin repeats indu	0.99	2.45
	449319	AA373630	Hs.188750	ESTs	1.56	3.28
50	418992	AW074143	Hs.87134	ESTs	1.88	2.20
	409367	AW382767		gb:PM0-HT0339-081199-001-h05 HT0339 Homo	1.30	2.50
	434973	AW449285	Hs.313636	EST	1.11	2.65
	408383	BE466959	Hs.144153	ESTs	1.30	2.44
	440100	BE382685	Hs.158549	ESTs, Weakly similar to T2D3_HUMAN TRANS	1.23	2.71
55	431995	AL122087	Hs.272304	Homo sapiens mRNA; cDNA DKFZp564C0371 (I	1.24	2.27
	427681	AB018263	Hs.180338	tumor necrosis factor receptor superfamily	1.70	1.68
	405146			C8001690*:gi15754446 ref NP_034760.1 ki	2.00	0.68
	436154	AA764950	Hs.119898	ESTs	1.43	3.00
	451233	AA047221	Hs.59752	ESTs	1.38	2.20
60	446855	AI814373	Hs.164175	ESTs	1.33	3.93
	448211	BE384592	Hs.6451	PRO0659 protein	1.48	2.73
	418283	S79895	Hs.83942	cathepsin K (pseudosclerosis)	1.33	2.68
	409609	AW444670	Hs.335685	ESTs	1.27	1.51
	450414	AI907735	Hs.21446	KIAA1716 protein	1.60	1.24
65	452929	AW954938	Hs.172816	neuregulin 1	2.01	3.70
	435112	AW976145	Hs.143198	Inhibitor of growth family, member 3	1.22	1.30
	439806	AA846824	Hs.180908	ESTs	0.80	2.04
	439910	H66765	Hs.339397	ESTs	1.28	2.16
	437886	BE264111	Hs.31314	retinoblastoma-binding protein 7	1.05	2.82
70	441354	AA931221	Hs.126813	ESTs	1.20	2.28
	428951	AL138153	Hs.300410	ESTs, Moderately similar to A47582 B-cel	1.50	1.83
	438272	AI167963	Hs.143700	ESTs, Weakly similar to S65824 reverse t	1.34	2.51
	429642	X68264	Hs.211579	melanoma cell adhesion molecule	1.18	1.18
	422121	AI757949	Hs.179833	ESTs	1.18	2.26
75	411184	AW821117		gb:PM2-ST0303-170100-003-g03 ST0303 Homo	1.18	2.21
	435871	AF257077	Hs.283627	eukaryotic translation initiation factor	1.17	1.57
	430570	AI417881	Hs.292464	ESTs	1.49	3.17
	431995	AL080197	Hs.272302	hypothetical protein	1.52	2.11

	451326	AW296946	Hs.256078	ESTs	1.19	2.18
	437046	BE149154		gb:RC2-HT0252-271099-017-c11 HT0252 Homo	1.18	2.25
	410154	F06959		gb:HSC1QD011 normalized infant brain cDN	1.41	2.05
5	434373	AI565566	Hs.168587	ESTs	1.39	1.33
	444552	AW295211	Hs.230777	ESTs	1.36	2.20
	411608	AW853441		gb:RC1-CT0252-030100-023-g09 CT0252 Homo	2.12	1.80
	440573	BE550891	Hs.270624	ESTs	2.19	2.17
	443047	AW157377	Hs.132910	ESTs	1.81	2.28
10	451473	AW298047	Hs.346198	ESTs	1.18	2.30
	416265	AA177088	Hs.190065	ESTs	2.37	3.38
	435375	AI733610	Hs.187832	ESTs	1.12	2.18
	401469			NM_022137*:Homo sapiens secreted modular	1.32	1.61
	456152	AA174126	Hs.332163	ESTs	1.26	2.50
15	415808	R21439	Hs.334578	Homo sapiens, clone IMAGE:3929520, mRNA	1.39	2.43
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	0.92	2.20
	435127	AJ217926	Hs.179863	EST	1.36	2.65
	420772	AW752656	Hs.222707	KIAA1718 protein	1.19	1.50
	456332	AA228357		gb:nc39d05.r1 NCI_CGAP_Pr2 Homo sapiens	1.45	3.57
20	444678	AI741513	Hs.143739	ESTs	1.43	1.62
	446175	AL036568	Hs.291	glutamyl aminopeptidase (aminopeptidase	1.00	1.53
	416463	H59241		Homo sapiens cDNA FLJ11095 fis, clone PL	1.44	2.13
	405158			ENSP00000243337:CDNA FLJ13984 fis, clone	1.38	2.68
	403903			C5001632*:gij10645308[gb]AAG21430.1 AC00	1.32	1.43
25	407271	X98937		gb:H.sapiens rearranged lg heavy chain (1.40	2.68
	413929	BE501689	Hs.75617	collagen, type IV, alpha 2	1.59	1.33
	450778	U81375	Hs.25450	solute carrier family 29 (nucleoside tra	1.17	1.10
	434274	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	1.92	2.80
	400075			Eos Control	1.76	2.60
30	433694	AI208611	Hs.12066	Homo sapiens cDNA FLJ11720 fis, clone HE	1.48	2.33
	454826	AW833676		gb:QV4-TT0008-181199-038-h04 TT0008 Homo	1.57	2.89
	415168	AA160805	Hs.199832	ESTs, Weakly similar to I78885 serine/th	2.08	1.76
	439486	AF086303	Hs.103185	ESTs	1.49	2.19
	403291			Target Exon	1.36	2.28
35	438618	AA897673	Hs.123457	ESTs	0.75	0.79
	455087	AW855389		gb:CM3-CT0275-191099-024-e06 CT0275 Homo	0.91	2.63
	408075	AA382881	Hs.42409	CGI-146 protein	1.46	2.15
	436826	AA731863	Hs.120276	ESTs	1.04	3.11
	408961	AW297475	Hs.323180	ESTs	1.25	1.39
40	424408	AI754813	Hs.146428	collagen, type V, alpha 1	1.64	2.05
	423300	AK000742	Hs.126774	L2DTL protein	1.47	3.44
	403217	AL134878		ribosomal protein, large P2	1.70	2.22
	437990	AI686579	Hs.121784	ESTs	2.14	1.69
	419156	AC002366	Hs.46329	amelogenin (X chromosome, amelogenesis i	1.40	1.45
45	411817	BE302900	Hs.72241	mitogen-activated protein kinase kinase	1.18	1.12
	425701	AA361850	Hs.322149	Human clone 137308 mRNA, partial cds	1.50	2.15
	418757	AI864193	Hs.169728	hypothetical protein FLJ13150	1.57	2.23
	415184	AA380436	Hs.211973	homolog of Yeast RRP4 (ribosomal RNA pro	1.32	2.09
	414918	AI219207	Hs.72222	hypothetical protein FLJ13459	1.61	1.50
50	401723			Target Exon	1.01	2.68
	439010	AW170332	Hs.75216	Homo sapiens cDNA FLJ13713 fis, clone PL	1.28	1.65
	449166	BE168981	Hs.23131	kinesin family member C3	1.64	2.58
	410642	AW792784		gb:CM0-UM0001-010300-258-h11 UM0001 Homo	1.54	1.90
	409556	D38616	Hs.54941	phosphorylase kinase, alpha 2 (liver)	1.63	1.21
55	439894	AA853077	Hs.300697	immunoglobulin heavy constant gamma 3 (G	0.76	0.61
	401913			ENSP00000249158*:CDNA	0.97	2.59
	406097			Target Exon	1.11	1.23
	414745	AA160511	Hs.5326	amino acid system N transporter 2; porcu	1.29	1.12
60	445752	AI733942	Hs.344887	ESTs	2.03	1.68
	408052	AW501117	Hs.283585	ESTs	1.32	1.72
	407256	AA204763	Hs.288036	IRNA isopentenylpyrophosphate transferas	1.01	2.09
	423264	AJ133439	Hs.126076	Glutamate receptor interacting protein	1.51	2.39
	418859	AA229558		gb:nc15d10.s1 NCI_CGAP_Pr1 Homo sapiens	1.40	2.35
	410370	AB037753	Hs.62767	KIAA1332 protein	1.34	2.00
65	417264	AA195100	Hs.188695	ESTs	1.09	2.61
	444909	AI933051	Hs.192280	ESTs	1.56	2.92
	419386	AA236867		ESTs, Weakly similar to I38022 hypotheti	1.14	2.28
	439212	AF087995	Hs.134877	ESTs	1.06	2.90
	437766	W69171	Hs.71741	ESTs, Highly similar to I38945 melanoma	1.25	2.28
70	448951	AI611221	Hs.334802	hypothetical protein FLJ10101	1.88	2.17
	401659			Target Exon	1.63	2.05
	419145	N99638		gb:za39g11.r1 Soares fetal liver spleen	2.63	3.85
	444813	AW054834	Hs.210356	ESTs	1.73	2.14
	433902	AW292820	Hs.144906	ESTs	1.88	2.46
75	403072			NM_003319*:Homo sapiens titin (TTN), mRN	1.32	2.91
	452484	AB033042	Hs.29679	cofactor required for Sp1 transcription	0.72	0.70
	456788	AA724612	Hs.133130	Homo sapiens mRNA; cDNA DKFZp566H0124 (f	1.90	3.40
	403315			Target Exon	1.22	2.00

	406432	AJ289116		CD1E antigen, e polypeptide	2.31	2.63
	457785	AA682670	Hs.160884	ESTs	0.96	2.38
	433259	AA580665	Hs.326082	ESTs	1.46	1.07
	436882	AW016722	Hs.194976	SH2 domain-containing phosphatase anchor	1.38	2.13
5	401473			Target Exon	1.47	2.04
	444816	Z48633	Hs.283742	H.sapiens mRNA for retroltransposon	1.64	2.15
	438029	H61502	Hs.10235	chromosome 5 open reading frame 4	1.44	2.25
	431830	Y16645	Hs.271387	small inducible cytokine subfamily A (Cy	1.26	2.21
	450817	N71597	Hs.29698	ESTs, Weakly similar to ZN91_HUMAN ZINC	2.20	2.90
10	404427			C6000068*:gij5453579[ref]NP_006120.1] bo	0.74	0.81
	430658	AW970093	Hs.24453	ESTs	1.45	2.55
	405723			Target Exon	1.60	2.28
	436896	AW977385	Hs.278815	ESTs	1.17	1.64
	411974	AW880414	Hs.84264	acidic protein rich in leucines	1.54	2.08
15	412528	AJ123478	Hs.32112	ESTs	1.72	2.85
	446425	AW285364	Hs.255418	ESTs	1.25	1.31
	424991	AA775471	Hs.241467	ESTs	0.62	0.37
	443100	AJ033188		gb:ow94e08.s1 Soares_fetal_liver_spleen_	1.15	2.34
20	445332	AJ220225	Hs.321057	ESTs	1.07	2.00
	414781	D50917	Hs.77293	KIAA0127 gene product	1.04	3.43
	421893	NM_001078	Hs.109225	vascular cell adhesion molecule 1	1.15	2.53
	424265	AF173901	Hs.144287	hair/enhancer-of-split related with YRP	1.26	2.00
	446667	BE161878	Hs.224805	ESTs	1.12	2.13
	426399	AA652588	Hs.301348	Homo sapiens cDNA FLJ13271 fis, clone OV	2.26	1.29
25	438190	AA780020	Hs.136798	ESTs, Moderately similar to KBF3_HUMAN N	1.44	2.07
	406972	M32053		gb:Human H19 RNA gene, complete cds.	1.38	2.11
	417086	AA194446		ESTs, Weakly similar to S55024 nebulin,	2.12	3.30
	446410	AJ361109	Hs.151721	ESTs, Weakly similar to I38022 hypothei	1.14	2.33
30	427674	NM_003528	Hs.2178	H2B histone family, member Q	1.24	1.00
	422526	AA311763	Hs.131056	ESTs	1.29	2.04
	439317	AF086127	Hs.50800	ESTs, Weakly similar to T47156 hypothei	1.26	2.12
	405126	AA063426		gb:z770c08.s1 Soares_pineal_gland_N3HPG	1.28	2.20
	412093	BE242691	Hs.14947	ESTs	0.87	2.58
35	420169	AA256126	Hs.16179	hypothetical protein FLJ23467	1.38	2.07
	426096	D87436	Hs.166318	lipin 2	2.00	2.25
	402551			NM_005012*:Homo sapiens receptor tyrosin	0.80	0.82
	405760			Target Exon	1.44	2.85
	402901			NM_025206*:Homo sapiens hypothetical pro	1.63	1.27
40	453982	AW014252	Hs.252837	ESTs	1.44	2.03
	424244	AV647184	Hs.143601	hypothetical protein hCLA-iso	1.40	1.18
	439984	BE559514	Hs.275425	hypothetical protein	1.30	2.15
	457297	AW968188		gb:EST380383 MAGE resequences, MAGJ Homo	1.64	3.17
	415054	AJ733907		gb:zo86h09.y5 Stralagene ovarian cancer	1.00	2.20
45	426273	AJ174861	Hs.190623	ESTs	1.19	1.16
	405187			NM_014272:Homo sapiens a disintegrin-lik	1.31	1.35
	413939	AL047051	Hs.199961	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.44	1.88
	427596	AA449505	Hs.270143	extracellular glycoprotein EMILIN-2 prec	2.06	1.50
	408049	AW076098	Hs.345588	desmoplakin (DPI, DPII)	2.01	3.90
50	406002			Target Exon	1.73	2.08
	408284	AW248254	Hs.44101	protein kinase PKNbeta	1.28	1.31
	431377	AW178807	Hs.246182	ESTs	1.40	2.70
	451456	AW386183	Hs.210305	ESTs	1.44	2.08
	427530	AA405093	Hs.126519	ESTs	1.07	1.12
	431957	AK002104	Hs.272246	hypothetical protein FLJ11292	1.27	2.89
55	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	1.74	1.28
	419600	AA448958	Hs.91481	NEU1 protein	1.13	1.15
	423314	AJ400661	Hs.127811	disintegrin metalloproteinase with throm	1.44	2.53
	451690	AW451469	Hs.209990	ESTs	1.41	2.49
60	454662	AW812715		gb:RC4-ST0185-271099-011-g01 ST0185 Homo	1.35	2.86
	454413	AI653672	Hs.40092	PNAS-123	1.79	2.03
	416861	AW977206	Hs.151858	ESTs	1.52	2.10
	415908	H08623	Hs.22833	ESTs	1.37	2.13
	438942	AW875398	Hs.6451	PRO0659 protein	1.80	1.55
65	407618	AW054922	Hs.53478	Homo sapiens cDNA FLJ12366 fis, clone MA	2.16	3.18
	429177	AA447527	Hs.207429	ESTs	1.74	3.19
	448357	N20169	Hs.108923	RAB38, member RAS oncogene family	0.77	0.73
	422008	AJ000534	Hs.110708	sarcoglycan, epsilon	1.52	4.08
	434461	AA744046	Hs.133350	ESTs, Weakly similar to I78885 serine/th	1.66	2.16
70	413489	BE144228		gb:MRO-HT0165-140200-009-d04 HT0165 Homo	1.28	2.23
	405551			Target Exon	1.11	1.19
	441183	BE562910	Hs.92679	Homo sapiens clone CDABP0014 mRNA sequen	1.20	1.20
	456034	AW450979		gb:UH-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su	1.98	2.53
	420611	AA594636	Hs.129929	ESTs	1.46	2.15
75	422061	BE178434	Hs.267995	ESTs, Moderately similar to G02654 ribos	1.42	2.30
	437908	AI082424		ESTs	1.38	2.21
	423052	M28214	Hs.123072	RAB3B, member RAS oncogene family	0.74	0.43
	401927			C17000914*:gij8394367[ref]NP_058549.1] s	2.26	2.14

5	432967	AA572949	Hs.207566	ESTs	1.52	2.28
	439159	AF087972	Hs.120938	ESTs	2.03	2.08
	415357	H22757	Hs.13471	ESTs	1.82	2.07
	442327	AA991745	Hs.42522	ESTs	1.48	2.88
	430186	AB020696	Hs.234791	KIAA0889 protein	1.46	2.23
	426971	AI809984	Hs.243209	ESTs, Weakly similar to NPA1_HUMAN NEURO	1.06	2.13
	422687	AW068823	Hs.119206	insulin-like growth factor binding prote	1.61	1.37
	432954	AI076345	Hs.214199	ESTs	1.19	2.84
10	429040	AL035542	Hs.248169	olfactory receptor, family 2, subfamily	1.25	1.44
	414169	AA136169	Hs.149335	ESTs	1.59	2.51
	419882	AA687313	Hs.190043	ESTs	1.20	2.50
	426900	AW163564	Hs.142375	ESTs	1.87	1.77
	418773	T39748	Hs.325474	Target CAT	1.35	2.02
15	439776	AL360140	Hs.176005	Homo sapiens mRNA full length insert cDN	1.32	2.10
	428712	AW085131	Hs.190452	KIAA0365 gene product	1.41	1.52
	408839	AW277084		gb:xp61h09.x1 NCI_CGAP_Ov39 Homo sapiens	1.14	2.03
	450492	AW290961	Hs.201815	ESTs	1.17	2.21
	434654	AI825942	Hs.139366	Homo sapiens clone L5 polyadenylated HER	1.62	2.31
20	457567	AW939074		gb:QV1-DT0069-010200-057-c12 DT0069 Homo	1.80	3.73
	452426	AI904823	Hs.31297	duodenal cytochrome b	2.15	1.84
	418559	AA225048	Hs.104207	ESTs	1.84	2.33
	439099	AB037800	Hs.5462	protein kinase C and casein kinase subst	1.07	1.15
	451984	R60571	Hs.27406	Homo sapiens mRNA; cDNA DKFZp566F1946 (f	1.18	1.22
25	420789	AI670057	Hs.199882	ESTs	2.24	2.55
	455396	AA236863	Hs.188894	ESTs, Weakly similar to APXL_HUMAN APICA	1.07	1.14
	402948			NM_025206:Homo sapiens hypothetical prot	2.41	1.83
	425405	AW296631	Hs.283403	ESTs	1.28	1.07
	439732	AW629604	Hs.167641	hypothetical protein from EUROIMAGE 1703	0.85	0.77
30	416784	AA334592	Hs.79914	lumican	1.88	1.27
	422531	AW967280	Hs.293894	ESTs, Weakly similar to HERC2 [Hsapiens	1.20	1.25
	415608	F12795	Hs.12286	ESTs, Moderately similar to ALU1_HUMAN A	1.03	2.31
	428671	BE297851	Hs.189482	zinc finger protein 179	1.26	2.20
	420007	H13700	Hs.31235	ESTs, Weakly similar to Y934_HUMAN HYPOT	1.60	2.25
35	400850			Target Exon	1.22	1.03
	404580			trichorhinophalangeal syndrome 1 gene (T	1.00	1.00
	407680	AW064284	Hs.279153	ESTs	1.02	2.28
	410420	AA224053	Hs.172405	cell division cycle 27	1.64	1.00
	421234	AA907153	Hs.190060	ESTs	1.76	1.45
40	426791	AA384910	Hs.46519	ESTs	1.12	2.15
	430439	AL133561		DKFZP434B061 protein	1.00	1.00
	434036	AI659131	Hs.197733	hypothetical protein MGC2849	1.00	1.00
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.40	1.00
	440304	BE159984	Hs.125395	ESTs	1.00	1.00
45	441699	AW511126	Hs.127572	ESTs	1.00	1.73
	443383	AI792453	Hs.166507	ESTs	2.04	1.00
	445660	AI702668	Hs.201955	ESTs	1.00	1.00
	453160	AI263307	Hs.239884	H2B histone family, member L	1.00	1.00
	456513	AA279143	Hs.88561	ESTs	1.00	1.40
50	457231	AI472022	Hs.301959	proline synthetase co-transcribed (bacte	0.98	0.63
	459565	W27085	Hs.209694	ESTs	1.00	1.00
	429317	AA831552	Hs.268016	Homo sapiens cDNA: FLJ21243 fis, clone C	1.00	1.00
	430971	M26150	Hs.248177	H3 histone family, member L	1.14	1.40
	408376	AW971303	Hs.292601	ESTs	1.08	1.60
55	411920	AW876263		gb:PMA-PT0019-131299-006-E09 PT0019 Homo	0.82	0.45
	457389	AW970989		gb:EST383074 MAGE resequences, MAGK Homo	0.92	0.71
	408565	BE502544	Hs.282244	ESTs, Weakly similar to peptidoglycan re	1.00	2.10
	438086	AA336519	Hs.83623	nuclear receptor subfamily 1, group I, m	1.00	1.00
	446779	AI341135	Hs.156084	ESTs	1.06	2.02
60	441691	AI015418	Hs.127556	ESTs	1.13	2.03
	402039			Target Exon	0.44	0.36
	437133	AB018319	Hs.5460	KIAA0776 protein	0.95	0.63
	438089	W05391		nuclear receptor subfamily 1, group I, m	3.12	1.00
	409582	R27430	Hs.271565	ESTs	1.00	1.00
65	428769	AW207175	Hs.106771	ESTs	1.00	1.48
	442868	AI022701	Hs.336984	ESTs	1.27	1.62
	439559	AW364675	Hs.173921	ESTs, Weakly similar to 2109260A B cell	1.00	1.33
	426958	R18845	Hs.172979	zinc finger protein 177	1.24	2.25
	419015	T79262	Hs.14463	ESTs	1.16	2.03
70	415806	AA169560		gb:zo89d08.r1 Stratagene ovarian cancer	1.00	1.33
	436110	AA704899	Hs.291651	ESTs, Weakly similar to I38022 hypothe	1.60	2.21
	458760	AI498631	Hs.111334	ferritin, light polypeptide	1.10	1.43
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	1.28	1.00
	438182	AW342140	Hs.182545	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.90	2.31
75	438091	AW373052		nuclear receptor subfamily 1, group I, m	4.70	1.00
	441633	AW558544	Hs.112242	normal mucosa of esophagus specific 1	2.48	1.00
	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	1.96	2.84
	416055	Z45423	Hs.13349	Homo sapiens cDNA FLJ14647 fis, clone NT	1.52	1.46

	417895	AA836392	Hs.56237	hypothetical protein FLJ20495	1.05	1.18
	422959	AV647015		paired immunoglobulin-like receptor beta	1.33	1.25
	408969	AW297929	Hs.328317	EST	1.88	2.07
5	409536	H59024	Hs.14485	Homo sapiens cDNA: FLJ23220 fis, clone A	1.18	2.38
	447449	AW137091	Hs.18624	KIAA1052 protein	1.07	1.13
	437315	AW976247	Hs.153248	ESTs	1.16	2.53
	459317	BRCA1b		Eos Control	1.36	1.32
	405137			Target Exon	1.11	1.18
	400366	M22333		Target	1.55	1.42
10	423413	AA325560	Hs.346401	ESTs	1.78	1.57
	433972	AI878910	Hs.278670	cisplatin resistance-associated overexpr	1.62	2.98
	440748	AW451780	Hs.130363	ESTs	1.42	2.14
	422637	AA399024	Hs.118836	myoglobin	1.46	2.38
	432342	AL036128	Hs.274404	plasminogen activator, tissue	1.67	1.10
15	442820	AW293459	Hs.172681	ESTs	1.02	1.13
	436573	AA723297	Hs.127138	ESTs	1.18	1.15
	403779			Target Exon	1.13	1.15
	447686	AI939440	Hs.345192	ESTs	1.66	2.78
	447506	R78778	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	1.44	2.48
20	425853	BE348404	Hs.24740	ESTs	1.40	2.75
	454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	1.52	2.00
	424132	AA335715	Hs.200299	ESTs	1.34	1.32
	421707	NM_014921	Hs.107054	lectomedin-2	1.09	1.14
	442871	AI290691	Hs.131393	ESTs	1.40	2.50
25	448489	AI523875		gb:lg97d04.x1 NCI_CGAP_CLL1 Homo sapiens	1.31	2.20
	436365	AW444548	Hs.163118	ESTs	1.07	1.12
	415733	AI052628	Hs.271570	ESTs, Weakly similar to 2109260A B cell	1.91	2.01
	413888	AA580288		gb:nn12d01.s1 NCI_CGAP_Co12 Homo sapiens	1.75	1.93
	408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	1.92	1.73
30	442959	AI025248	Hs.6927	ESTs	1.05	1.12
	409610	AW444736	Hs.27854	ESTs	1.62	2.45
	424793	AI559696	Hs.298885	ESTs	1.37	2.78
	449977	C16939	Hs.297848	ESTs	1.52	4.57
35	414051	BE244127		gb:TCBAP1E0661 Pediatric pre-B cell acut	1.68	2.84
	422400	AA974434	Hs.128353	ESTs	1.04	2.20
	443908	AW295791	Hs.13040	G protein-coupled receptor 86	1.47	2.10
	439316	AF086126	Hs.118208	Homo sapiens cDNA FLJ11727 fis, clone HE	2.08	0.59
	438505	AA808948	Hs.173776	ESTs, Moderately similar to ALU1_HUMAN A	1.44	2.73
40	436186	AK001084	Hs.333498	Homo sapiens cDNA FLJ10222 fis, clone HE	2.17	1.00
	453740	AL120295	Hs.311809	ESTs, Moderately similar to PC4259 ferri	1.88	2.58
	431756	R69465	Hs.255889	ESTs	1.12	1.30
	424487	T08754	Hs.6259	KIAA1698 protein	1.15	1.15
	435392	R07195	Hs.19918	ESTs	1.38	2.64
45	430068	AA464964		gb:zx80f10.s1 Soares ovary tumor NbHOT H	0.92	2.12
	418741	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	1.44	2.51
	411664	BE065069	Hs.270833	amphiregulin (schwannoma-derived growth	1.94	2.33
	416586	D44643	Hs.14144	secreted modular calcium-binding protein	1.72	2.68
	419612	AI498267	Hs.110613	KIAA0421 protein	2.28	2.46
50	435800	AI248285	Hs.118348	ESTs	1.42	2.45
	433363	AA584829	Hs.275163	non-metastatic cells 2, protein (NM23B)	2.07	2.53
	422936	AA319278		gb:EST21478 Adrenal gland tumor Homo sap	1.46	1.22
	413358	BE259160	Hs.75313	aldo-keto reductase family 1, member B1	1.43	1.43
	435357	N71620	Hs.118173	ESTs	1.44	2.93
55	441063	AA913819	Hs.188025	ESTs	1.20	2.80
	450724	R55428		gb:yj79b05.r1 Soares breast 2NbHBst Homo	1.44	4.18
	430446	AF131782	Hs.241438	Homo sapiens clone 24941 mRNA sequence	1.03	2.34
	401577			NM_000761:Homo sapiens cytochrome P450,	1.13	1.22
	403978			C5000010*:gij10440464[dbj]BAB15765.1] (A	1.22	1.66
60	459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	2.72	4.60
	416708	H78836	Hs.181900	ESTs, Moderately similar to ALU1_HUMAN A	1.36	2.03
	451410	AL110235	Hs.26358	DKFZP566K1924 protein	1.51	2.29
	451159	AW298631	Hs.27721	Wolf-Hirschhorn syndrome candidate 1-lik	1.33	1.09
	448455	AI252625	Hs.269860	ESTs, Moderately similar to S65657 alpha	0.83	0.40
65	444020	R92962	Hs.35052	ESTs	1.66	2.50
	414623	BE391050		gb:601285674F1 NIH_MGC_44 Homo sapiens c	1.84	3.88
	454915	AW841619		gb:RC1-CN0017-120200-012-b09 CN0017 Homo	1.14	2.10
	444064	W85970	Hs.16292	ESTs	0.80	0.63
	454353	AW389693	Hs.300700	hypothetical protein FLJ20727	1.30	2.10
70	447794	AI424999	Hs.161445	EST	1.26	2.05
	426686	AI362802	Hs.171814	parathyromin	1.16	1.11
	435815	AA700482	Hs.113157	ESTs	1.66	2.73
	432482	L19267	Hs.275924	dystrophin myotonia-containing WD repea	1.10	1.15
	431062	AA491270	Hs.187946	ESTs	1.44	2.60
75	429191	AF065215	Hs.198161	phospholipase A2, group IVB (cytosolic)	1.35	1.06
	424456	AA341017	Hs.25549	hypothetical protein FLJ20898	1.21	3.45
	451124	AI186203	Hs.31432	cardiac ankyrin repeat protein	1.23	2.10
	432828	AB042326	Hs.287402	chondroitin 4-sulfotransferase	1.11	2.71

	431868	BE246400	Hs.285176	acetyl-Coenzyme A transporter	1.03	3.10
	429321	AA449921		gb:zx37g07.r1 Soares_tetal_fetus_Nb2HF8_	1.68	2.93
	417890	R79048		gb:yi87g02.r1 Soares_placenta_Nb2HP_Homo	1.32	1.80
5	439590	AF086410		gb:Homo sapiens full length insert cDNA	1.32	2.43
	420232	AW450051	Hs.256295	ESTs	1.28	2.26
	418927	BE349635	Hs.190284	ESTs	1.46	1.23
	441940	AW298115	Hs.128152	ESTs	1.34	1.34
	401090			C9000193*.g 6330729 dbj BAA86547.1 (AB	1.50	1.40
10	409136	AW206670	Hs.50748	chromosome 21 open reading frame 18	1.02	2.38
	438267	AW205708	Hs.292725	ESTs, Weakly similar to T18818 hypotheti	1.28	2.25
	422482	AI439905	Hs.344476	gb:ti57g08.x1 NCL_CGAP_Lym12 Homo sapien	1.05	2.81
	420067	TS2431	Hs.94795	Homo sapiens mRNA; cDNA DKFZp564O222 (fr	1.77	2.40
	442180	AA983913	Hs.128929	ESTs	1.76	2.38
	434256	AI378817	Hs.191847	ESTs	1.05	2.06
15	444519	AI160304	Hs.28313	ESTs	0.55	0.63
	454459	AW855738	Hs.17767	KIAA1554 protein	1.10	2.05
	455988	BE177983		gb:RC3-HT0600-230300-021-g10 HT0600 Homo	1.70	2.64
	444510	AI367823	Hs.146872	ESTs	1.44	2.08
	456210	N49729	Hs.156875	ESTs	1.64	2.65
20	450569	AW192334	Hs.38218	ESTs	1.78	2.71
	414921	BE390551	Hs.77628	steroidogenic acute regulatory protein r	1.05	1.12
	401381			C14000165.g 12698069 dbj BAB21853.1 (A	0.63	0.85
	439998	BE559554	Hs.61790	hypothetical protein FLJ23338	1.06	1.14
	453762	AW977286	Hs.17428	RBP1-like protein	1.42	2.68
25	419403	AA744520	Hs.87734	ESTs, Weakly similar to nonsyndromic hea	0.99	2.17
	423736	AW936874		gb:RC1-DT0029-120100-011-407 DT0029 Homo	2.05	1.56
	421186	AI798039	Hs.270563	ESTs, Moderately similar to T12512 hypot	1.29	1.31
	426435	AI827946	Hs.124854	hypothetical brain protein my040	1.36	1.59
	439312	AA833902	Hs.270745	ESTs	1.60	2.50
30	407924	BE537128	Hs.299797	ESTs	1.51	1.15
	409692	AI500724		KIAA1550 protein	1.72	2.21
	415449	H15034		gb:ym20a03.s1 Soares Infant brain 1N1B H	1.50	2.13
	423436	R21176	Hs.100926	ESTs	1.18	2.60
	458697	AI797713	Hs.156471	ESTs	1.54	2.20
35	415770	M79237		gb:EST01385 Subtracted Hippocampus, Stra	1.49	1.55
	449279	AI962312	Hs.224976	ESTs, Weakly similar to CRX_HUMAN CONE-R	2.50	3.60
	429735	AA458759	Hs.188794	ESTs	1.84	2.31
	442124	R66412	Hs.129013	Homo sapiens cDNA FLJ14309 fis, clone PL	1.10	1.19
40	412557	AA761612	Hs.291557	ESTs	1.10	1.18
	409335	NM_001502	Hs.53985	glycoprotein 2 (zymogen granule membrane	1.18	1.12
	430526	AF181862	Hs.242407	G protein-coupled receptor, family C, gr	1.35	2.39
	420855	AA281092	Hs.33417	Homo sapiens cDNA: FLJ22806 fis, clone K	1.22	2.09
	450567	AA033904	Hs.269235	ESTs	1.60	2.20
	414197	W44877	Hs.55501	ESTs	1.06	2.08
45	448800	AI571294	Hs.298889	ESTs, Moderately similar to ALLU1_HUMAN A	1.65	2.79
	421338	AA287443		gb:zs52c10.r1 NCL_CGAP_GCB1 Homo sapiens	1.47	2.90
	412679	BE144762		gb:CMO-HT0180-041099-065-b04 HT0180 Homo	1.32	2.53
	417882	R22311		gb:yh26c09.r1 Soares placenta Nb2HP Homo	1.58	2.43
50	425112	AW953291	Hs.64211	hypothetical protein MGC5601	0.70	0.63
	401658			C16000210.g 12585542 sp O14771 Z213_HUM	1.68	2.04
	409325	AW377549	Hs.17865	ESTs	1.68	2.21
	437402	AI553976	Hs.121191	ESTs	1.20	2.35
	433455	AA360439	Hs.89319	ESTs	0.98	2.53
55	457329	AI634860	Hs.247043	type 1 tumor necrosis factor receptor sh	0.59	0.43
	434830	AW852235		gb:QV0-CT0225-230300-169-e11 CT0225 Homo	1.24	1.12
	450696	AI654223	Hs.16026	hypothetical protein FLJ23191	1.44	2.53
	446098	AW072215	Hs.208470	ESTs	1.38	2.93
	443310	BE552018	Hs.133152	ESTs	0.85	0.83
60	424015	N95696	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	1.42	2.26
	420229	AA256675	Hs.194058	ESTs, Weakly similar to AF252293 1 PAR3	1.70	2.39
	403371			Target Exon	1.50	3.43
	410744	H86002		gb:ys92b01.r1 Soares retina N2b5HR Homo	1.32	2.13
	424160	T74062		gb:yc81f01.r1 Soares Infant brain 1N1B H	1.30	2.17
65	438818	AW979008	Hs.222487	ESTs	1.98	2.43
	438791	AA825750	Hs.129983	ESTs	1.12	2.15
	411206	AW827390	Hs.16689	ESTs	1.17	2.58
	432211	BE274530	Hs.273333	hypothetical protein FLJ10986	0.42	0.30
	448918	AB011152	Hs.22572	KIAA0580 protein	1.54	2.63
	424496	AI733451	Hs.167165	hypothetical protein FLJ12975	1.39	2.25
70	410730	AW368860		DnaJ (Hsp40) homolog, subfamily B, membe	1.84	3.23
	457581	AA578512		gb:nh22e11.s1 NCL_CGAP_Pr1 Homo sapiens	1.21	1.09
	435353	AW243062	Hs.190348	ESTs	1.90	2.98
	417029	AW952192	Hs.273385	guanine nucleotide binding protein (G pr	1.21	1.24
	433682	AA642418	Hs.17381	ESTs	1.18	2.23
75	424915	R42755	Hs.23096	ESTs	1.60	2.73
	442201	AW516704	Hs.208726	ESTs	1.74	3.20
	429111	AI870811	Hs.7579	KIAA1151 protein	1.27	1.40

	429282	N27596	Hs.21342	ESTs	1.84	3.73
	436604	AW105129	Hs.242158	ESTs	1.27	2.70
	448712	W01046	Hs.333371	Homo sapiens clone TA40 untranslated mRNA	0.79	2.70
5	412274	AA101443		gb:zn74a07.r1 Stratagene NT2 neuronal pr	1.40	2.53
	403859			C5001408*gl 12621134 ref NP_075244.1 M	1.76	2.00
	451521	AA018237	Hs.126189	gb:ze53a02.r1 Soares retina N2b4HR Homo	1.48	2.51
	443210	AI692649	Hs.9451	hypothetical protein MGC13168	1.44	2.60
	442722	AL048889	Hs.131029	ESTs, Weakly similar to B28096 line-1 pr	1.20	2.25
10	400840			Target Exon	0.66	0.60
	454639	AW811633		gb:RC2-ST0158-091099-011-d05 ST0158 Homo	1.23	1.41
	439864	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	1.77	2.12
	410725	AW799279		gb:RC0-UM0051-210300-012-h06 UM0051 Homo	1.08	2.55
	423430	AF112481	Hs.128501	RAD54, S. cerevisiae, homolog of, B	1.94	2.29
	450717	T94709		gb:ye35d09.r1 Stratagene lung (937210) H	1.56	2.64
15	400314	NM_018949	Hs.192720	G protein-coupled receptor 14	0.89	0.87
	434947	AA654320	Hs.183819	Homo sapiens cDNA FLJ12304 fis, clone MA	1.19	2.14
	453582	AW854339	Hs.33476	hypothetical protein FLJ11937	1.24	2.19
	409005	AW299806	Hs.297256	ESTs	1.24	2.03
20	406584			Target Exon	1.52	2.37
	420203	AA256374	Hs.191069	ESTs	1.16	1.37
	406156			Target Exon	1.18	1.17
	422132	AB002337	Hs.112078	KIAA0339 gene product	1.08	1.16
	441371	AW452292	Hs.197354	ESTs	1.19	2.00
25	434807	AA364183	Hs.323443	hypothetical protein FLJ11806	1.30	2.76
	424542	AI860558	Hs.272009	ESTs, Weakly similar to ALU2_HUMAN ALU S	1.48	2.48
	450893	AK002185	Hs.25625	hypothetical protein FLJ11323	1.15	1.57
	418481	M81945	Hs.85289	CD34 antigen	2.16	1.76
	443077	AI459490	Hs.60090	Homo sapiens cDNA FLJ13595 fis, clone PL	1.36	2.41
30	437521	AA758756	Hs.121380	ESTs	1.07	2.05
	430265	L36033	Hs.237356	stromal cell-derived factor 1	2.34	1.35
	446898	AV660906	Hs.184411	albumin	1.52	1.33
	429725	AA457367	Hs.191638	ESTs	1.38	3.00
	425114	AW409763	Hs.50699	ESTs, Weakly similar to 2109260A B cell	1.13	2.34
35	419879	Z17805	Hs.93584	Homer, neuronal immediate early gene, 2	1.62	1.71
	435284	AA879470	Hs.96849	Homo sapiens cDNA FLJ11492 fis, clone HE	1.20	2.50
	415634	F13165	Hs.12549	ESTs, Weakly similar to 2109260A B cell	1.46	2.35
	420565	AI806770	Hs.30258	ESTs	1.39	3.85
	419494	W01060	Hs.34382	ESTs	1.10	1.75
40	458183	AL031591	Hs.7370	phosphatidylinositol transfer protein, b	1.28	2.24
	416620	RS3080	Hs.35035	ESTs	1.81	2.58
	431356	AW499632	Hs.288512	Homo sapiens cDNA FLJ11632 fis, clone HE	1.42	2.03
	433282	BE539101	Hs.5324	hypothetical protein	0.33	0.20
	456898	NM_001928	Hs.155597	D component of complement (adipsin)	1.50	0.95
45	458126	AW979136	Hs.124629	ESTs	1.34	1.32
	414005	AA134489	Hs.269379	ESTs	1.52	2.07
	411496	AW849241		gb:IL3-CT0215-210200-088-E03 CT0215 Homo	1.10	2.21
	451147	AA016982	Hs.64341	ESTs	1.53	2.29
	450238	T89693	Hs.138777	ESTs	1.32	2.28
50	449284	BE502240	Hs.38592	hypothetical protein FLJ23342	1.46	1.40
	449479	AI797619	Hs.197659	ESTs	0.72	0.68
	403066			Target Exon	1.32	1.19
	410118	AW590680	Hs.110802	von Willebrand factor	1.72	2.54
	437674	AI749921	Hs.205377	ESTs	1.38	2.21
55	431065	AA491286	Hs.128792	ESTs	1.30	2.08
	416352	H78006	Hs.19553	ESTs	1.05	1.14
	452565	BE066552		gb:RC3-BT0333-300300-017-h08 BT0333 Homo	1.46	2.53
	418115	AW005376	Hs.173280	ESTs	1.20	0.98
60	422031	R66895	Hs.28788	ESTs	1.37	1.37
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	1.64	2.20
	457683	AI821877	Hs.140002	ESTs, Moderately similar to ALU7_HUMAN A	1.03	2.35
	435521	W23814	Hs.6361	mitogen-activated protein kinase kinase	0.73	0.59
	438874	H02780	Hs.347520	gb:yl41a11.r1 Soares placenta Nb2HP Homo	1.56	2.73
	441167	AA921754	Hs.211781	ESTs	1.74	2.12
65	455917	BE156765		gb:RC1-HT0370-120100-012-c09 HT0370 Homo	1.29	1.35
	419058	AW675039	Hs.1227	aminolevulinatase, delta, dehydratase	2.04	1.83
	408651	BE266928	Hs.17126	hypothetical protein MGC15912	1.30	1.23
	442737	AB002319	Hs.8663	KIAA0321 protein	0.85	0.79
	407134	TS1588		gb:yb27e06.s1 Stratagene fetal spleen (9	1.23	0.97
70	447492	AI381619	Hs.20188	ESTs	1.26	2.28
	437840	AA884836	Hs.292014	ESTs	2.05	2.29
	412294	AA689219	Hs.117176	poly(A)-binding protein, nuclear 1	1.47	3.55
	419909	AL136653	Hs.93575	decidual protein induced by progesterone	1.10	2.18
	432569	AI131140	Hs.152434	ESTs	1.34	1.83
75	412252	AW903782		gb:CM4-NN1032-190400-527-g09 NN1032 Homo	1.26	2.00
	444298	Z17870		gb:HSDHII020 Stratagene cDNA library Hum	1.36	2.68
	445261	T79759	Hs.250651	ESTs, Weakly similar to I38022 hypothe	0.95	2.23
	418315	T06475	Hs.124962	Homo sapiens, clone IMAGE:3510191, mRNA,	0.82	0.82

	440357	AA379353	Hs.20950	phospholysine phosphohistidine inorganic	0.83	0.68
	440867	AI417007	Hs.166338	ESTs	1.45	1.50
	410956	AW938322		gb:PM1-DT0054-231299-002-c02 DT0054 Homo	1.06	2.95
5	446574	AI310135	Hs.335933	ESTs	1.54	2.45
	447912	AW576549	Hs.165728	ESTs, Weakly similar to I38022 hypothe	1.22	2.07
	457741	BE044740		gb:hm55g10.x1 NCI_CGAP_RDF1 Homo sapiens	1.89	2.08
	433762	AA732484	Hs.169399	ESTs	1.24	2.58
	418156	W17056	Hs.83623	nuclear receptor subfamily 1, group I, m	3.71	1.38
10	409282	AW966480		gb:EST378554 MAGE resequences, MAGI Homo	1.70	1.70
	425169	AW292500	Hs.128514	ESTs	1.13	1.12
	458497	AI161428	Hs.75916	splicing factor 3b, subunit 2, 145kD	1.26	2.28
	405673			NM_022775:Homo sapiens hypothetical prot	2.00	1.00
	442691	AW341438	Hs.278036	ESTs	1.38	2.28
15	424316	AA676403	Hs.145078	regulator of differentiation (in S. pomb	1.06	2.10
	444608	AI174683	Hs.329863	ESTs	1.95	1.82
	447345	BE247767	Hs.18166	KIAA0870 protein	1.26	2.10
	438488	AW979249		gb:EST391359 MAGE resequences, MAGP Homo	1.68	2.63
	428946	D42046	Hs.194665	DNA2 (DNA replication helicase, yeast, h	1.32	2.33
20	403214			NM_016232*:Homo sapiens interleukin 1 re	1.02	2.15
	404495			C8001441*:gij8923061 refNP_060114.1 hy	2.20	2.49
	443471	AW236939	Hs.172154	Homo sapiens clone FLB3442 PRO0872 mRNA,	1.58	1.74
	437116	AL049253	Hs.190162	ESTs	1.22	2.53
	451357	AB020640	Hs.26319	Human DNA sequence from clone RP3-467L1	0.94	2.35
25	408255	AW807321		gb:MR4-ST0062-240300-003-g05 ST0062 Homo	1.12	1.39
	448931	AI597805	Hs.192671	ESTs	1.30	3.29
	422343	AI628633	Hs.346823	gb:ty77d05.x1 NCI_CGAP_Kid11 Homo sapien	1.86	2.32
	407140	AA059106	Hs.271780	ESTs, Weakly similar to I38022 hypothe	1.37	1.01
	429187	AA447648	Hs.163872	ESTs, Weakly similar to S65657 alpha-1C-	1.74	1.55
30	423614	AI457640	Hs.206632	ESTs	1.48	2.83
	428073	AA446167	Hs.47385	ESTs	1.24	2.00
	415732	AA167566	Hs.271570	ESTs, Weakly similar to 2109260A B cell	1.31	2.34
	412634	U55984	Hs.289088	heat shock 90kD protein 1, alpha	0.42	0.22
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	1.94	1.27
35	415007	BE244332	Hs.77770	adaptor-related protein complex 3, mu 2	0.78	0.71
	402654			Target Exon	0.90	0.85
	457974	AW842353	Hs.321717	ESTs, Weakly similar to S22765 heterogen	0.86	0.90
	405340			C2002952:gil1345964 sp P10079 FBP1_STRPU	1.46	2.33
40	426259	BE395776	Hs.168640	ankylosis, progressive (mouse) homolog	1.63	2.75
	442237	AW905607	Hs.24567	ESTs, Weakly similar to KBF3_HUMAN NUCLE	1.08	3.38
	456370	AA234938	Hs.87384	ESTs	0.77	2.83
	407041	X15673		gb:Human pTR2 mRNA for repetitive sequen	2.00	1.84
	452001	AI827675	Hs.274281	fidgetin	1.38	2.03
	445137	AI733837	Hs.145661	ESTs	1.60	3.00
45	440808	AK001339	Hs.7432	hypothetical protein FLJ10477	1.17	2.10
	404418			Target Exon	1.90	3.36
	447658	AI916872	Hs.213424	ESTs	1.90	2.21
	434414	AI798376		gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens	1.58	1.24
	400834			NM_002240*:Homo sapiens potassium inward	1.25	2.33
50	449542	AW857362	Hs.268855	ESTs, Weakly similar to I38022 hypothe	1.46	1.28
	441043	AA913422	Hs.192104	ESTs	1.26	1.09
	403391			C3001164*:gil1730196 sp P50573 GAR3_RAT	1.46	2.55
	449129	AI631602	Hs.258949	ESTs	1.27	2.48
	418321	D63477	Hs.84087	KIAA0143 protein	0.56	0.52
55	426789	F06596	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	1.31	2.06
	443679	AK001810	Hs.9670	hypothetical protein FLJ10948	1.34	1.22
	428554	R46070	Hs.6407	ESTs	1.04	2.08
	401890			Target Exon	1.24	1.14
	419501	AW843822		gb:CM4-CN0045-010200-514-f08 CN0045 Homo	1.74	1.38
60	457096	AI809202	Hs.208343	ESTs, Weakly similar to carboside sulf	0.82	0.87
	426123	AA370352		gb:EST82246 Prostate gland I Homo sapien	1.28	2.35
	449445	AW197349	Hs.232197	ESTs	1.24	2.13
	430683	AC004862	Hs.247768	Homo sapiens PAC clone RP4-697H17 from 7	1.30	2.00
	440642	AI744995		ESTs, Moderately similar to ALU4_HUMAN A	1.29	2.44
65	455236	AW875972		gb:CM3-PT0014-071299-051-b05 PT0014 Homo	1.78	2.95
	449622	AW013915	Hs.196578	ESTs	1.42	2.20
	415116	AA160363	Hs.269956	ESTs	2.02	1.03
	457269	AI338993	Hs.134535	ESTs	1.93	1.35
	427877	AW138725	Hs.178057	ESTs	1.91	2.42
70	454631	AW811324		gb:IL3-ST0141-131099-017-A02 ST0141 Homo	1.00	3.13
	458390	AI792585	Hs.133272	ESTs, Weakly similar to ALUC_HUMAN !!!	1.02	2.21
	435844	AA700856	Hs.59651	ESTs, Weakly similar to I78885 serine/th	0.85	0.81
	427237	AA399964	Hs.97763	ESTs	1.57	1.44
	408855	T83061	Hs.319946	Homo sapiens mRNA for KIAA1727 protein,	1.20	3.13
	442151	AI733404	Hs.128865	ESTs	1.50	2.13
75	412708	R26830	Hs.106137	ESTs, Weakly similar to CGHU7L collagen	1.16	3.00
	417262	AA195276	Hs.263858	ESTs, Moderately similar to B34087 hypot	1.25	2.40
	419362	N64116	Hs.24624	hypothetical protein FLJ21945	1.38	2.48

	447248	AW295831	Hs.6496	ESTs	1.56	2.03
	415622	F13010	Hs.12400	ESTs	1.48	2.30
	414065	AW515373	Hs.271249	Homo sapiens cDNA FLJ13580 fis, clone PL	1.26	2.88
	414585	W46954	Hs.334716	hypothetical protein MGC16291	1.24	2.05
5	443197	Z43613		gb:HSC1GD091 normalized infant brain cDN	1.11	2.04
	428266	AJ382001	Hs.43590	ESTs	1.09	2.03
	447083	AJ472124	Hs.157757	ESTs	1.66	3.53
	412302	AW936334		gb:QV4-DT0021-281299-070-g05 DT0021 Homo	1.74	3.00
	445555	AW974013		ESTs	1.32	1.29
10	453117	AW162044	Hs.104203	hypothetical protein MGC12981	0.73	0.81
	436757	AW975663	Hs.293404	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.21	1.88
	431976	AA719001	Hs.291065	ESTs	1.23	2.01
	430557	AA482910	Hs.279664	ESTs	1.64	2.65
	438744	BE314727	Hs.75721	profilin 1	0.85	0.85
15	439325	AF086139	Hs.150423	cyclin-dependent kinase 9 (CDC2-related	1.16	2.05
	438117	AA328041	Hs.194329	hypothetical protein FLJ21174	0.79	0.76
	401686			NM_014587*:Homo sapiens SRY (sex determi	1.32	2.31
	420269	U72937	Hs.96264	alpha thalassemia/mental retardation syn	0.78	0.53
20	434288	AW189075	Hs.116265	fibrillin3	2.42	4.23
	433215	AB040912	Hs.191098	hypothetical protein FLJ11598	1.36	1.36
	413429	BE139117	Hs.278881	ESTs	1.30	2.98
	426417	AA377908	Hs.13254	ESTs	1.36	1.77
	413882	AA132973	Hs.184492	ESTs	1.55	2.10
25	413346	AA128566		gb:z24h06.r1 Soares_pregnant_uterus_NbH	1.29	1.77
	445020	AI205655	Hs.147221	ESTs	1.90	2.00
	418175	AW967054	Hs.206312	ESTs, Weakly similar to I38022 hypothei	1.60	3.70
	429582	AJ569068	Hs.22247	ESTs	1.06	2.38
	409134	AW340389	Hs.250585	ESTs	1.64	2.57
30	415642	U19878	Hs.336224	transmembrane protein with EGF-like and	0.73	2.33
	435887	F13625	Hs.124183	ESTs	1.10	2.33
	440513	BE407106	Hs.65907	Homo sapiens, clone IMAGE:3959816, mRNA,	0.85	2.03
	419711	C02621	Hs.159282	ESTs	1.22	2.00
	434249	AA987537	Hs.129875	ESTs	1.29	2.48
35	437355	AL359557	Hs.306508	Homo sapiens mRNA; cDNA DKFZp762O1415 (f	1.86	2.08
	428360	H10291	Hs.30974	ESTs	1.40	2.05
	435339	AJ358300	Hs.129827	ESTs	1.38	2.18
	435345	AW360966	Hs.6653	ESTs	1.49	2.27
	435105	AJ878982	Hs.131859	Homo sapiens F-box protein FBX11 mRNA, p	1.78	2.33
40	459645	AA074346	Hs.250715	ESTs	1.50	2.40
	449691	AA002143	Hs.21413	solute carrier family 12, (potassium-chl	0.74	0.69
	425955	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha	1.42	2.76
	437272	AW975957		gb:EST388066 MAGE resequences, MAGN Homo	1.00	2.16
	456955	NM_006925	Hs.166975	splicing factor, arginine/serine-rich 5	0.84	0.81
45	421362	AK000050	Hs.103853	hypothetical protein FLJ20043	1.30	2.21
	457926	AA452378	Hs.11637	Homo sapiens mRNA; cDNA DKFZp547J125 (fr	1.27	2.12
	444557	AI167637	Hs.146924	ESTs	1.83	2.35
	434476	AW585820	Hs.84264	acidic protein rich in leucines	1.43	3.80
	458059	AW015588	Hs.137232	ESTs, Weakly similar to S65657 alpha-1C-	1.30	2.23
50	413595	AW235215	Hs.16145	ESTs	2.10	2.43
	417281	R98773	Hs.268883	ESTs	1.26	2.10
	445689	BE158869		gb:QV0-HT0398-210100-096-f08 HT0398 Homo	1.15	2.15
	423249	AA323682	Hs.125374	ESTs, Weakly similar to S26689 hypothei	1.76	1.50
	408366	AW511255	Hs.346442	ESTs	1.74	2.91
55	441359	AJ435179	Hs.126820	ESTs	2.43	1.59
	413068	BE063792		gb:QV3-BT0295-260100-066-d06 BT0295 Homo	1.52	2.09
	441322	AW071851	Hs.130628	ESTs	1.42	2.10
	409124	AW292809	Hs.50727	N-acetylglucosaminidase, alpha- (Sanfil	1.11	2.20
	432413	AK000257	Hs.274505	Homo sapiens mRNA; cDNA DKFZp564A216 (tr	1.10	2.25
60	425391	AI248252	Hs.160672	ESTs	1.17	2.38
	443861	AW449462	Hs.134743	ESTs	1.44	2.30
	454609	AW810204		gb:MR4-ST0125-021199-017-d08 ST0125 Homo	2.30	1.33
	425893	AA629895		gb:ad43b07.s1 Stratagene lung carcinoma	1.76	2.51
	443611	NM_014397	Hs.9625	NIMA (never in mitosis gene a)-related k	1.81	2.90
65	410359	R38624	Hs.106313	ESTs	1.78	2.05
	406308			NM_025192:Homo sapiens hypothetical prot	1.92	2.24
	432476	T94344	Hs.326263	ESTs	1.40	2.45
	435073	AA664078		gb:ac04a05.s1 Stratagene lung (937210) H	1.66	2.26
	420581	AA278469	Hs.151940	ESTs	1.48	2.58
70	435579	AI332373	Hs.156924	ESTs	1.46	2.68
	439633	AF086464	Hs.86248	ESTs	1.40	2.48
	430551	AA481150	Hs.136343	ESTs	1.40	2.28
	450855	T97988	Hs.295605	mannosidase, alpha, class 2A, member 2	1.48	2.40
	444326	AI939357	Hs.270710	ESTs	0.88	2.28
75	412149	R49355	Hs.273824	ESTs	1.58	2.19
	455116	AW857271		gb:CMO-CT0307-210100-158-g09 CT0307 Homo	1.56	2.50
	449626	AA774247	Hs.301637	zinc finger protein 258	0.60	0.53
	410047	AI167810	Hs.132390	zinc finger protein 36 (KOX 18)	0.66	0.58

	418865	AW117500	Hs.104241	ESTs	1.58	2.63
	402762			ENSP00000235171*:GAP junction beta-4 pro	0.81	0.82
	436449	AI418027	Hs.120361	ESTs	1.46	1.46
5	403488			ENSP00000201948:KARYOPHERIN BETA2B HOMOL	1.38	2.23
	431235	AA318271	Hs.250905	hypothetical protein	1.14	2.55
	448576	AB026730	Hs.21495	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	0.70	0.78
	408100	AW205382	Hs.42676	KIAA0781 protein	1.36	2.66
	433436	AW162474		Bruno (Drosophila) -like 6, RNA binding	1.50	2.15
	422337	R38572		gb:yc87c11.s1 Soares infant brain 1N1B H	2.23	1.71
10	426160	AA206020	Hs.167460	splicing factor, arginine/serine-rich 3	1.08	2.09
	447008	BE010189		nuclear receptor subfamily 1, group I, m	1.26	1.27
	420141	AA702961	Hs.124103	ESTs, Weakly similar to I38344 titin, ca	1.46	2.60
	423840	AA332434	Hs.72465	ESTs, Weakly similar to non-lens beta ga	1.26	2.47
	447793	AI424924	Hs.211203	ESTs	2.38	1.83
15	407328	AA508857	Hs.187748	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.11	2.54
	432451	AW972771	Hs.292471	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.63	2.05
	421311	N71848	Hs.283609	hypothetical protein PRO2032	0.51	0.44
	444649	AW207523	Hs.197628	ESTs	1.21	2.24
	448688	R94570	Hs.266869	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.91	3.25
20	428847	AI954833	Hs.98881	ESTs	1.48	2.66
	413750	BE161453		gb:IL2-HT0437-290200-045-A06 HT0437 Homo	1.22	1.00
	429355	AW973253	Hs.292689	ESTs	1.86	2.35
	427798	AA412499	Hs.104779	ESTs	1.82	2.33
25	431179	AI338644	Hs.195432	aldehyde dehydrogenase 2 family (mitocho	0.80	2.00
	451719	AI373532	Hs.157910	ESTs	1.29	3.85
	438094	AI821755	Hs.131805	ESTs, Weakly similar to A56194 thromboxa	1.74	2.54
	418504	BE159718	Hs.85335	Homo sapiens mRNA; cDNA DKFZp564D1462 (f	0.52	0.49
	407414	AF072164		gb:Homo sapiens HSFE-1 mRNA, partial cds	1.67	2.28
	416410	H53777	Hs.36822	ESTs	1.85	2.28
30	439141	AI241470	Hs.268982	ESTs	1.08	2.28
	441181	AA416925	Hs.121076	peptidylprolyl isomerase (cyclophilin)-I	1.81	2.02
	434482	AF143331	Hs.16073	ESTs	1.22	2.00
	455757	BE079531		gb:RC5-BT0624-240300-013-D08 BT0624 Homo	1.53	2.16
35	425787	AA363867	Hs.155029	ESTs	0.76	2.13
	405727			CX001244:gi11420428[ref][XP_004814.1] be	1.70	2.21
	441846	AW850980		gb:IL3-CT0220-150200-068-803 CT0220 Homo	1.16	2.14
	451945	BE504055	Hs.211420	ESTs	0.84	2.73
	438432	AW444990	Hs.258800	ESTs, Weakly similar to I38022 hypotheti	1.60	2.43
40	451140	AW411354	Hs.26002	LIM domain binding 1	1.14	1.20
	407341	AA918886	Hs.204918	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.03	2.42
	453041	AI680737	Hs.289068	Homo sapiens cDNA FLJ11918 fis, clone HE	1.69	3.43
	437613	R19892	Hs.10267	MIL1 protein	1.16	2.11
	451507	AW291109	Hs.208787	ESTs, Weakly similar to T31611 hypotheti	1.22	2.05
45	430259	BE550182	Hs.127826	RaiGEF-like protein 3, mouse homolog	2.85	1.00
	453669	AL049029	Hs.7258	hypothetical protein FLJ22021	0.75	0.64
	455065	AW854352		gb:RC3-CT0255-200100-024-g10 CT0255 Homo	1.49	2.20
	442220	AL037800	Hs.8148	selenoprotein T	0.50	0.18
	437936	AW798475	Hs.288549	hypothetical protein FLJ14710	1.50	2.44
	442556	AL137781	Hs.8379	Homo sapiens mRNA; cDNA DKFZp586L2424 (f	0.54	0.37
50	405223			Target Exon	1.09	2.80
	437225	AW975982	Hs.292935	ESTs	1.03	2.47
	421101	AF010446	Hs.101840	major histocompatibility complex, class	0.72	0.57
	436200	R51386	Hs.124881	ESTs	1.64	2.93
55	402025			NM_021624:Homo sapiens histamine H4 rece	1.52	2.28
	407019	U49973		gb:Human Tigger1 transposable element, c	2.40	2.12
	451305	AW003571	Hs.211191	ESTs, Weakly similar to A46010 X-linked	1.24	3.23
	423450	AJ290445	Hs.128759	KIAA0524 protein	1.64	2.13
	423139	AW402725	Hs.288560	hypothetical protein FLJ21106	1.61	2.28
60	451763	AW294647	Hs.233634	hypothetical protein FLJ14220	1.39	2.08
	456915	AI915689	Hs.212781	EST	1.62	2.02
	452829	AI955579	Hs.63368	ESTs, Weakly similar to TRHY_HUMAN TRICH	0.60	0.41
	446383	T05816	Hs.92511	ESTs	2.08	1.48
	432576	AW157424	Hs.165954	ESTs, Weakly similar to I38022 hypotheti	1.88	2.49
	433820	AI401627	Hs.174067	ESTs	1.30	2.00
65	419719	AA844700	Hs.39297	ESTs, Moderately similar to ALU1_HUMAN A	1.33	2.00
	415868	H06728	Hs.21017	ESTs	1.34	2.08
	420738	NM_004185	Hs.258575	wingless-type MMTV integration site fami	1.42	2.29
	446614	AK001733	Hs.15562	hypothetical protein FLJ10871	0.79	0.78
70	404167			NM_021956*:Homo sapiens glutamate recept	1.62	2.55
	417074	Z49878	Hs.81131	guanidinoacetate N-methyltransferase	0.72	0.75
	401215			C12000457*:gi17512178[pl][T30337] polypr	1.14	2.08
	421600	AW893889	Hs.323231	Homo sapiens cDNA FLJ11946 fis, clone HE	1.88	2.66
	426248	T18988	Hs.293668	ESTs	1.17	3.44
	454523	AW803980		gb:PMO-UM0084-240300-001-G11 UM0084 Homo	1.34	2.40
75	420656	AA279098	Hs.187636	ESTs	1.22	2.43
	402833			C1002508:gi16691937[emb][CAB65797.1] (ALO	1.31	2.00
	438910	AA827921	Hs.291858	ESTs, Weakly similar to ALUC_HUMAN IIII	1.39	3.13

	416170	H42454	Hs.220645	ESTs	0.99	2.18
	433598	AJ762836	Hs.271433	ESTs, Moderately similar to ALU2_HUMAN A	2.04	1.28
	417699	T91491	Hs.119670	ESTs	1.36	2.50
5	459605	AL045773		gb:DKFZp434F246_r1 434 (synonym: hies3)	1.21	2.13
	453204	R10799	Hs.191990	ESTs	3.12	2.98
	458971	AL119206	Hs.126257	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.34	2.09
	457040	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	1.68	2.00
	400414	AF083118	Hs.283968	Homo sapiens CATX-2 mRNA, complete cds	1.70	2.54
10	426263	AI908774	Hs.259785	camitine palmitoyltransferase I, liver	0.96	2.14
	439334	AI148976	Hs.112062	ESTs	1.50	2.45
	455527	AW984479		gb:PM1-HN0012-220300-001-b12 HN0012 Homo	1.46	2.28
	408084	AL040832	Hs.160422	Homo sapiens clone PP902 unknown mRNA	1.61	2.23
	432059	AF227131	Hs.272387	taste receptor, type 2, member 4	1.66	2.15
15	429791	AW015667	Hs.119427	ESTs	1.51	2.83
	438695	AI885190	Hs.156089	ESTs, Weakly similar to repressor protei	1.19	2.03
	458139	AI525711	Hs.253147	ESTs	1.42	2.10
	413035	BE155563		gb:PM4-HT0352-171199-001-C05 HT0352 Homo	1.62	2.30
	422444	AA310688		gb:EST181501 Jurkat T-cells V Homo sapie	1.38	2.05
20	409546	AW410190	Hs.250624	hypothetical protein MGC4473	1.87	2.18
	411432	AW846272		gb:QV0-CT0179-300999-024-d12 CT0179 Homo	1.04	2.03
	445327	AI220082	Hs.147722	ESTs	1.16	2.10
	424628	AB011136	Hs.151385	KIAA0564 protein	0.61	0.63
	440197	AW340708	Hs.317714	pallid (mouse) homolog, pallidin	0.56	0.39
25	408894	BE081731		gb:QV2-BT0635-220400-158-e04 BT0635 Homo	1.50	2.45
	422776	AA316987	Hs.129846	ESTs	1.36	2.20
	428255	AJ627478	Hs.187670	ESTs	1.34	2.40
	412484	AA112090	Hs.269961	ESTs	0.97	2.00
	432789	D26361	Hs.3104	KIAA0042 gene product	1.44	2.73
30	430100	AA766178	Hs.291601	ESTs, Highly similar to T00350 hypothei	1.06	2.02
	419528	AA244000	Hs.222365	ESTs	1.34	2.06
	441793	AA968459	Hs.158785	ESTs	1.80	2.70
	429468	AF033579		T-box 10	0.71	0.61
	410248	AA166553	Hs.268171	ESTs	2.55	2.10
35	401818			NM_000664*:Homo sapiens acetyl-Coenzyme	1.76	2.58
	451724	AI903765		gb:UT-BT037-301298-102 BT037 Homo sapien	1.64	2.28
	431866	NM_012098	Hs.8025	angiotensin-like 2	1.56	2.36
	432719	AW935411	Hs.314460	ESTs	1.36	2.25
	418977	AA233094	Hs.191517	ESTs	2.06	3.60
40	404220			C6000989*:gil7573285[emb]CAB87644.1} (AL	1.54	2.23
	446708	BE549905	Hs.231754	ESTs	1.35	2.16
	453823	AL137967		gb:DKFZp761D2315_r1 761 (synonym: hamy2)	1.42	2.38
	422050	AA302741	Hs.25786	ESTs, Moderately similar to JC5238 galac	1.40	2.50
	400704			Target Exon	1.48	1.00
45	406104			Target Exon	1.22	2.03
	411008	AW813238		gb:MR3-ST0191-020200-207-d04 ST0191 Homo	1.00	2.13
	426582	AA381797	Hs.281121	ESTs	1.35	2.45
	430853	AI734179	Hs.105876	ESTs	1.43	2.23
	432420	AL044659	Hs.43791	ESTs	1.15	2.03
50	403197			C2002793*:gil1353148[sp]Q09568[YR86_CAE	0.52	0.47
	432407	AA221036		gb:zr0312.r1 Stratagene NT2 neuronal pr	1.93	2.23
	414996	AW747800	Hs.55016	hypothetical protein FLJ21935	1.56	2.72
	401016			ENSP00000227126:NAALADASE II PROTEIN.	1.25	2.45
	433335	AA584134	Hs.269454	ESTs	1.31	2.24
55	459668	BE244127		gb:TCBAP1E0661 Pediatric pre-B cell acut	1.16	2.03
	437722	AW292947	Hs.122872	ESTs, Weakly similar to JU0033 hypothei	3.75	2.72
	452277	AL049013	Hs.28783	KIAA1223 protein	0.33	0.26
	425712	AA412548	Hs.21423	ESTs, Moderately similar to ALU1_HUMAN A	1.34	2.21
	427598	AA406057	Hs.97998	ESTs	1.06	2.05
60	412565	M85975	Hs.344069	gb:EST02500 Fetal brain, Stratagene (cat	1.24	2.59
	422043	AL133649	Hs.110953	retinoic acid induced 1	0.48	0.41
	421814	L12350	Hs.108623	thrombospondin 2	0.48	2.45
	413645	AA130992		gb:zo15e02.s1 Stratagene colon (937204)	1.32	2.45
	435563	AF210317	Hs.95497	solute carrier family 2 (facilitated glu	0.39	0.28
65	452396	H10302	Hs.112577	ESTs	1.60	2.45
	440612	BE561384		gb:601344969F1 NIH_MGC_8 Homo sapiens cD	1.08	2.60
	454721	AW815588		gb:QV0-ST0216-061299-066-a09 ST0216 Homo	1.44	1.65
	417796	AA206141	Hs.6786	ESTs	1.68	3.85
	432864	D16217	Hs.279607	calpastatin	0.43	0.35
70	454480	AA088375	Hs.22612	hypothetical protein DKFZp566D1346	2.19	1.91
	434490	AF143870	Hs.15246	ESTs	2.26	2.07
	418797	AA515814		gb:ng64b03.s1 NCI_CGAP_Lip2 Homo sapiens	1.42	2.55
	403871			C5001783*:gil780367[gb]AAB05844.1} (L416	1.60	2.63
	441283	AA927670	Hs.131704	ESTs	1.31	3.63
75	442250	AW290871	Hs.129121	ESTs	1.14	2.38
	456747	AL037357	Hs.125864	tropomodulin 2 (neuronal)	1.61	1.26
	425757	AA363171		gb:EST72986 Ovary II Homo sapiens cDNA 5	1.29	2.95
	405494			C2001837*:gil12697903[gb]BAB21770.1} (A	2.09	1.00

	432250	AA452088	Hs.274170	Opa-interacting protein 2	1.26	2.71
	431911	AK000156	Hs.272193	Homo sapiens cDNA FLJ20149 fis, clone CO	1.46	2.60
	413923	AI733852	Hs.199957	ESTs	1.62	2.10
	449590	AA694070	Hs.268835	ESTs	1.20	2.53
5	438467	AA608027	Hs.123277	ESTs	1.48	2.10
	432121	AI824879	Hs.211286	ESTs, Weakly similar to 1207289A reverse	1.27	3.13
	412298	AW936300		gb:QV4-DT0021-281299-070-a04 DT0021 Homo	1.42	2.60
	408519	AA679082	Hs.43481	hypothetical protein DKFZp564K192	1.84	3.70
	416067	T79732	Hs.14633	ESTs	1.11	3.08
10	420497	AW206285	Hs.253548	ESTs	1.90	2.48
	405704			NM_001844*:Homo sapiens collagen, type I	1.42	2.90
	423443	AI432601	Hs.168812	Homo sapiens cDNA FLJ14132 fis, clone MA	1.42	2.03
	415904	Z44679	Hs.336391	ESTs	1.62	2.94
	413786	AW613780	Hs.13500	ESTs	0.33	0.17
15	404031			C5001700*:gij9256616[ref]NP_061761.1 pr	1.94	2.29
	457412	N40711	Hs.333300	hypothetical protein FLJ14026	1.92	3.20
	439719	AF086554	Hs.326048	Homo sapiens mRNA; cDNA DKFZp434M0420 (f	1.62	2.30
	418161	AI950754	Hs.81716	ESTs	1.81	2.42
	425894	AW954011	Hs.180711	ESTs	0.92	2.20
20	419988	W39388	Hs.55336	Homo sapiens, clone MGC:17421, mRNA, com	1.34	2.57
	439668	AI091277	Hs.302634	frizzled (Drosophila) homolog 8	1.67	2.66
	450177	AI698091	Hs.107845	ESTs	1.50	2.25
	459704	AA719572	Hs.274441	Homo sapiens mRNA; cDNA DKFZp434N011 (fr	1.27	3.35
	410357	AW663614		gb:hj22e04.x1 NCI_CGAP_LJ8 Homo sapiens	0.69	0.59
25	459234	AI940425		gb:CMO-CT0052-150799-024-c04 CT0052 Homo	1.67	2.08
	421313	NM_014923	Hs.103329	KIAA0970 protein	0.57	0.26
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	1.80	2.73
	423086	AB028994	Hs.123420	KIAA1061 protein	0.40	0.56
	425980	AA366951		gb:EST77963 Pancreas tumor III Homo sapi	1.33	2.50
30	423185	BE299590	Hs.125078	omithine decarboxylase antizyme 1	0.60	0.56
	410840	AW806924		gb:QV4-ST0023-160400-172-h10 ST0023 Homo	1.50	2.88
	403917			Target Exon	1.82	2.02
	437384	AI674710	Hs.174397	ESTs	1.26	2.05
	444389	AW439340	Hs.189720	ESTs	1.26	2.13
35	443318	AI051603	Hs.133141	ESTs	1.46	2.20
	441093	AI698138	Hs.126918	ESTs	1.40	2.35
	439432	AI984203	Hs.57874	ESTs	0.88	2.18
	454629	AW811114		gb:MR2-ST0131-111199-016-a04 ST0131 Homo	1.96	2.31
	406207			Target Exon	2.77	2.55
40	444872	AI936264		p30 DBC protein	1.48	2.45
	401908			C17000154:gij12003980[gb]AAG43830.1 AF21	1.15	2.28
	404730			Target Exon	1.84	2.78
	457498	AI732230	Hs.191737	ESTs	1.49	2.55
45	448471	AA158617	Hs.21276	collagen, type IV, alpha 3 (Goodpasture	0.37	0.36
	438978	AI095207	Hs.307972	ESTs	1.57	2.39
	418786	AI795317	Hs.203594	Homo sapiens uncharacterized gastric pro	2.86	3.34
	400416	AF083130		Homo sapiens CATX-14 mRNA, partial cds	2.03	1.55
	450446	AI696334	Hs.14450	ESTs	1.32	2.38
	419791	AI579909	Hs.105104	ESTs	0.41	0.27
50	449436	AA860329	Hs.279307	hypothetical protein DKFZp434i2117	2.01	1.50
	430808	L08603	Hs.247980	melanocortin 4 receptor	1.09	2.18
	443116	AI033397	Hs.132225	ESTs	1.30	2.25
	437923	BE088433	Hs.334696	hypothetical protein KIAA1335	1.40	2.50
	403294			Target Exon	0.98	2.18
55	436007	AI247716	Hs.232168	ESTs	1.38	1.00
	430649	AB040941	Hs.247713	KIAA1508 protein	1.52	2.85
	437271	AL137445	Hs.28846	Homo sapiens mRNA; cDNA DKFZp566O134 (fr	1.29	2.59
	444500	AV651273	Hs.282966	ESTs, Moderately similar to 2109260A B c	1.22	2.05
	447434	R16890	Hs.137135	ESTs	1.72	2.85
60	400830			NM_025006:Homo sapiens hypothetical prot	2.04	2.68
	428114	AI821548	Hs.98363	ESTs, Weakly similar to I38022 hypotheti	1.09	2.74
	409688	AI150485		gb:qf38a10.x1 Soares_testis_NHT Homo sap	1.67	1.38
	440781	BE561823	Hs.281434	Homo sapiens cDNA FLJ14028 fis, clone HE	1.28	2.50
	442662	U78168	Hs.8578	Rap1 guanine-nucleotide-exchange factor	1.92	2.28
65	443078	M78728	Hs.132694	Homo sapiens cDNA: FLJ23149 fis, clone L	1.42	2.03
	440179	AI990151	Hs.125904	ESTs	1.49	2.63
	446780	R31107		gb:yh61g01.s1 Soares_placenta Nb2HP Homo	1.96	2.78
	444173	AI126432	Hs.149493	ESTs	1.50	2.10
	417939	R53863	Hs.337512	ESTs, Weakly similar to ALUB_HUMAN !!!!	1.60	2.03
70	428490	BE301738	Hs.49806	ESTs, Weakly similar to A46010 X-linked	0.47	0.44
	443869	AI141520	Hs.151464	ESTs, Weakly similar to ALUC_HUMAN !!!!	1.25	2.68
	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	2.12	1.15
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	0.64	0.48
	454701	AW854930		gb:PM0-CT0263-201099-003-005 CT0263 Homo	1.30	2.33
75	439795	N77294	Hs.194294	ESTs	1.17	2.33
	425546	BE409762	Hs.26118	hypothetical protein MGC13033	1.17	2.85
	411245	AW833441		gb:QV4-TT0008-271099-020-g01 TT0008 Homo	1.90	3.98

	434957	AF283775	Hs.35380	x 001 protein	0.47	0.41
	425724	AA362525		gb:EST72223 Namalwa B cells I Homo sapie	1.38	2.63
	446847	T51454	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	0.34	0.28
5	453216	AL137566	Hs.32405	Homo sapiens mRNA; cDNA DKFZp586G0321 (f	1.28	2.19
	421718	AL117574		Homo sapiens mRNA; cDNA DKFZp434L2221 (f	2.04	1.79
	415924	H18047	Hs.335821	ESTs	2.02	3.17
	450850	AA648886	Hs.151999	ESTs	1.68	2.45
	443153	AI371823	Hs.34079	ESTs	1.13	2.41
10	434420	AA668278	Hs.194864	hypothetical protein FLJ22578	1.34	2.38
	426126	AL118747	Hs.26691	ESTs	1.31	2.25
	421926	AA300591		gb:EST13437 Testis tumor Homo sapiens cD	1.48	2.40
	459563	AI590487	Hs.49760	gb:tt77d04.x1 NCI_CGAP_HSC3 Homo sapiens	1.74	3.33
	453006	AI362575	Hs.303171	ESTs	1.17	2.24
	437223	C15105	Hs.330716	Homo sapiens cDNA FLJ14368 fis, clone HE	0.54	0.46
15	417016	AA837098	Hs.269933	ESTs	1.04	2.18
	420223	N27807	Hs.286	ribosomal protein L4	2.08	3.10
	425303	AA354785		gb:EST63098 Jurkat T-cells V Homo sapien	2.18	2.85
	400375	NM_014115		NM_014115: Homo sapiens PRO0113 protein	1.83	2.14
20	456169	Y07909	Hs.79368	epithelial membrane protein 1	1.54	2.08
	409707	AA861773	Hs.313501	ESTs	0.79	0.84
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	1.46	2.06
	443152	AI803470	Hs.204529	KIAA1806 protein	1.07	2.43
	452714	AW770994	Hs.30340	hypothetical protein KIAA1165	0.45	0.34
25	415110	H04043		gb:yj45c03.r1 Soares placenta Nb2HP Homo	1.62	2.07
	443251	BE185436	Hs.278839	ESTs	1.34	2.05
	433441	R37094	Hs.13742	ESTs	1.76	2.05
	434612	R76513	Hs.301183	molecule possessing ankyrin repeats Indu	0.83	2.88
	417807	R17806	Hs.269452	gb:yj09b06.r1 Soares infant brain 1NIB H	1.30	2.23
30	426902	AI125334	Hs.97408	ESTs	1.94	2.20
	436028	AA731124	Hs.120931	ESTs	2.01	1.73
	428878	AA436884	Hs.48926	ESTs	1.22	2.17
	439749	AL389942	Hs.157752	Homo sapiens mRNA full length insert cDN	1.32	2.75
	442435	AI986208	Hs.244760	ESTs, Highly similar to B34087 hypothe	2.09	3.13
35	416527	T62507	Hs.11038	ESTs	1.66	2.12
	441808	AW118601	Hs.127887	ESTs, Moderately similar to 1609195B blo	1.22	2.58
	417054	AF017060	Hs.174151	aldehyde oxidase 1	2.57	1.48
	446536	AC002563	Hs.15767	cltron (rho-interacting, serine/threonin	1.16	2.23
	418442	AI873471	Hs.186898	ESTs	1.39	2.26
40	416640	BE262478	Hs.79404	neuron-specific protein	0.31	0.26
	403146			Target Exon	1.49	2.18
	457397	AW969025	Hs.109154	ESTs	1.32	2.26
	439189	AI951185	Hs.144630	nuclear receptor subfamily 2, group F, m	1.76	2.90
	423969	AI830571	Hs.34969	hypothetical protein DKFZp566N034	1.18	2.00
45	459683	AI674906	Hs.199460	gb:wc73f02.x1 NCI_CGAP_Pan1 Homo sapiens	1.74	2.00
	426826	AK001890	Hs.172654	guanine nucleotide binding protein beta	2.04	1.60
	414482	BE522743	Hs.301064	arfatpin 1	0.40	0.29
	438027	N93047	Hs.19131	transcription factor Dp-2 (E2F dimerizat	1.08	2.40
	408623	AW811978	Hs.254037	ESTs	1.64	3.08
50	433765	AA909619	Hs.112668	ESTs	1.52	2.02
	417132	N56605	Hs.269053	ESTs	1.64	2.51
	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	0.28	0.16
	435186	AL119470	Hs.145631	ESTs	1.74	3.10
	411107	AW958042	Hs.95870	PTD015 protein	0.49	0.24
55	406930	U04691		gb:Human olfactory receptor (OR17-219) g	2.21	3.88
	411026	AW813786		gb:RC3-ST0197-120200-015-b05 ST0197 Homo	1.64	1.03
	415766	H01613	Hs.50628	adaptor-related protein complex 4, sigma	1.64	2.51
	446018	AW631111	Hs.249727	gb:hh92e12.y1 NCI_CGAP_GU1 Homo sapiens	1.56	2.48
	440125	AW238410	Hs.253888	ESTs	1.46	2.25
60	449832	AA694264	Hs.60049	ESTs	1.27	2.33
	431899	AA521381	Hs.187726	ESTs	1.11	2.53
	431531	BE142052	Hs.62654	kringle-containing transmembrane protein	1.06	2.00
	441077	AI241273	Hs.15312	ESTs	1.12	2.13
	426799	H14843	Hs.303154	popeye protein 3	0.61	0.51
65	419480	BE536584	Hs.122546	hypothetical protein FLJ23017	1.88	2.38
	455908	BE156306		gb:QV0-HT0367-150200-114-h04 HT0367 Homo	1.77	2.55
	403332			Target Exon	1.46	2.60
	455753	BE075124		gb:PM1-BT0585-110200-003-h02 BT0585 Homo	1.40	2.43
	404429			Target Exon	1.31	2.01
70	438941	AF075047	Hs.31864	ESTs	1.34	2.21
	428745	AA433896	Hs.201634	ESTs	1.72	2.06
	411567	AW851630		gb:MR2-CT0222-211099-002-h06 CT0222 Homo	1.60	2.70
	458714	R20916	Hs.344777	ESTs	0.93	2.07
	426839	M74782	Hs.172689	interleukin 3 receptor, alpha (low affin	1.39	2.71
75	444539	AI955765	Hs.146907	ESTs, Weakly similar to 2004399A chromos	1.66	2.18
	407322	AA171892	Hs.324570	ESTs, Weakly similar to ALU3_HUMAN ALU S	1.30	2.65
	453826	AL138129		gb:DKFZp547F152_r1 547 (synonym: hibr1)	1.52	2.73
	435695	AA694324	Hs.257675	ESTs	1.24	2.00

	402294		Target Exon	1.80	3.08
	417759	R13567	ESTs	1.63	2.58
	417527	AA203524	gb:zx55e10.r1 Soares_fetal_liver_spleen_	1.52	2.02
	427526	AA405062	gb:zu12e04.r1 Soares_testis_NHT Homo sap	2.03	1.90
5	455300	AW691707	gb:CM3-NT0090-040500-171-e02 NT0090 Homo	1.12	2.20
	448121	AL045714	hypothetical protein DKFZp564F013	0.93	2.28
	415855	AJ921875	gb:wp07e04.x1 NCL_CGAP_Kid12 Homo sapien	1.43	2.08
	425702	N59555	gb:yv76f05.s1 Soares fetal liver spleen	1.61	2.80
10	441056	H37860	ESTs	1.11	2.10
	400311	AF072164	Homo sapiens HSFE-1 mRNA, partial cds	2.04	2.95
	451478	NM_012331	methionine sulfoxide reductase A	0.50	0.20
	425288	AA354502	gb:EST62799 Jurkat T-cells V Homo sapien	0.99	2.08
	456397	W28339	PTD010 protein	1.11	2.29
15	405654		C12001521:gil7513934 pir T31081 cca3 pr	2.30	1.00
	405151	AJ088196	Homo sapiens clone IMAGE:451939, mRNA se	1.21	2.60
	418851	AA287987	ESTs, Weakly similar to 1207289A reverse	1.28	2.60
	406016		Target Exon	0.57	0.48
	440903	AJ458079	ESTs	2.02	1.61
20	445026	W90337	ESTs, Moderately similar to 2109260A B c	1.56	2.23
	414182	AA136301	KIAA1105 protein	1.32	2.55
	457048	AA400352	ESTs	1.54	2.05
	440542	AA899143	ESTs, Weakly similar to PC4259 ferritin	1.48	2.15
	422857	R71461	gb:yi51h07.r1 Soares placenta Nb2HP Homo	1.42	2.78
25	445948	AW444562	ESTs	1.50	2.48
	454002	BE299567	ESTs, Moderately similar to ALU8_HUMAN A	1.31	2.25
	413656	T91703	gb:ye20g09.s1 Stratagene lung (937210) H	2.10	1.69
	420441	AJ986160	dual specificity phosphatase 6	0.99	2.33
	412062	H09124	Homo sapiens cDNA: FLJ23573 fis, clone L	2.14	1.61
30	408991	BE501816	ESTs	1.76	2.83
	432534	AW361626	hypothetical protein FLJ11240	0.41	0.28
	435136	R27299	ESTs	0.76	3.40
	451052	AA281504	Homo sapiens cDNA: FLJ22165 fis, clone H	2.16	1.85
	413928	AA442498	ESTs, Moderately similar to Z195_HUMAN Z	1.30	2.00
35	439448	AA970788	ESTs	1.87	2.23
	403344		NM_000341:Homo sapiens solute carrier fa	1.36	2.22
	418056	AA524886	gb:nh34f02.s1 NCL_CGAP_P13 Homo sapiens	1.42	2.85
	435428	AJ791746	ESTs	2.44	1.32
	419964	AA811657	ESTs	1.32	2.08
40	440926	AW196772	ESTs	1.80	2.65
	452625	AA724771	ESTs	1.64	2.18
	452797	AJ369787	ESTs	1.47	3.16
	436120	AJ248193	ESTs	1.41	2.83
	449567	AJ990790	ESTs	1.48	2.45
45	409628	AB021865	potassium voltage-gated channel, Shal-re	1.70	2.23
	416617	H69311	ESTs	1.83	2.04
	452266	AJ767250	ESTs	0.58	0.43
	404606		Target Exon	1.47	3.75
	401814		Target Exon	2.00	1.91
50	428403	AJ393048	leucine rich repeat (in FLJ) Interactin	0.33	0.21
	433390	AA586950	Homo sapiens mRNA; cDNA DKFZp761G18121 (2.00	4.90
	451443	AW295527	ESTs	1.87	2.25
	411188	BE161168	gb:PMO-HT0425-170100-002-a10 HT0425 Homo	2.15	1.69
	452704	AA027823	Homo sapiens PNAS-130 mRNA, complete cds	2.64	1.65
55	424060	X92108	H.sapiens mRNA for subtelomeric repeat s	2.40	2.58
	433331	AJ738815	ESTs	1.46	2.10
	428520	AA331901	hypothetical protein FLJ10097	0.44	0.19
	439492	AF086310	ESTs	0.42	0.26
	426736	AA431615	ESTs	1.90	2.45
60	416225	AA577730	ESTs, Weakly similar to PC4259 ferritin	2.72	6.25
	404917		Target Exon	1.60	2.15
	448955	AW207597	ESTs	2.08	1.75
	402797		Target Exon	2.12	1.37
	457951	U23860	gb:Human clone mcag19 chromosome 16 CTG	1.72	2.00
65	426982	AA149707	ubiquitin-like 3	0.36	0.17

TABLE 8B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

75	Pkey	CAT Number	Accession
	408139	10421_1	AA451966 NM_016370 AB036693 AL139228 R58124 AI634847 AL119333 W07356 AI334284 H29050 AI92685 AA652438 AW172843 W19794 N21460 AJ743862 AW130622 AA991348 AJ204553 AA992664 N80848 AA699329 AI824676 R26624 R49653 AW807321 AW807262 AW177104 AW807319 AW807115 AW807344 AW807324 AW178116 BE141575 AW845849 AW807105 AW845868 BE140942 AW807178 AW807167 AW807398 AW807320 AW807306 AW845866
	408255	1049351_1	

408283	1050275_1	BE141579 AW807555 AW807502 BE141596 AW845845 AW807500 AW845854 AW807480 AW807486 AW807478 AW178109 AW807228 AW807374 AW807125 AW846124 AW807470 AW807477 AW807510 AW807208 BE141573 AW807465
408839	1085657_1	AW277084 R27662 R26970 D79194
409126	110159_1	AA063426 AW962323 AW408063 AA063503 AA772927 AW753492 BE175371 AA311147
409282	111512_1	AW966480 AA069840 AA384646
409291	1115745_1	AW373472 AW373484 BE071899 BE071898
409367	1123651_1	AW382767 BE153835 BE153702 BE153572
409688	114831_3	AI150485 AW938392 AA076894 AW883422
409692	114869_1	AI500724 AA399661 AA397891 AI471084 AI423511 T07531 AI094336
409894	1157906_1	BE081731 AW861738 AW503629 BE081969
410154	117950_1	F06959 Z43559 AA082002
410357	1197159_1	AW663614 BE046540 BE045760 AW827443 BE046544
410642	1213736_1	AW792784 Z44444 H06639
410725	1218207_1	AW799279 AW799395 AW799392 AW799276 AW799479 H57885
410730	121847_1	AW368860 AA457091 AI903441 AA088823 W88852 AW979154 AA826016 R94779
410744	1219485_1	H85002 W92289 AW801558 AW801324 AW801270 AW801307 AW801351 AW801357 AW801299 AW801609 AW801356 AW801420 AW801425 AW801358 AW801429 AW801428 AW801427 AW801424 AW801306
410840	1223800_1	AW806924 AW866537 AW866473 AW866298 AW866390 AW866478 AW866454 AW866309 AW866539 AW866521 AW866547 AW866517 AW866403 AW866369
410956	1227882_1	AW938322 AW938307 AW938320 AW938323 AW811840
411008	1229027_1	AW813238 AW813474 AW813334 AW816081 AW813296 AW813363 AW813397 AW813327 AW813328 AW816031 AW816140
411026	1229373_1	AW813786
411141	1233793_1	AW819561 AW819682 AW819663 AW819688 AW819499 AW819498 AW819690 BE065081
411184	1234977_1	AW821117 AW855541 AW855405 AW855374
411188	1235093_1	BE161168 BE162466 AW821260
411245	1236412_1	AW833441 AW833552 AW833700 AW833610 AW833673 AW833675
411347	1239834_1	AW838126 AW838294 AW838247 AW838251 AW838292 AW838299 AW838374
411432	1245636_1	AW845272 AW846564 AW846545 AW846285 AW846135 AW846317 AW846200 AW846265 AW846326 AW846196 AW846357 AW846153 AW846286 AW846319 AW846277 AW846381 AW846438 AW846481 AW846352
411496	1248073_1	AW849241 AW849569 AW849243
411567	1249774_1	AW851630 AW851703 AW851735 AW851723 AW851708 AW851712
411590	125064_1	T96183 T64070 AA094134
411608	1251259_1	AW853441 BE145228 BE145218 BE145162 BE145283
411652	1252836_1	AW855393 AW855560 AW855424
411880	1263110_1	AW872477 BE088101 T05990
411918	1265807_1	AW876354 AW876179 AW876318 AW876290 AW876234 AW876125 AW876199 AW876198
411920	1265812_1	AW876263 AW876257 AW876261 AW876273 AW876231 AW876398 AW876334 AW876134 AW876371 AW876308 AW876314 AW876328 AW876169 AW876331 AW876426 AW876407 AW876412 AW876322 AW876363 AW876218 AW876240 AW876141 AW876138 AW876326 AW876181 AW876131 AW876378 AW876206 AW876191 AW876188 AW876376 AW876289 AW876415 AW876209 AW876366 AW876343 AW876347 AW876165
412085	1276467_1	AW891667 H93096
412252	1285293_1	AW903782 AW903668 AW903672 AW903763 AW903784
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30	457581	359936_1	AA578512 AA595535 BE177533
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	459234	945240_1	AI940425

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TABLE 8C

	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
40	Strand:	Indicates DNA strand from which exons were predicted.
	NI_position:	Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	NI_position
45	400704	8118864	Minus	63110-63241
	400830	8570385	Plus	157683-163035
	400834	8705192	Plus	121863-122288
	400840	9188586	Plus	113882-114121
50	400850	1927150	Minus	4506-4691
	400881	2842777	Minus	91446-91603,92123-92265
	401016	8117441	Plus	126234-126359,128050-128236
	401090	8492704	Minus	201281-201460
	401215	9858408	Plus	103739-103919
55	401241	4827300	Minus	30503-30844,31056-31248
	401335	9884881	Plus	15736-16352
	401381	8570226	Minus	118629-119146,119392-119657
	401400	7708226	Minus	33028-33585
	401469	6682292	Minus	125521-125639
60	401473	7249001	Plus	115142-117305
	401577	9280797	Minus	139377-139674,141195-141281,142217-142340
	401658	9100664	Plus	89638-90028
	401659	7689875	Minus	183379-183521
	401686	6468551	Plus	5005-5426,6810-7042
65	401723	7656694	Plus	147273-147503
	401814	7408052	Plus	136003-136726
	401818	7467933	Minus	10964-11084,11674-11817
	401890	8516144	Plus	148955-149396,149569-150002
	401908	8698760	Minus	126888-127024
70	401913	9369520	Minus	33753-33904
	401927	3873185	Minus	112000-112137
	402025	7547159	Plus	173835-173998
	402039	7770432	Plus	560-1294
	402049	8072512	Plus	100065-100419
75	402085	7249154	Plus	90533-90687,94949-95158
	402241	7690131	Minus	125073-125206,130996-131125
	402294	2282012	Minus	2575-3000
	402305	7328724	Plus	40832-41362

	402366	9454515	Plus	195808-196863
	402551	9856793	Minus	37346-37633
	402654	8076879	Plus	44058-44803
5	402685	8318556	Plus	58962-59294
	402762	9230904	Minus	123298-124035
	402797	3421043	Minus	15758-15930
	402833	8918545	Plus	26987-27778
	402901	8894222	Minus	175426-175667
10	402948	9368458	Minus	143456-143626,143808-143935
	403066	8954202	Plus	158189-158433
	403072	8954241	Plus	141829-142006
	403146	9799812	Plus	162877-163118
	403197	9930749	Plus	79990-80237
15	403214	7630945	Minus	76723-77027,79317-79484
	403217	7630969	Plus	54089-54163,55427-55623
	403290	8083176	Plus	19288-20076
	403291	7230870	Plus	95177-95435
	403294	8096496	Plus	41565-41881
20	403315	8247953	Minus	125117-125287
	403332	8568139	Minus	31409-31674
	403344	8569726	Plus	70823-70990
	403362	8571772	Plus	64099-64260
	403371	9087278	Plus	105655-106050
25	403391	9438337	Plus	42410-42544,83317-83540,86840-86922,87970-88110
	403488	9966615	Minus	12450-12753
	403536	8076924	Plus	34972-35182
	403779	8018040	Minus	95602-95969
	403859	7708954	Plus	113738-113858
30	403871	7709282	Plus	104545-104757
	403903	7710671	Minus	101165-102597
	403917	7710849	Plus	109718-109847,109927-110202
	403978	8576014	Plus	97326-97808
	404031	7671252	Plus	171477-172316
35	404167	9926594	Minus	77030-77280
	404220	6706820	Plus	46107-46439
	404286	2326514	Plus	51086-51301
	404418	7382420	Minus	153339-153481,155099-155294
	404427	7407959	Plus	127170-127358
40	404429	7407979	Plus	31352-31498
	404440	7528051	Plus	80430-81581
	404495	8151634	Minus	59449-60477
	404580	6539738	Minus	240588-241589
	404606	9212936	Minus	22310-23269
45	404730	8389582	Plus	119832-120016,124110-124275
	404917	7341851	Plus	49330-49498
	405033	7107731	Minus	142358-142546
	405137	8570507	Plus	158969-159423
	405146	9438278	Minus	102529-102633
50	405158	9966252	Plus	42873-43056,43815-43949
	405187	7229826	Plus	117025-117170,118567-118736
	405223	7239614	Plus	106184-106313
	405340	6094635	Plus	49644-49760
	405494	8050952	Minus	70284-70518
55	405551	1552506	Plus	12525-12997
	405654	4895155	Minus	53624-53759
	405667	4726099	Plus	5798-5914
	405673	4589984	Plus	50700-50842
	405704	4204244	Plus	138842-139051
60	405723	9801668	Plus	114896-115831
	405727	9838331	Minus	78865-79664
	405760	6066938	Minus	37424-38045
	405779	7280331	Minus	33048-33856
	405944	7883702	Minus	5143-5684
65	406002	8247797	Minus	154007-154579
	406016	8272661	Plus	41341-41940
	406097	7107918	Minus	36698-37269
	406104	9124028	Plus	35309-35977
	406156	7144867	Plus	379-597
70	406207	5923650	Minus	162607-162800
	406300	6479046	Minus	19234-19401
	406308	9211532	Plus	358408-358651
	406314	9211609	Minus	12899-13011,18022-18136
	406317	9211652	Plus	108018-108410
75	406432	9256504	Plus	3804-3930,4026-4120,4929-5109
	406490	7711309	Minus	80295-80480
	406584	3983530	Minus	3989-4497

TABLE 9A: Genes predictive of no bladder cancer progression

	Pkey:	Unique Eos probeset identifier number				
	ExAccn:	Exemplar Accession number, Genbank accession number				
5	UnigeneID:	Unigene number				
	Unigene Title:	Unigene gene title				
	R1	80th percentile of Ta or T1 tumor Als from patients who did not upstage divided by the 80th percentile of Ta or T1 tumor Als from patients who did upstage				
	R2	median of Ta or T1 tumor Als from patients who did not upstage divided by the median of Ta or T1 tumor Als from patients who upstaged				
10	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
	408000	L11690	Hs.198589	bullous pemphigoid antigen 1 (230/240kD)	4.64	5.88
	412129	M21984	Hs.73454	troponin T3, skeletal, fast	4.54	5.10
	459290	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg	4.37	1.63
	400844			NM_003105*:Homo sapiens sortilin-related	3.69	5.90
15	419555	AA244416		gbnc07d11.s1 NCI_CGAP_Pr1 Homo sapiens	3.61	2.03
	414522	AW518944	Hs.76325	step II splicing factor SLU7	3.60	1.00
	440509	BE410132	Hs.134202	ESTs, Weakly similar to T17279 hypotheti	3.58	1.04
	445182	AW189787		ESTs	3.57	2.70
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	3.56	1.48
20	421314	BE440002	Hs.180324	Homo sapiens, clone IMAGE:4183312, mRNA,	3.28	3.25
	429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	3.25	2.50
	430702	U56979	Hs.278568	H factor 1 (complement)	3.20	2.70
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	3.20	2.30
	420729	AW964897	Hs.290825	ESTs	3.20	1.53
	433376	AJ249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	3.00	4.10
	420028	AB014680	Hs.8786	carbohydrate (N-acetylglucosamine-6-O) s	2.94	2.78
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	2.93	1.43
	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	2.93	1.33
30	428030	AJ915228	Hs.11493	Homo sapiens cDNA FLJ13536 fis, clone PL	2.92	2.47
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	2.89	3.33
	414407	AA147026	Hs.76704	ESTs	2.87	2.87
	450779	AW204145	Hs.155044	ESTs	2.78	1.86
	411243	AB039886	Hs.69319	CA11	2.73	1.00
35	417878	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	2.68	2.32
	441519	NM_014056	Hs.7917	DKFZP564K247 protein	2.67	2.98
	446619	AJ076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	2.66	1.00
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	2.64	1.77
	426252	BE176980	Hs.28917	ESTs	2.63	7.30
	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	2.60	2.53
40	429429	AA829725	Hs.334437	hypothetical protein MGC4248	2.59	3.34
	427450	AB014526	Hs.178121	KIAA0626 gene product	2.57	2.28
	420180	AJ004035	Hs.25191	ESTs	2.56	1.68
	434061	AW024973	Hs.283675	NPD009 protein	2.54	2.10
	422070	AF149785	Hs.111126	pituitary tumor-transforming 1 interacti	2.54	3.25
45	419355	AA428520	Hs.90061	progesterone binding protein	2.53	3.63
	446215	AW821329	Hs.14368	SH3 domain binding glutamic acid-rich pr	2.52	4.38
	432442	AJ672516	Hs.178485	ESTs, Weakly similar to S65657 alpha-1C-	2.50	4.60
	447887	AA114050	Hs.19949	caspase 8, apoptosis-related cysteine pr	2.49	2.23
	401155			Target Exon	2.48	2.30
50	404530			Target Exon	2.48	1.00
	446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	2.48	2.35
	436476	AA326108	Hs.33829	bHLH protein DEC2	2.47	2.88
	446535	AF257175	Hs.15250	peroxisomal D3,D2-enoyl-CoA isomerase	2.46	2.19
55	408636	BE294925	Hs.46680	CGI-12 protein	2.45	1.60
	420962	NM_005904	Hs.100602	MAD (mothers against decapentaplegic, Dr	2.44	3.75
	427008	Z45258	Hs.286013	short coiled-coil protein	2.42	3.40
	459711	BE368801	Hs.21858	trinucleotide repeat containing 3	2.40	2.78
	407910	AA650274	Hs.41295	fibronectin leucine rich transmembrane p	2.40	1.00
60	410337	M83822	Hs.62354	cell division cycle 4-like	2.39	3.88
	435029	AF167706	Hs.19280	cysteine-rich motor neuron 1	2.39	3.23
	437181	AJ306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	2.39	1.00
	410968	AA199907	Hs.67397	homeo box A1	2.38	1.33
	422511	AJ076442	Hs.117938	collagen, type XVII, alpha 1	2.38	6.40
65	450775	AA902384	Hs.73853	bone morphogenetic protein 2	2.38	2.71
	442433	BE243044	Hs.8309	KIAA0747 protein	2.37	3.68
	454000	AA040620	Hs.5672	hypothetical protein AF140225	2.36	1.14
	447701	BE619526	Hs.255527	hypothetical protein MGC14128	2.36	2.02
	427985	AJ770170	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	2.36	2.18
	442257	AW503831	Hs.323370	Human EST clone 25267 mariner transposon	2.35	3.53
70	454070	N79110	Hs.21276	collagen, type IV, alpha 3 (Goodpasture	2.35	3.60
	418452	BE379749	Hs.85201	C-type (calcium dependent, carbohydrate-	2.35	2.48
	421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	2.35	1.00
	407793	AW080879	Hs.236572	gbxc38g04.x1 NCI_CGAP_Co20 Homo saplens	2.35	1.21
	442061	AA774284	Hs.285728	abl-interactor 12 (SH3-containing protei	2.34	3.03
75	402845			ENSP00000246267:KIAA0444 PROTEIN (FRAGME	2.34	1.52
	411407	R00903	Hs.169793	ribosomal protein L32	2.34	0.77
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	2.34	0.72

	424637	NM_015057	Hs.151411	KIAA0916 protein	2.32	2.56
	413804	T64682		gb:yc48b02.r1 Stratagene liver (937224)	2.32	1.46
	411060	NM_006074	Hs.318501	Homo sapiens mRNA full length insert cDN	2.32	2.90
5	430028	BE564110	Hs.227750	Target CAT	2.32	2.28
	417720	AA205625	Hs.208067	ESTs	2.32	2.09
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	2.31	1.13
	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	2.30	4.38
	444745	AF117754	Hs.11861	thyroid hormone receptor-associated prol	2.30	1.86
10	408179	AL042465	Hs.43445	poly(A)-specific ribonuclease (deadenyli	2.29	2.19
	442679	R53718	Hs.107882	hypothetical protein FLJ10659	2.29	2.79
	458949	AW291777	Hs.346137	ESTs, Weakly similar to T08599 probable	2.28	1.85
	407191	AA608751		gb:ae56h07.s1 Stratagene lung carcinoma	2.27	2.42
	448367	AI955411	Hs.94109	Homo sapiens cDNA FLJ13634 fis, clone PL	2.27	1.18
15	405155			Target Exon	2.26	1.94
	445594	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	2.26	1.55
	417458	NM_005655	Hs.82173	TGFB inducible early growth response	2.25	1.95
	430315	NM_004293	Hs.239147	guanine deaminase	2.24	1.84
	411945	AL033527	Hs.92137	v-myc avian myelocytomatosis viral oncog	2.24	2.73
20	408937	AA210734	Hs.291386	ESTs	2.24	3.18
	431474	AL133990	Hs.190642	CEGP1 protein	2.23	1.00
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	2.22	4.08
	420997	AK001214	Hs.100914	hypothetical protein FLJ10352	2.22	2.15
	420164	AW339037	Hs.24908	ESTs	2.22	2.16
25	414099	U11313	Hs.75760	sterol carrier protein 2	2.21	4.05
	424800	AL035588	Hs.153203	MyoD family inhibitor	2.21	3.53
	459005	AA447679	Hs.144558	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.21	2.90
	416290	NM_000016	Hs.79158	acyl-Coenzyme A dehydrogenase, C-4 to C-	2.20	4.00
	439208	AK000299	Hs.180952	dynactin 4 (p62)	2.20	1.88
30	401563			C15001262:gi7304981 ref NP_038528.1 ca	2.20	1.77
	404687			C9000375:gi11994617 dbj BAB02754.1 (A	2.19	2.60
	443303	U67319	Hs.9216	caspase 7, apoptosis-related cysteine pr	2.19	2.08
	439866	AA280717	Hs.6727	Ras-GTPase activating protein SH3 domain	2.19	2.21
35	400835	AW853954		chromosome 2 open reading frame 2	2.18	3.00
	456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Or	2.18	2.45
	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	2.17	1.83
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	2.17	2.67
	451131	AI267586	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	2.17	1.71
	406038	Y14443		zinc finger protein 200	2.17	1.71
40	434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	2.17	1.00
	441623	AA315805		desmoglein 2	2.17	1.81
	459244	AW503990	Hs.142442	HP1-BP74	2.17	4.03
	424720	M89907	Hs.152292	SWI/SNF related, matrix associated, acti	2.17	2.93
	404204			ENSP00000252204:Zinc finger protein 165	2.17	1.02
45	453987	AA323750	Hs.235026	Homo sapiens, clone IMAGE:4247529, mRNA,	2.16	2.85
	411400	AA311919	Hs.69851	nucleolar protein family A, member 1 (H/	2.16	3.60
	454949	AW847318	Hs.290131	KIAA1819 protein	2.16	1.96
	409223	AA312572	Hs.6241	phosphoinositide-3-kinase, regulatory su	2.16	1.48
	418030	BE207573	Hs.83321	neuromedin B	2.16	2.07
50	433364	AI075407	Hs.296083	ESTs, Moderately similar to I54374 gene	2.16	2.32
	459511	AI142379		gb:qg64c01.r1 Soares_testis_NHT Homo sap	2.16	1.85
	437559	AI678033	Hs.121476	ESTs	2.15	1.43
	418827	BE327311	Hs.47166	HT021	2.15	3.84
	417470	AF112219	Hs.82193	esterase D/ornithineglutathione hydrolase	2.15	1.74
55	421012	X53281	Hs.101025	basic transcription factor 3	2.15	1.26
	448772	AW390822	Hs.301528	L-kynurenine/alpha-aminoacidipate aminotra	2.15	4.05
	439601	AB029032	Hs.6606	KIAA1109 protein	2.15	2.15
	434417	AL110157	Hs.3843	Homo sapiens mRNA; cDNA DKFZp586F2224 (f	2.15	1.45
	424865	AF011333	Hs.153563	lymphocyte antigen 75	2.15	2.63
60	400752			NM_003105:Homo sapiens sortilin-related	2.14	2.67
	438916	AW188464	Hs.101515	ESTs	2.14	2.38
	430024	AI808780	Hs.227730	Integrin, alpha 6	2.14	2.00
	409345	AI949109		hypothetical protein FLJ20783	2.14	1.40
	421939	BE169531	Hs.109727	TAK1-binding protein 2; KIAA0733 protein	2.13	1.58
65	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	2.13	2.67
	419591	AF090900	Hs.91393	Homo sapiens cDNA: FLJ21887 fis, clone H	2.13	2.00
	458025	AI275406	Hs.32450	gb:ql63c10.x1 Soares_NhHMPu_S1 Homo sapi	2.12	0.89
	428582	BE336699	Hs.185055	BENE protein	2.12	2.65
	422749	W01076	Hs.278573	CD59 antigen p18-20 (antigen identified	2.12	2.73
70	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	2.11	0.91
	456421	AL157485	Hs.91973	hypothetical protein	2.11	2.51
	421508	NM_004833	Hs.105115	absent in melanoma 2	2.11	3.13
	402750			NM_021797:Homo sapiens eosinophil chemo	2.09	1.79
	406274			Target Exon	2.09	1.60
75	406897	M57417		gb:Homo sapiens mucin (mucin) mRNA, part	2.09	1.00
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	2.09	2.92
	445320	AA503887	Hs.167011	Homo sapiens cDNA: FLJ21362 fis, clone C	2.09	3.20
	442271	AF000652	Hs.8180	syndecan binding protein (syntenin)	2.09	1.90

5	428336	AA503115	Hs.183752	microsaminoprotein, beta-	2.08	1.15
	405165			ENSP00000238974: Homeobox protein NKX2-3	2.07	2.83
	416999	AW195747	Hs.21122	hypothetical protein FLJ11830 similar to	2.07	3.71
	453865	AA307279	Hs.35947	methyl-CpG binding domain protein 4	2.07	1.71
	439924	AI985897	Hs.125293	ESTs	2.07	1.00
10	439004	AW979062		gb:EST391172 MAGE resequences, MAGP Homo	2.07	2.13
	407955	BE536739	Hs.109909	ESTs	2.06	1.91
	412998	BE046254		gb:hn38g09.x2 NC1_CGAP_RDF2 Homo sapiens	2.06	2.58
	414013	AA766605	Hs.47099	hypothetical protein FLJ21212	2.05	5.00
	415249	R40515	Hs.21248	ESTs	2.05	2.18
15	427332	R09418	Hs.261101	ESTs, Weakly similar to I38022 hypotheti	2.05	3.35
	426521	AF161445	Hs.170219	hypothetical protein	2.05	1.00
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	2.05	6.03
	423851	R39505	Hs.133342	Homo sapiens clone 24566 mRNA sequence	2.05	1.88
	410028	AW576454	Hs.346502	ESTs	2.04	1.95
20	406575			Target Exon	2.04	1.56
	457148	AF091035	Hs.184627	KIAA0118 protein	2.04	3.11
	449924	VY30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	2.04	2.42
	429837	NM_003896	Hs.225839	siatyltransferase 9 (CMP-NeuAcLactosyl	2.04	1.97
	440675	AW005054	Hs.47883	ESTs, Weakly similar to KCC1_HUMAN CALCI	2.04	2.06
25	411988	AA455459	Hs.164480	ESTs, Weakly similar to T50609 hypotheti	2.04	2.65
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	2.04	2.35
	446187	AK001241	Hs.14229	hypothetical protein FLJ10379	2.04	2.03
	420838	AW118210	Hs.42321	ESTs	2.03	1.00
	445481	AW661846	Hs.346630	ESTs	2.03	2.49
30	448175	BE296174	Hs.225160	hypothetical protein FLJ13102	2.03	2.25
	410600	AW575742		ESTs, Moderately similar to S65657 alpha	2.02	2.10
	401177			Target Exon	2.02	2.59
	448474	AI792014	Hs.13809	hypothetical protein FLJ10648	2.02	4.23
	434782	NM_005032	Hs.4114	plastin 3 (T isoform)	2.02	1.48
35	424125	M31669	Hs.1735	inhibin, beta B (activin AB beta polypep	2.02	2.93
	424241	AW995948	Hs.182339	Homo sapiens pyruvate dehydrogenase kina	2.02	2.63
	424673	AA345051	Hs.294092	ESTs, Weakly similar to I38022 hypotheti	2.02	3.43
	414721	X90392	Hs.77091	ribosomal protein L10	2.02	1.89
	429869	AI907018	Hs.15977	Target CAT	2.02	1.47
40	439177	AW820275	Hs.76611	ESTs, Weakly similar to I38022 hypotheti	2.01	1.94
	437175	AW968078	Hs.87773	protein kinase, cAMP-dependent, catalyti	2.01	1.64
	452046	AB018345	Hs.27657	KIAA0802 protein	2.01	4.31
	417615	BE548641	Hs.82314	hypoxanthine phosphoribosyltransferase 1	2.01	6.75
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	2.00	2.75
45	408232	AL137269	Hs.43899	Homo sapiens mRNA: cDNA DKFZp434C1714 (f	2.00	2.02
	408409	AW838181	Hs.278337	Homo sapiens cDNA FLJ11537 fis, clone HE	2.00	1.95
	433256	AW604447	Hs.339408	ESTs, Weakly similar to S26689 hypotheti	2.00	0.91
	426969	AI936504	Hs.2083	CDC-like kinase 1	2.00	3.60
	442053	R35343	Hs.24968	Human DNA sequence from clone RP1-233G16	2.00	1.95
50	444916	AB028956	Hs.12144	KIAA1033 protein	2.00	1.23
	452286	AI358570	Hs.123933	ESTs, Weakly similar to ZN91_HUMAN ZINC	2.00	5.30
	414906	AA157911	Hs.72200	ESTs	1.99	1.22
	414176	BE140638	Hs.75794	endothelial differentiation, lysophospha	1.99	3.83
	414557	AA340111	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	1.99	2.31
55	452846	AA082160	Hs.63368	ESTs, Weakly similar to TRHY_HUMAN TRICH	1.99	3.43
	408437	AW957744	Hs.278469	lactimal proline rich protein	1.98	2.15
	439205	AF087990	Hs.42758	Homo sapiens, clone IMAGE:3354845, mRNA,	1.98	2.28
	442506	BE566411		ESTs	1.98	3.95
	447731	AA373527	Hs.19385	CGI-58 protein	1.98	2.67
60	410579	AK001628	Hs.64691	KIAA0483 protein	1.97	2.43
	426716	NM_006379	Hs.171921	sama domain, Immunoglobulin domain (Ig),	1.97	2.50
	456141	AI751357	Hs.288741	Homo sapiens cDNA: FLJ22256 fis, clone H	1.97	3.03
	419576	AK002060	Hs.91251	hypothetical protein FLJ11198	1.96	2.88
	407241	M34516		gb:Human omega light chain protein 14.1	1.96	1.09
65	420654	AI681270	Hs.99824	BCE-1 protein	1.96	1.75
	448586	AF285120	Hs.283734	CGI-204 protein	1.95	3.28
	408089	H59799	Hs.42644	thioredoxin-like	1.95	4.00
	421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C	1.95	2.12
	452518	AA280722	Hs.24758	ESTs, Weakly similar to I38022 hypotheti	1.95	3.45
70	432015	AL157504	Hs.159115	Homo sapiens mRNA: cDNA DKFZp586O0724 (f	1.94	2.80
	434263	N34895	Hs.44648	ESTs	1.94	4.60
	409829	M33552	Hs.56729	lymphocyte-specific protein 1	1.94	1.79
	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	1.94	2.30
	401835			Target Exon	1.94	2.27
75	406557			C5000893:gi6226859 pP38525 EFG_THEMEA	1.94	3.28
	440062	AI350518	Hs.129692	ESTs	1.94	3.18
	410442	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	1.94	2.70
	457281	BE253012	Hs.153400	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.94	2.60
	420230	AL034344	Hs.284186	forkhead box C1	1.93	2.28
	452970	NM_012238	Hs.31176	sirtuin (silent mating type information	1.93	4.35
	403728			Target Exon	1.92	1.70

5	415789	H01581	gb:yl33f08.r1 Soares placenta Nb2HP Homo	1.92	2.15
	406759	AA654582	Hs.77039 ATP synthase, H transporting, mitochondr	1.92	2.10
	442073	AW973443	Hs.8086 RNA (guanine-7-) methyltransferase	1.92	4.43
	438023	AF204883	Hs.6048 FEM-1 (C.elegans) homolog b	1.92	4.00
	445502	AW379160	Hs.12813 DKFZP434J214 protein	1.92	2.13
	405474		NM_001093*:Homo sapiens acetyl-Coenzyme	1.92	2.58
	430007	NM_014892	Hs.227502 KIAA1116 protein	1.92	3.78
	439937	AF151906	Hs.6776 CGI-148 protein	1.91	2.32
10	418068	AW971155	Hs.293902 ESTs, Weakly similar to ISHUS protein d	1.91	1.88
	444630	AI753230	Hs.323562 hypothetical protein DKFZp564K142	1.91	1.61
	451184	T87943	Hs.173538 transcription factor 7-like 2 (T-cell sp	1.90	3.35
	414715	AA587891	Hs.904 amylo-1,6-glucosidase, 4-alpha-glucanotr	1.90	3.55
	445841	AL080115	Hs.13370 DKFZP564G0222 protein	1.90	1.46
15	425284	AF155568	Hs.348043 NS1-associated protein 1	1.90	3.65
	437943	NM_016353	Hs.5943 rec	1.89	1.73
	442426	AI373062	Hs.332938 hypothetical protein MGC5370	1.89	2.79
	400111		Eos Control	1.89	3.84
	437762	T78028	Hs.154679 synaptotagmin I	1.89	1.00
20	404069		Target Exon	1.89	2.51
	434809	AW974687	gb:EST386776 MAGE resequences, MAGM Homo	1.88	2.35
	414220	BE298094	Hs.323806 gb:601118231F1 NIH_MGC_17 Homo sapiens c	1.88	1.00
	422506	R20909	Hs.300741 sorcin	1.87	2.99
	417439	AW602154	Hs.82143 E74-like factor 2 (ets domain transcript	1.87	1.13
25	404391		Target Exon	1.87	3.00
	420187	AK001714	Hs.95744 hypothetical protein similar to ankyrin	1.86	2.93
	446950	AA305800	Hs.5672 hypothetical protein AF140225	1.86	1.90
	400634		C10000818*:gil7661882[refl]NP_055697.1 K	1.86	2.80
	408455	C19034	Hs.288613 Homo sapiens cDNA FLJ14175 fis, clone NT	1.86	1.32
30	422366	T83882	Hs.97927 ESTs	1.85	1.44
	452170	AF064801	Hs.28285 patched related protein translocated in	1.85	2.64
	430504	AV650537	Hs.247309 succinate-CoA ligase, GDP-forming, beta	1.85	1.81
	426484	AA379658	Hs.272759 KIAA1457 protein	1.85	2.60
	411809	AW993680	gb:RC3-BN0034-290200-013-d08 BN0034 Homo	1.85	2.10
35	431129	AL137751	Hs.263671 Homo sapiens mRNA; cDNA DKFZp434I0812 (f	1.84	3.70
	412843	AF007555	Hs.74624 protein tyrosine phosphatase, receptor I	1.84	2.58
	401512		NM_014080:Homo sapiens dual oxidase-like	1.84	1.52
	415969	H11294	Hs.31047 ESTs	1.84	3.08
	444736	AA533491	Hs.23317 hypothetical protein FLJ14681	1.84	1.20
40	426418	M90464	Hs.169825 collagen, type IV, alpha 5 (Alport syndr	1.84	2.35
	416968	AA412686	Hs.97955 ESTs	1.84	2.18
	442961	BE614474	Hs.289074 F-box only protein 22	1.84	2.18
	418650	BE386750	Hs.86978 prolyl endopeptidase	1.84	1.98
	420923	AF097021	Hs.273321 differentially expressed in hematopoieti	1.84	1.00
45	432634	F06459	Hs.289113 cytochrome b5 reductase 1 (BSR-1)	1.83	3.93
	442485	BE092285	Hs.29724 hypothetical protein FLJ13187	1.83	3.10
	427699	AW965076	Hs.180378 hypothetical protein 669	1.83	3.03
	447387	AI268331	Hs.102237 lubby super-family protein	1.83	1.78
	418663	AK001100	Hs.41690 desmocollin 3	1.82	1.53
50	419733	AW382955	Hs.224961 Homo sapiens cDNA FLJ14415 fis, clone HE	1.82	1.00
	409267	NM_012453	Hs.52515 transducin (beta)-like 2	1.81	1.57
	413341	H78472	Hs.191325 ESTs, Weakly similar to T18967 hypotheti	1.81	2.05
	423810	AL132685	Hs.132955 BCL2/adenovirus E1B 19kD-interacting pro	1.81	1.98
	416274	AW160404	Hs.79126 guanine nucleotide binding protein 10	1.80	1.91
55	400843		NM_003105*:Homo sapiens sortilin-related	1.80	4.88
	442187	N23532	Hs.288963 Homo sapiens cDNA: FLJ23034 fis, clone L	1.80	2.61
	458285	AW295984	Hs.255595 ESTs, Weakly similar to A46302 PTB-assoc	1.80	2.33
	413753	U17760	Hs.75517 laminin, beta 3 (nicotin (125kD), kalinin	1.80	3.17
	428004	AA449563	Hs.151393 glutamate-cysteine ligase, catalytic sub	1.80	1.00
60	401613		Target Exon	1.79	2.66
	407173	T64349	gb:yc10d08.s1 Stralagene lung (937210) H	1.79	2.30
	443145	AI049671	Hs.307763 EST, Weakly similar to I38022 hypothetic	1.79	2.00
	418596	AW976721	Hs.293327 ESTs	1.79	3.92
	437374	AL359571	Hs.44054 ninein (GSK3B interacting protein)	1.79	1.24
65	439569	AW602168	Hs.222399 CEGP1 protein	1.79	2.39
	430677	Z26317	Hs.94560 desmoglein 2	1.78	2.02
	436749	AA584890	Hs.5302 lectin, galactoside-binding, soluble, 4	1.78	0.96
	453016	AW295466	Hs.232051 ESTs, Weakly similar to dJ403A15.3 [H.s	1.78	2.60
	426885	AA393130	Hs.193894 ESTs, Weakly similar to A47582 B-cell gr	1.78	2.47
70	452848	AI417193	Hs.288912 hypothetical protein FLJ22604	1.78	2.17
	412560	R24601	Hs.72249 CCR4-NOT transcription complex, subunit	1.78	3.13
	411821	BE299339	Hs.193516 threa-PDZ containing protein similar to	1.78	1.55
	428788	AF082283	Hs.17448 B-cell CLL/lymphoma 10	1.78	2.36
	443963	AA878183	Hs.259737 Homo sapiens cDNA FLJ13618 fis, clone PL	1.78	2.20
75	435479	AF197137	Hs.75187 ATP synthase, H transporting, mitochondr	1.77	2.03
	413073	AL038165	Hs.75187 translocase of outer mitochondrial membr	1.77	2.29
	442473	W27992	gb:43d19 Human retina cDNA randomly prime	1.77	2.93
	418060	AA211589	Hs.208047 ESTs	1.77	4.19

	400773		NM_003105*:Homo sapiens sortilin-related	1.77	1.76	
	400175		Eos Control	1.77	2.04	
	421501	M29971	Hs.1384	Q-6-methylguanine-DNA methyltransferase	1.77	2.32
5	451234	AJ914901	Hs.24052	ESTs, Weakly similar to I38022 hypothe	1.77	2.43
	423332	AJ091466	Hs.127241	sorting nexin 7	1.76	1.82
	423960	AA164516	Hs.136309	SH3-containing protein SH3GLB1	1.76	2.00
	450489	AJ697990	Hs.346002	ESTs	1.76	3.15
	457265	AB023212	Hs.225967	KIAA0995 protein	1.76	2.37
10	413076	U10564	Hs.75188	wee1 (S. pombe) homolog	1.75	2.18
	421948	L42583	Hs.334309	keratin 6A	1.75	1.00
	453578	R06875	Hs.81810	ESTs	1.75	3.10
	412430	AW675064	Hs.73875	fumarylacetoacetate hydrolase (fumarylac	1.75	2.14
	439396	BE562958	Hs.74346	hypothetical protein MGC14353	1.75	1.78
15	431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	1.75	2.36
	449538	AI559444	Hs.104679	ESTs	1.75	3.07
	453146	AI338952	Hs.32194	ESTs	1.74	2.82
	426122	NM_006925	Hs.166975	splicing factor, arginine/serine-rich 5	1.74	2.88
	408989	AW361666	Hs.49500	KIAA0746 protein	1.74	2.07
20	441715	AI929453	Hs.342655	Homo sapiens cDNA FLJ13289 fis, clone OV	1.74	2.06
	412718	X79204	Hs.74520	spinocerebellar ataxia 1 (olivopontocere	1.74	2.46
	450798	AW167780	Hs.50438	ESTs	1.74	2.02
	445537	AJ245671	Hs.12644	EGF-like-domain, multiple 6	1.73	2.58
	400190			Eos Control	1.73	2.40
25	416309	R84694	Hs.79194	cAMP responsive element binding protein	1.73	1.48
	410219	T98226	Hs.171952	occludin	1.73	2.75
	419814	AW402478	Hs.93213	BCL2-antagonist/killer 1	1.73	2.70
	448625	AW970786	Hs.178470	hypothetical protein FLJ22662	1.73	2.07
	422387	AA309996	Hs.148656	ESTs, Weakly similar to T12453 hypothe	1.73	2.02
30	417386	AL037228	Hs.82043	D123 gene product	1.73	2.44
	405812			Target Exon	1.72	2.94
	436270	C03769	Hs.339669	Homo sapiens, clone IMAGE:3947554, mRNA,	1.72	2.85
	409855	AW502461		gb:U1-HF-BR0p-giv-b-08-0-ULr1 NIH_MGC_5	1.72	2.63
35	411442	N25956	Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone NT	1.72	1.88
	400846			sortilin-related receptor, L(DLR class)	1.72	1.63
	401660			Target Exon	1.72	2.63
	402190			C19000835*:gij10946730[ref]NP_067362.1]	1.72	3.33
	439191	AA281177	Hs.41182	Homo sapiens DC47 mRNA, complete cds	1.71	2.17
40	410444	W73484	Hs.132554	gb:z54e04.s1 Soares_fetal_heart_NbHH19W	1.71	2.70
	430393	BE185030	Hs.241305	estrogen-responsive B box protein	1.71	1.33
	445066	AI343931	Hs.149383	ESTs	1.71	2.32
	411299	BE409857	Hs.69499	hypothetical protein	1.71	2.92
	408246	N55669	Hs.333823	mitochondrial ribosomal protein L13	1.71	2.00
	454054	AI336329	Hs.301519	Homo sapiens cDNA FLJ12536 fis, clone NT	1.71	1.93
45	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	1.70	3.70
	427820	BE222494	Hs.180919	inhibitor of DNA binding 2, dominant neg	1.70	1.60
	400750			Target Exon	1.70	2.82
	455842	BE145837		gb:MR0-HT0208-101299-202-c07 HT0208 Homo	1.70	2.17
50	429966	BE081342	Hs.283037	HSPC039 protein	1.70	1.18
	418444	AI902899	Hs.85155	butyrate response factor 1 (EGF-response	1.70	2.47
	437450	AL390154	Hs.26954	Homo sapiens mRNA; cDNA DKFZp762G123 (fr	1.70	3.03
	415738	BE539367	Hs.295953	ESTs, Weakly similar to AF220049 1 uncha	1.70	2.34
	405245			Target Exon	1.70	1.99
	408483	AA464836	Hs.291079	ESTs, Weakly similar to T27173 hypothe	1.70	2.05
55	413611	BE153275		gb:PM0-HT0335-180400-008-e11 HT0335 Homo	1.70	2.05
	410190	AW072328	Hs.59728	Homo sapiens mRNA; cDNA DKFZp566C0546 (f	1.69	2.20
	434608	AA805443	Hs.179909	hypothetical protein FLJ22995	1.69	2.36
	432170	T56887	Hs.18282	KIAA1134 protein	1.69	1.83
	448182	AF244137	Hs.20597	host cell factor homolog	1.69	2.11
60	436293	AI601188	Hs.120910	ESTs	1.69	2.37
	448524	AB032948	Hs.21356	hypothetical protein DKFZp762K2015	1.68	2.48
	404231			Target Exon	1.68	2.50
	453906	AW444952	Hs.257054	ESTs	1.68	2.45
	437967	BE277414	Hs.5947	mel transforming oncogene (derived from	1.68	1.00
65	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	1.68	3.51
	448813	AF169802	Hs.22142	cytochrome b5 reductase b5R.2	1.68	1.69
	429162	AK001250	Hs.197642	hypothetical protein FLJ10388	1.68	3.13
	425556	H27225	Hs.9444	hypothetical protein FLJ13114	1.67	2.02
	405630			Target Exon	1.67	3.00
70	421405	AA251944	Hs.104058	CGI-29 protein	1.67	3.25
	422640	M37984	Hs.118845	troponin C, slow	1.67	1.23
	450857	AA629075	Hs.190090	ESTs	1.67	2.48
	451668	Z43948	Hs.326444	cartilage acidic protein 1	1.66	2.55
	433821	AW182416		ESTs	1.66	2.65
75	405595			NM_000721*:Homo sapiens calcium channel,	1.66	2.23
	433892	AI929357	Hs.323966	Homo sapiens clone H63 unknown mRNA	1.66	1.97
	443558	AA376798	Hs.286122	MDS024 protein	1.66	2.00
	412141	AI183838	Hs.48938	hypothetical protein FLJ21802	1.66	2.65

	424685	W21223	Hs.151734	nuclear transport factor 2 (placental pr	1.66	2.88
	400845			NM_003105*:Homo sapiens sortilin-related	1.66	1.61
	447816	NM_007233	Hs.274329	TP53 target gene 1	1.66	2.63
	404438			Target Exon	1.66	2.34
5	451543	AA397651	Hs.301959	proline synthetase co-transcribed (bacte	1.65	2.08
	433233	AB040927	Hs.301804	KIAA1494 protein	1.65	3.13
	420938	AL049698	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	1.65	1.37
	435438	H84421	Hs.4890	ubiquitin-conjugating enzyme E2E 3 (homo	1.65	2.35
10	431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	1.65	1.00
	433235	AB040929	Hs.35089	contactin 3 (plasmacytoma associated)	1.65	1.44
	439632	AW410714	Hs.334437	hypothetical protein MGC4248	1.65	2.35
	409324	W76202	Hs.343812	lipic acid synthetase	1.65	2.00
	452207	NM_014517	Hs.28423	upstream binding protein 1 (LBP-1a)	1.65	2.33
15	423630	AB011132	Hs.129952	KIAA0560 gene product	1.65	2.13
	443358	H65417	Hs.17757	pleckstrin homology domain-containing, f	1.65	1.63
	427417	AA341061	Hs.177861	CGI-110 protein	1.64	1.28
	450353	AI244661	Hs.103296	ESTs, Weakly similar to S65657 alpha-1C-	1.64	1.60
	445677	H96577	Hs.6838	ras homolog gene family, member E	1.64	1.91
20	447503	AA115496	Hs.336898	Homo sapiens, Similar to RIKEN cDNA 1810	1.64	2.04
	431234	AL389985	Hs.301637	zinc finger protein 258	1.64	1.53
	418032	AW964695	Hs.9436	Homo sapiens, clone MGC:15763, mRNA, com	1.64	2.05
	407796	AA195509	Hs.39733	postsynaptic protein CRIP1	1.64	2.30
	445298	AF187813	Hs.14637	kidney- and liver-specific gene	1.64	2.05
25	439578	AW263124	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	1.64	2.26
	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	1.64	2.10
	433646	AA603319	Hs.155195	ESTs	1.64	2.05
	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	1.64	1.00
	419982	AA252544	Hs.55610	solute carrier family 30 (zinc transport	1.64	2.16
30	401603			NM_022041*:Homo sapiens giant axonal neu	1.64	2.73
	431604	AF175265	Hs.264190	vacuolar protein sorting 35 (yeast homol	1.64	2.75
	400788			O600994*:gij10435784 dbj BAB14668.1 (A	1.63	2.04
	416221	BE513171	Hs.79086	mitochondrial ribosomal protein L3	1.63	2.64
	422491	AA338548	Hs.117546	neuronatin	1.63	0.96
35	424737	BE301883	Hs.152707	glioblastoma amplified sequence	1.63	3.45
	416078	AL034349	Hs.79005	protein tyrosine phosphatase, receptor t	1.63	1.39
	403988			C5001831:gij11056014 ref NP_067651.1 ac	1.62	2.11
	411486	N85785	Hs.181165	eukaryotic translation elongation factor	1.62	2.63
	407874	AI766311	Hs.289047	Homo sapiens cDNA FLJ14059 fis, clone HE	1.62	2.19
40	446700	AW206257	Hs.156326	Human DNA sequence from clone RP11-145L2	1.62	3.03
	438184	AA779897	Hs.122125	ESTs	1.62	2.79
	405502			C7000609*:gij628012 pir A53933 myosin I	1.62	2.55
	447050	NM_016314	Hs.17200	STAM-like protein containing SH3 and ITA	1.62	2.48
	457961	AA772119	Hs.270721	ESTs, Weakly similar to I38022 hypotheti	1.62	2.30
45	436774	AW975810	Hs.159054	hypothetical protein FLJ13224	1.62	2.17
	414893	AA215295	Hs.77578	ubiquitin specific protease 9, X chromos	1.62	2.03
	456660	AI299739	Hs.99601	hypothetical protein FLJ12553	1.62	2.25
	405806			Target Exon	1.62	2.15
	421205	AL137540	Hs.102541	netrin 4	1.62	1.00
50	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	1.62	1.74
	427016	AA397525	Hs.191579	ESTs	1.61	2.16
	458182	AI147996	Hs.155833	ESTs, Weakly similar to spliceosomal pro	1.61	2.74
	451109	F11875	Hs.5534	Homo sapiens cDNA FLJ12961 fis, clone NT	1.61	2.59
	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	1.61	1.78
55	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	1.61	2.10
	447532	AK000614	Hs.18791	hypothetical protein FLJ20607	1.61	1.75
	439944	AA856767	Hs.124623	ESTs	1.61	2.41
	414692	H06831	Hs.164557	ESTs, Moderately similar to ALUC_HUMAN1	1.60	3.05
	433187	R53995	Hs.293381	ESTs, Moderately similar to ALU7_HUMAN A	1.60	2.63
60	446825	BE266822	Hs.344097	filamin A, alpha (actin-binding protein-	1.60	2.43
	441166	AA921738	Hs.132473	ESTs	1.60	2.69
	425571	AJ007292	Hs.158306	ephrin-A2	1.60	1.49
	406836	AW514501	Hs.156110	immunoglobulin kappa constant	1.60	1.08
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	1.60	1.47
65	449268	AW369278	Hs.23412	hypothetical protein FLJ20160	1.60	2.89
	400772			NM_003105*:Homo sapiens sortilin-related	1.60	2.57
	445733	BE295568	Hs.13225	UDP-Gal:betaGlcNAc beta 1,4- galactosylt	1.60	2.03
	428172	U09387	Hs.182828	zinc finger protein 136 (clone pHZ-20)	1.60	2.68
	421887	AW161450	Hs.109201	CGI-86 protein	1.59	1.39
70	418127	BE243982	Hs.83532	membrane cofactor protein (CD46, trophob	1.59	1.67
	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	1.59	2.19
	434938	AW500718	Hs.8115	Homo sapiens, clone MGC:16169, mRNA, com	1.59	2.26
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomas	1.59	1.76
	418067	AI127958	Hs.83393	cystatin E/M	1.59	1.26
75	427127	AW802282	Hs.22265	pyruvate dehydrogenase phosphatase	1.59	2.25
	451938	AI354355	Hs.16697	down-regulator of transcription 1, TBP-b	1.59	2.10
	407325	AA291180	Hs.328476	ESTs, Weakly similar to alternatively sp	1.58	2.43
	410796	Z44547	Hs.3731	ESTs, Moderately similar to I38022 hypot	1.58	1.28

5	417343	AA197132	Hs.231581	myosin, heavy polypeptide 1, skeletal mu	1.58	2.84
	416643	U62531	Hs.79410	solute carrier family 4, anion exchanger	1.58	1.26
	400847			NM_003105*:Homo sapiens sortilin-related	1.58	1.48
	436760	AW606927	Hs.5306	hypothetical protein DKFZp586F1122 simil	1.57	1.57
	433427	A1816449	Hs.171889	cholinephosphotransferase 1	1.57	1.64
10	451986	BE246996	Hs.318401	hypothetical protein DKFZp564D1378	1.57	1.83
	426901	A1929568	Hs.146668	KIAA1253 protein	1.57	2.23
	426028	NM_0011110	Hs.172028	a disintegrin and metalloproteinase doma	1.57	3.07
	444604	AW327695	Hs.11441	chromosome 1 open reading frame 8	1.57	1.86
	439686	W40445	Hs.235857	ESTs, Weakly similar to I38022 hypotheti	1.57	3.07
15	426996	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	1.57	2.01
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	1.57	2.83
	418942	A1566004	Hs.141269	Homo sapiens cDNA: FLJ21550 fis, clone C	1.57	1.21
	418555	A1417215	Hs.87159	hypothetical protein FLJ12577	1.56	3.08
	402358			NM_021155*:Homo sapiens CD209 antigen (C	1.56	2.05
20	419749	X73608	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	1.56	2.08
	404977			Insulin-like growth factor 2 (somatomedi	1.56	5.50
	441872	BE567100	Hs.154938	hypothetical protein MDS025	1.56	2.30
	415503	U36601	Hs.78473	N-deacetylase/N-sulfotransferase (hepara	1.56	2.56
	451743	AW074266	Hs.23071	ESTs	1.56	1.85
25	423184	NM_004428	Hs.1624	ephrin-A1	1.56	1.41
	408041	AW138782	Hs.243607	ESTs	1.56	2.21
	416777	AF146760	Hs.79844	DKFZP564M1416 protein	1.56	2.00
	428013	AF151020	Hs.181444	hypothetical protein	1.56	1.53
	410072	BE384447	Hs.16034	hypothetical protein MGC13186	1.55	1.52
30	411495	AP000693	Hs.70359	KIAA0136 protein	1.55	2.88
	408162	AA933833	Hs.118527	ESTs	1.55	2.70
	413350	U02556	Hs.75307	t-complex-associated-testis-expressed 1-	1.55	1.99
	422010	AA302049	Hs.31181	Homo sapiens cDNA: FLJ23230 fis, clone C	1.55	1.60
	425229	AU076961	Hs.155212	methylmalonyl Coenzyme A mutase	1.55	2.57
35	425184	BE278288	Hs.155048	Lutheran blood group (Auberger b antigen	1.55	1.45
	419011	H56244	Hs.89552	glutathione S-transferase A2	1.55	2.77
	417538	AW050865	Hs.275711	hypothetical protein MGC2452	1.55	2.76
	409806	AW500960		gb:U1-HF-BP0p-aly-b-01-0-U1r1 NIH_MGC_5	1.55	2.45
	402737			Target Exon	1.54	2.58
40	419825	A1754011	Hs.7326	ESTs	1.54	1.00
	410001	AB041036	Hs.57771	kallikrein 11	1.54	0.62
	407813	AL120247	Hs.40109	KIAA0872 protein	1.54	2.33
	415906	A1751357	Hs.288741	Homo sapiens cDNA: FLJ22256 fis, clone H	1.54	2.77
	427886	AA417083	Hs.104789	ESTs	1.54	2.60
45	437018	AA889078	Hs.187033	ESTs	1.54	2.48
	415049	N67334	Hs.50158	ESTs	1.54	2.57
	422315	U16296	Hs.115176	T-cell lymphoma invasion and metastasis	1.54	2.57
	413715	AW851121	Hs.75497	Homo sapiens cDNA: FLJ22139 fis, clone H	1.54	1.98
	447144	A1630759	Hs.17481	Homo sapiens clone 24606 mRNA sequence	1.54	2.48
50	438924	BE535511		transmembrane trafficking protein	1.53	3.08
	445166	A1656116	Hs.147451	ESTs	1.53	2.08
	414073	AF068293	Hs.75737	pericentriolar material 1	1.53	1.70
	402378			Target Exon	1.53	2.83
	452316	AA298484	Hs.61265	ESTs, Moderately similar to G786_HUMAN P	1.53	1.60
55	450374	AA397540	Hs.60293	Homo sapiens clone 122482 unknown mRNA	1.53	3.59
	402817			C1003551:gi5678593 ref NP_033547.1 win	1.53	2.75
	406837	R70292	Hs.156110	immunoglobulin kappa constant	1.53	1.01
	410573	AF151057	Hs.64595	aminoadipate-semialdehyde dehydrogenase-	1.53	1.23
	426359	AA376409	Hs.10862	Homo sapiens cDNA: FLJ23313 fis, clone H	1.53	0.67
60	434445	A1349306	Hs.11782	ESTs	1.53	2.80
	452717	AW160399	Hs.30376	hypothetical protein	1.53	2.01
	420465	AL080276	Hs.70488	similar to prokaryotic-type class I pept	1.53	2.25
	437404	AA858974	Hs.180992	ESTs	1.53	2.00
	459192	AW176180		gb:RC2-BT0214-010999-001-E07 BT0214 Homo	1.52	3.20
65	446457	A1300580	Hs.345281	ESTs, Moderately similar to ALU1_HUMAN A	1.52	2.35
	441466	AW673081	Hs.54828	ESTs	1.52	1.99
	421810	AK001718	Hs.108530	hypothetical protein FLJ10856	1.52	2.98
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	1.52	2.47
	414882	D79994	Hs.77546	Homo sapiens cDNA: FLJ21983 fis, clone H	1.52	2.55
70	442169	W21813	Hs.8125	Homo sapiens mRNA; cDNA DKFZp586E1521 (f	1.52	1.31
	404349			Target Exon	1.52	2.74
	416278	AA356365	Hs.79137	protein-L-isoaspartate (D-aspartate) O-m	1.52	2.93
	431846	BE019924	Hs.271580	uropod 1B	1.52	1.01
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	1.52	0.93
75	442670	BE410050	Hs.11859	hypothetical protein FLJ13188	1.52	2.70
	441617	AA581863	Hs.178485	Homo sapiens cDNA FLJ13919 fis, clone Y7	1.52	1.65
	440079	A1557284	Hs.6900	ring finger protein 13	1.52	1.76
	432831	A1821702	Hs.115959	ESTs, Weakly similar to I38022 hypotheti	1.52	2.13
	414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	1.52	2.13
	442149	AB014550	Hs.8118	KIAA0650 protein	1.52	1.00
	457747	AW975000		gb:EST387105 MAGE resequences, MAGN Homo	1.51	2.38

5	419433	AA814807	Hs.7395	hypothetical protein FLJ23182	1.51	2.50
	431812	AA515902	Hs.130650	ESTs	1.51	1.64
	415477	NM_002228	Hs.78465	v-jun avian sarcoma virus 17 oncogene ho	1.51	2.62
	447580	AJ953360	Hs.133487	ESTs	1.51	2.02
	416926	H03109	Hs.108920	HT018 protein	1.51	2.22
10	442755	W57656	Hs.109701	ubiquitin-like 5	1.51	1.34
	448694	AA478756	Hs.194477	E3 ubiquitin ligase SMURF2	1.51	2.24
	422675	BE018517	Hs.119140	eukaryotic translation initiation factor	1.51	1.49
	404397			ENSP00000251675* KIAA1550 protein (Fragm	1.51	2.18
	412927	AA284018	Hs.75063	human Immunodeficiency virus type I enha	1.51	1.33
15	402371			Target Exon	1.51	3.22
	431730	AF208856	Hs.268122	hypothetical protein	1.51	1.57
	417715	AW969587	Hs.86366	ESTs	1.51	1.59
	451117	AA015752	Hs.205173	ESTs	1.50	2.70
	434727	H43374	Hs.7890	Homo sapiens mRNA for KIAA1671 protein,	1.50	3.53
20	442297	NM_006202	Hs.89901	phosphodiesterase 4A, cAMP-specific (dun	1.50	2.24
	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	1.50	1.13
	452658	N88604	Hs.30212	thyroid receptor interacting protein 15	1.50	1.62
	428695	AJ355647	Hs.189999	purinergic receptor (family A group 5)	1.50	1.00
	438967	H30340	Hs.173705	Homo sapiens cDNA: FLJ22050 fis, clone H	1.50	1.05
25	419847	AW390601	Hs.184544	Homo sapiens, clone IMAGE:3355383, mRNA,	1.50	2.53
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (1.49	0.97
	433265	AB040971	Hs.35096	KIAA1538 protein	1.49	1.44
	408136	AL041135	Hs.42959	KIAA1012 protein	1.49	2.24
	455485	AA102287	Hs.26756	hypothetical protein FLJ20896	1.49	2.40
30	418863	AL135743	Hs.25566	ESTs, Weakly similar to 2004399A chromos	1.49	2.84
	405193			C7000789:gil1943947[gblAAC48716.1] (U901	1.48	2.20
	408948	AW296713	Hs.221441	ESTs	1.48	2.20
	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	1.48	2.24
	405932			C15000305:gil3806122[gblAAC69198.1] (AF0	1.48	1.48
35	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	1.48	1.16
	422355	AW403724	Hs.300697	coagulation factor VII (serum prothrombi	1.48	1.20
	428044	AA093322	Hs.301404	RNA binding motif protein 3	1.48	2.38
	418166	AW501907	Hs.261734	Homo sapiens cDNA: FLJ22807 fis, clone K	1.48	1.28
	430453	BE387080	Hs.3903	Cdc42 effector protein 4; binder of Rho	1.48	2.73
40	401600	BE247275		U5 snRNP-specific protein, 116 kD	1.48	2.53
	432638	AJ017717		chromosome 21 open reading frame 15	1.48	2.03
	405194			C7000789:gil1943947[gblAAC48716.1] (U901	1.48	2.00
	416179	R19015	Hs.79067	MAD (mothers against decapentaplegic, Cr	1.48	1.25
	450272	AJ075170	Hs.20010	ESTs	1.48	2.35
45	413709	BE158687		gb:CMO-HT0395-280100-169-b09 HT0395 Homo	1.48	2.08
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	1.48	1.00
	410418	D31382	Hs.63325	transmembrane protease, serine 4	1.47	1.91
	435656	BE545586	Hs.278712	Homo sapiens cDNA FLJ11074 fis, clone PL	1.47	2.26
	404769			NM_007037* Homo sapiens a disintegrin-II	1.47	1.24
50	420132	BE079847	Hs.301914	gb:RC6-BT0627-220300-012-D06 BT0627 Homo	1.47	2.00
	448356	AL120837	Hs.20993	high-glucose-regulated protein 8	1.47	2.90
	421628	AL121317	Hs.106210	hypothetical protein FLJ10813	1.47	4.08
	449059	AJ000566	Hs.98135	hypothetical protein FLJ20559	1.47	3.13
	449029	N28989	Hs.22891	solute carrier family 7 (cationic amino	1.47	1.06
55	422119	AJ277829	Hs.111862	KIAA0590 gene product	1.47	1.51
	438713	H16902		ESTs	1.47	2.39
	418248	NM_005000	Hs.83916	NM_005000* Homo sapiens NADH dehydrogena	1.47	1.00
	419125	AA642452	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	1.46	2.20
	420548	AA278246	Hs.920	ESTs	1.46	2.13
60	424258	AA433848	Hs.107882	hypothetical protein FLJ10659	1.46	1.98
	414683	S78296	Hs.76888	hypothetical protein MGC12702	1.46	1.45
	427045	H86504	Hs.173328	protein phosphatase 2, regulatory subuni	1.46	2.31
	446646	BE552004	Hs.26192	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.46	1.30
	427257	AJ026805	Hs.97726	ESTs	1.46	2.48
65	422971	AJ879223	Hs.145409	RAB, member of RAS oncogene family-like	1.46	1.05
	451334	AJ122691	Hs.13268	ESTs	1.46	2.12
	403326			C2000428*gil7705383[ref]NP_057536.1] GC	1.46	2.40
	453827	AF201948	Hs.35660	BUP protein	1.46	1.65
	423599	AJ805664	Hs.31731	peroxiredoxin 5	1.46	1.56
70	410691	AW239228	Hs.65450	reticulum 4	1.46	1.49
	430688	AL022101	Hs.104991	hypothetical protein similar to preferen	1.46	2.45
	438083	AJ949940	Hs.121924	ESTs	1.46	2.00
	430713	AA351647	Hs.2642	eukaryotic translation elongation factor	1.45	1.60
	437325	AF142481	Hs.5548	I-box and leucine-rich repeat protein 5	1.45	1.26
75	403342			Target Exon	1.45	2.21
	438808	M73980	Hs.129053	Homo sapiens NOTCH 1 (N1) mRNA, complete	1.45	2.40
	446493	AK001389	Hs.15144	hypothetical protein DKFZp564O043	1.45	3.65
	414895	AW894856	Hs.116278	Homo sapiens cDNA FLJ13571 fis, clone PL	1.44	2.71
	442072	AJ740832	Hs.12311	Homo sapiens clone 23570 mRNA sequence	1.44	1.08
	425723	NM_014420	Hs.159311	dickkopf (Xenopus laevis) homolog 4	1.44	2.24
	432901	AJ554929	Hs.281866	ATPase, H transporting, lysosomal (vacuo	1.44	1.63

	412210	AW901492		gb:RCO-NN1012-270300-031-h10 NN1012 Homo	1.44	2.15
	421685	AF189723	Hs.106778	ATPase, Ca transporting, type 2C, member	1.44	1.83
	428115	AB023194	Hs.300855	KIAA0977 protein	1.44	1.31
5	442358	BE567985	Hs.18585	ESTs, Moderately similar to ALU4_HUMAN A	1.44	2.47
	414685	L39874	Hs.76894	dCMP deaminase	1.44	1.25
	413798	AA336708	Hs.75546	capping protein (actin filament) muscle	1.44	1.26
	410937	AA218564	Hs.67052	vacuolar protein sorting 26 (yeast homolog)	1.44	1.41
	400397	AJ270770		transcription factor 7-like 2 (T-cell sp)	1.44	3.43
	405902			Target Exon	1.44	2.65
10	433976	AA620987	Hs.190268	ESTs	1.44	2.46
	405376			Target Exon	1.44	2.28
	436086	Z43133	Hs.9961	Homo sapiens cDNA: FLJ21954 fis, clone H	1.44	1.34
	418182	AW016405	Hs.16648	ESTs	1.44	2.35
	430307	BE513442	Hs.238944	hypothetical protein FLJ10631	1.43	1.55
15	434524	AA443164	Hs.23259	hypothetical protein FLJ13433	1.43	2.05
	417821	BE245149	Hs.82643	protein tyrosine kinase 9	1.43	2.15
	404744			Target Exon	1.43	1.99
	405418			Target Exon	1.43	2.83
	402899			Target Exon	1.43	2.40
20	451608	AA384525	Hs.26745	hypothetical protein	1.43	1.22
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR)	1.43	2.45
	401041			C11000425.gij4507721[ref]NP_003310.1} i	1.43	2.90
	417839	AJ815732	Hs.82712	fragile X mental retardation, autosomal	1.43	2.84
	409245	AA361037	Hs.288036	tRNA isopentenylpyrophosphate transferase	1.43	2.65
25	447808	NM_007265	Hs.19673	suppressor of S. cerevisiae gcr2	1.43	2.00
	456492	AA330047	Hs.191187	ESTs	1.43	2.73
	449244	AW859979	Hs.32204	ESTs	1.42	1.57
	413094	H24184	Hs.25413	TOLLIP protein	1.42	1.33
	452407	AA582909	Hs.29353	brain-specific protein p25 alpha	1.42	2.50
30	407674	AW064061	Hs.279145	ESTs	1.42	2.35
	441297	AW403084	Hs.7766	ubiquitin-conjugating enzyme E2E 1 (homo)	1.42	2.20
	421832	W51778	Hs.323949	kangal 1 (suppression of tumorigenicity)	1.42	1.48
	426348	BE466586	Hs.17433	hypothetical protein FLJ20957	1.42	1.83
	432554	AJ479813	Hs.278411	NCK-associated protein 1	1.42	2.46
35	431735	AW977724	Hs.75868	thymosin, beta 4, X chromosome	1.42	1.30
	429853	NM_004376	Hs.226581	COX15 (yeast) homolog, cytochrome c oxid	1.42	1.50
	444037	AV647686	Hs.42733	CHMP1.5 protein	1.42	1.38
	402144			Target Exon	1.42	2.38
40	456758	AA325170	Hs.224627	ESTs, Weakly similar to FAHUA alpha-act	1.42	2.23
	452322	BE566343	Hs.28988	glutaredoxin (thioltransferase)	1.42	2.18
	426863	AL137657	Hs.172803	hypothetical protein MGC10327	1.41	1.38
	410684	AA088500	Hs.170298	ESTs	1.41	1.28
	401784			NM_002280*:Homo sapiens keratin, hair, a	1.41	1.37
45	427523	BE242779	Hs.179526	upregulated by 1,25-dihydroxyvitamin D-3	1.41	1.32
	449269	AI564682	Hs.175870	ESTs	1.41	1.37
	406467			Target Exon	1.41	1.80
	444339	T96555	Hs.31562	ESTs	1.41	2.94
	431563	AI027643	Hs.120912	ESTs	1.41	1.41
50	413343	BE392026	Hs.334346	hypothetical protein MGC13045	1.41	1.21
	447537	AW295072	Hs.346408	ESTs, Weakly similar to AF193556 1 sacsi	1.41	2.07
	428211	AA424211	Hs.183176	ESTs	1.41	1.25
	406248			Target Exon	1.41	2.40
	437412	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	1.41	1.39
55	414653	M24486	Hs.76768	procollagen-proline, 2-oxoglutarate 4-di	1.41	1.33
	403885			Target Exon	1.41	2.58
	439459	AF086279	Hs.58013	ESTs	1.41	2.08
	419075	T84266	Hs.123927	ESTs	1.41	2.84
	405022			Target Exon	1.40	2.55
60	401346	BE041451		hypothetical protein	1.40	2.38
	415660	AI909007	Hs.78563	ubiquitin-conjugating enzyme E2G 1 (homo)	1.40	2.38
	448023	AI693299	Hs.170388	ESTs	1.40	2.38
	435962	AA702820	Hs.291294	ESTs	1.40	2.10
	432480	AA205475	Hs.275865	ribosomal protein S18	1.40	1.37
65	414309	AK000639	Hs.75884	DKFZP588A011 protein	1.40	1.18
	440256	U23841	Hs.18851	hypothetical protein FLJ10875	1.40	1.91
	413809	L25851	Hs.851	integrin, alpha E (antigen CD103, human)	1.40	2.80
	408176	AK001553	Hs.43436	adenylate kinase 3 alpha like	1.40	2.73
	433960	AW629188	Hs.188929	ESTs	1.40	1.99
70	404178			C6001430*.gij4503521[ref]NP_001559.1} mu	1.40	2.83
	402449			Target Exon	1.40	1.51
	455604	BE011183		gb:PM3-BN0218-100500-003-d09 BN0218 Homo	1.40	2.30
	429221	AI821060	Hs.198271	Target CAT	1.40	1.22
	422122	AA383642	Hs.111894	lysosomal-associated protein transmembra	1.40	1.42
	406231			Target Exon	1.40	2.60
75	405879			Target Exon	1.40	2.73
	450936	AI033745		gb:ow23a10.x1 Soares_parathyroid_tumor_N	1.40	1.13
	403381			ENSP00000231844*:Ecotropic virus integra	1.39	6.03

5	453258	AW293134	Hs.32597	ring finger protein (C3H2C3 type) 6	1.39	3.20
	448261	BE244072	Hs.20815	macrophage erythroblast attacher	1.39	1.33
	427666	AJ791495	Hs.180142	calmodulin-like skin protein (CLSP)	1.39	2.30
	413859	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	1.39	1.53
	407704	BE315072	Hs.78768	malignant cell expression-enhanced gene/	1.39	1.34
10	430138	AA936296	Hs.234265	DKFZP586G011 protein	1.39	2.38
	432841	M93425	Hs.62	protein tyrosine phosphatase, non-recept	1.39	2.88
	444051	N48373	Hs.10247	activated leucocyte cell adhesion molecu	1.39	1.34
	440704	M69241	Hs.162	insulin-like growth factor binding prote	1.39	1.61
	450092	AW139606	Hs.221057	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.39	2.78
15	400275			NM_006513:Homo sapiens seryl-tRNA synth	1.39	2.03
	403725			Target Exon	1.39	2.03
	443211	AJ128388	Hs.143655	ESTs	1.39	1.83
	421510	AK000919	Hs.105191	hypothetical protein FLJ10057	1.39	2.83
	430071	AA355986	Hs.232068	transcription factor 8 (represses interl	1.38	3.54
20	451545	AJ802128	Hs.208647	ESTs	1.38	2.21
	439897	NM_015310	Hs.6763	KIAA0942 protein	1.38	3.65
	423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	1.38	1.00
	410344	AW978436	Hs.62515	KIAA0494 gene product	1.38	2.25
	404439			ENSP00000067222:Mitochondrial 28S ribos	1.38	2.25
25	448581	NM_002709	Hs.21537	protein phosphatase 1, catalytic subunit	1.38	1.47
	408569	BE066047	Hs.86412	chromosome 9 open reading frame 5	1.38	1.27
	447643	H10767	Hs.238465	nGAP-like protein	1.38	1.22
	401593			Target Exon	1.38	2.58
	403807			NM_031889:Homo sapiens enamelin (ENAM),	1.38	2.38
30	406356	N47812		CGI-35 protein	1.38	2.25
	401886			NM_021783:Homo sapiens XEDAR (XEDAR), mR	1.38	2.00
	421110	AJ250717	Hs.1355	cathepsin E	1.38	8.93
	427449	AW946384	Hs.178112	DNA segment, single copy probe LNS-CAVL	1.38	1.44
	427451	AJ690916	Hs.178137	transducer of ERBB2, 1	1.38	2.81
35	440681	AW449696	Hs.166547	ESTs	1.38	2.95
	419590	AF005043	Hs.91390	poly (ADP-ribose) glycohydrolase	1.38	2.10
	446044	H57567	Hs.13572	calcium modulating ligand	1.37	2.62
	400967			Target Exon	1.37	3.12
	414506	AF075337	Hs.76293	thymosin, beta 10	1.37	1.18
40	402599			NM_021186:Homo sapiens zona pellucida g	1.37	2.68
	422932	AI191813	Hs.308220	ESTs	1.37	2.38
	433889	AK002082	Hs.3623	hypothetical protein FLJ11220	1.37	2.23
	429802	H09548	Hs.5367	ESTs, Weakly similar to I38022 hypothe	1.37	2.25
	443856	AK000574	Hs.9908	nitrogen fixation cluster-like	1.37	1.28
45	453489	AA300067	Hs.33032	hypothetical protein DKFZp434N185	1.37	2.15
	424670	W61215	Hs.116651	epithelial V-like antigen 1	1.37	1.66
	428995	AW004975	Hs.194716	MAD (mothers against decapentaplegic, Dr	1.37	1.33
	441551	AA318224	Hs.296141	ESTs	1.37	2.95
	450528	NM_014072	Hs.25063	PRO0461 protein	1.37	1.19
50	427605	NM_000997	Hs.337445	ribosomal protein L37	1.37	1.31
	459237	AA031675	Hs.31917	Homo sapiens, clone MGC.9658, mRNA, comp	1.37	2.50
	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B	1.37	1.31
	404906			NM_025213:Homo sapiens spectrin, beta, n	1.36	3.08
	436246	AW450963	Hs.119991	ESTs	1.36	1.00
55	441478	AA350018	Hs.301342	hypothetical protein MGC4342	1.36	1.43
	419715	AF070523	Hs.92384	vitamin A responsive, cytoskeleton relat	1.36	1.28
	426251	M24283	Hs.168383	intercellular adhesion molecule 1 (CD54)	1.36	2.16
	400129			Eos Control	1.36	2.03
	450447	AF212223	Hs.25010	hypothetical protein P15-2	1.36	2.13
60	434697	AL133033	Hs.4084	KIAA1025 protein	1.36	2.01
	430308	BE540865	Hs.238990	cyclin-dependent kinase inhibitor 1B (p2	1.36	2.03
	434767	AF153201		C2H2 (Kruppel-type) zinc finger protein	1.36	2.87
	459729	AL037285	Hs.289848	EST, Weakly similar to ALU4_HUMAN ALU SU	1.36	1.27
	426653	AA530892	Hs.171695	dual specificity phosphatase 1	1.35	2.20
65	408912	AB011084	Hs.46924	KIAA0512 gene product; ALEX2	1.35	2.68
	409844	AW502336		gb:U1-HF-BR0p-aka-b-05-Q-U1.r1 NIH_MGC_5	1.35	2.29
	402517			Target Exon	1.35	2.10
	447042	AB035863	Hs.182217	succinate-CoA ligase, ADP-forming, beta	1.35	1.25
	405000			Target Exon	1.35	2.32
70	452065	AK000360	Hs.27721	Wolf-Hirschhorn syndrome candidate 1-lik	1.35	2.36
	404666			C9000748:gi8324209[gb]AAB34384.2 (S775	1.35	2.55
	451081	AJ078645	Hs.431	murine leukemia viral (bmt-1) oncogene h	1.35	1.70
	427979	BE379776	Hs.181309	proleosome (prosome, macropain) subunit,	1.35	2.23
	435825	R16702	Hs.91147	ESTs	1.35	2.39
75	426469	BE297886	Hs.293970	methylmalonate-semialdehyde dehydrogenas	1.35	1.40
	447002	BE242866	Hs.16933	HepA-related protein	1.34	2.88
	410946	AW811502		gb:QV2-ST0145-061299-015-b04 ST0145 Homo	1.34	2.02
	454383	AW500332	Hs.11114	hypothetical protein dJ1181N3.1	1.34	2.13
	440512	AA887845	Hs.19673	suppressor of S. cerevisiae gcr2	1.34	2.05
	409655	AW502208		gb:U1-HF-BR0p-aju-a-09-Q-U1.r1 NIH_MGC_5	1.34	2.63
	447390	X95384	Hs.18426	translational inhibitor protein p14.5	1.34	1.00

5	450293	N36754	Hs.171118	hypothetical protein FLJ00026	1.34	2.45
	445831	NM_006055	Hs.13351	LanC (bacterial lanthiotic synthetase c	1.34	1.60
	418610	AW24593	Hs.223394	hypothetical protein MGC2742	1.34	1.39
	441946	AW298716	Hs.120775	ESTs	1.34	2.30
	446192	H49944	Hs.14231	selenoprotein W, 1	1.34	1.17
	416285	BE537973	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	1.34	2.22
	425590	A1954686	Hs.158321	beaded filament structural protein 2, ph	1.34	2.50
	407498	U28131		gb:Human HMGL-C chimeric transcript mRNA	1.34	2.13
10	441331	A1216764	Hs.149971	ESTs, Moderately similar to ALUB_HUMAN I	1.34	2.05
	411789	AF245505	Hs.72157	Adlcan	1.34	1.27
	420542	NM_000505	Hs.1321	coagulation factor XII (Hageman factor)	1.33	1.25
	413892	A1878921	Hs.75607	myristoylated alanine-rich protein kinas	1.33	1.41
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	1.33	1.99
	414861	AL119396	Hs.77508	glutamate dehydrogenase 1	1.33	1.66
15	421687	AL035306	Hs.106823	hypothetical protein MGC14797	1.33	2.18
	410846	AW807057		gb:MR4-ST0062-031199-018-b03 ST0062 Homo	1.33	2.07
	443937	R66571	Hs.24601	ESTs	1.33	2.02
	432360	BE045243	Hs.274416	Target CAT	1.33	1.12
20	443119	AA312264	Hs.7980	hypothetical protein MGC12966	1.33	2.68
	438464	AA659735	Hs.324743	protein phosphatase 4 regulatory subunit	1.33	1.99
	401371			ENSP00000198192:BA438F9.1 (novel protei	1.33	1.10
	405443			Target Exon	1.33	2.11
	453764	BE008180	Hs.282846	Homo sapiens cDNA FLJ14353 fis, clone Y7	1.33	2.88
25	424924	AL039103	Hs.153834	pumilio (Drosophila) homolog 1	1.33	1.24
	453555	N23574	Hs.123649	ESTs, Moderately similar to ALU7_HUMAN A	1.33	2.23
	404343			C7002191:gil5053028[gb]AAD38811.1JAF155	1.33	1.04
	412383	AW947577		gb:RC0-MT0004-140300-031-b09 MT0004 Homo	1.33	2.06
	404250			Target Exon	1.33	2.53
30	413899	AF083892	Hs.75608	flgh1 junction protein 2 (zona occludens	1.33	2.81
	422716	A1702835	Hs.124475	ESTs, Weakly similar to YEF4_YEAST HYPOT	1.33	2.30
	448862	A1351979	Hs.152717	hypothetical protein FLJ13725	1.33	1.08
	409540	AW409569		gb:fn01e09.x1 NIH_MGC_17 Homo sapiens cD	1.33	2.18
	431186	NM_012249	Hs.250697	ras-like protein	1.32	1.39
35	402754			NM_022469: Homo sapiens hypothetical pro	1.32	1.16
	420798	W93774	Hs.99936	keratin 10 (epidermolytic hyperkeratosis	1.32	2.02
	459710	A1701596	Hs.121592	ESTs	1.32	2.70
	435192	AK000739	Hs.4835	eukaryotic translation initiation factor	1.32	2.22
	401383			Target Exon	1.32	2.18
40	453394	AW960474	Hs.40289	ESTs	1.32	2.20
	421820	AW662990	Hs.294133	heme-binding protein	1.32	1.24
	444047	A1097452	Hs.135095	ESTs	1.32	2.95
	440860	R10482	Hs.132876	ESTs	1.32	2.83
	425808	AA364109	Hs.177990	ESTs	1.32	2.11
45	456558	BE410992	Hs.258730	heme-regulated initiation factor 2-alpha	1.32	2.05
	447015	AB033029	Hs.16953	KIAA1203 protein	1.32	1.30
	414015	AA340987	Hs.75693	prolylcarboxypeptidase (angiotensinase C	1.32	1.39
	414843	BE386038	Hs.77492	heterogeneous nuclear ribonucleoprotein	1.32	1.28
	424058	AL121516	Hs.138617	thyroid hormone receptor interactor 12	1.32	2.01
50	401196			Target Exon	1.32	2.13
	450147	AW373713	Hs.146324	CGI-145 protein	1.32	1.32
	422699	BE410590	Hs.119257	ems1 sequence (mammary tumor and squamou	1.32	1.33
	405172			Target Exon	1.32	2.11
	434087	AF116675	Hs.334476	hypothetical protein PRO1942	1.32	2.30
55	416720	H05435	Hs.11110	hypothetical protein MGC2508	1.32	2.18
	426621	NM_001329	Hs.171391	C-terminal binding protein 2	1.32	1.53
	442685	AB033017	Hs.8594	KIAA1191 protein	1.32	1.43
	443879	Z28462	Hs.9927	Homo sapiens mRNA; cDNA DKFZp564D156 (fr	1.31	2.24
	405180	NM_002649		phosphoinositide-3-kinase, catalytic, ga	1.31	1.36
60	417365	D50683	Hs.82028	transforming growth factor, beta recepto	1.31	0.98
	402087			Target Exon	1.31	1.31
	429323	NM_001649	Hs.2391	apical protein, Xenopus laevis-like	1.31	2.05
	409935	AW511413	Hs.278025	ESTs	1.31	1.20
	430235	BE268048	Hs.236494	RAB10, member RAS oncogene family	1.31	1.31
	400172			Eos Control	1.31	1.05
65	421742	AW970004	Hs.107528	androgen induced protein	1.31	1.79
	404273			Target Exon	1.31	2.35
	416204	AW972270	Hs.144054	ESTs	1.31	2.15
	435076	AW298113	Hs.92909	SON DNA binding protein	1.31	2.05
70	452497	AA732153	Hs.27865	Homo sapiens cDNA: FLJ21333 fis, clone C	1.30	1.57
	404596			Target Exon	1.30	2.23
	419080	AW150835	Hs.18878	hypothetical protein FLJ21620	1.30	1.15
	427195	W27230	Hs.173912	eukaryotic translation initiation factor	1.30	1.34
	438129	AA778647		gb:af87d03.s1 Soares_testis_NHT Homo sap	1.30	2.55
75	402138			Target Exon	1.30	2.09
	404029			NM_018936: Homo sapiens protocadherin be	1.30	2.83
	402731	AL042818		E3 ubiquitin ligase SMURF1	1.30	3.32
	458766	AW183618	Hs.55610	solute carrier family 30 (zinc transport	1.30	1.56

5	434585	AW451715	Hs.184075	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.30	2.73
	417219	AW973473	Hs.220936	ESTs	1.30	2.45
	428125	AA393071	Hs.182579	leucine aminopeptidase	1.30	2.00
	416188	BE157260	Hs.79070	v-myc avian myelocytomatosis viral oncog	1.30	1.00
	444681	AJ243937	Hs.288316	chromosome 6 open reading frame 9	1.30	0.94
10	408621	X57809	Hs.181125	immunoglobulin lambda locus	1.29	1.02
	436653	AW410458	Hs.5258	chromosome 11 open reading frame2	1.29	1.20
	417250	N58241	Hs.332115	ESTs	1.29	3.43
	434978	AA321238	Hs.4310	eukaryotic translation initiation factor	1.29	1.91
	448079	R76981		thyroid hormone receptor-associated prot	1.29	2.01
15	450626	AW190989	Hs.1508	insulin-degrading enzyme	1.29	2.09
	456059	BE543127	Hs.336948	Homo sapiens, clone IMAGE:3530891, mRNA,	1.29	2.23
	417809	H75797	Hs.233550	zinc finger protein 208	1.29	2.20
	454771	AW819939	Hs.273629	ESTs	1.29	2.10
	413895	BE178160		gb:RC3-HT0600-060400-022-h10 HT0600 Homo	1.29	2.08
20	404649			Target Exon	1.29	1.32
	440676	NM_004987	Hs.112378	LJM and senescent cell antigen-like doma	1.29	2.08
	405891			Target Exon	1.29	2.00
	418965	AI002238	Hs.11482	splicing factor, arginine/serine-rich 11	1.29	2.41
	412824	AW958075	Hs.11261	small proline-rich protein 2A	1.29	1.27
25	420037	BE295598	Hs.135569	hypothetical protein FLJ14708	1.29	1.23
	459221	BE246522	Hs.306121	leukocyte receptor cluster (LRC) encoded	1.28	2.48
	458651	AW612481	Hs.104105	ESTs	1.28	2.35
	422984	W28614		chorionic somatomammotropin hormone 1 (p	1.28	1.37
	459365	BE087754		gb:MR4-BT0358-140400-006-g10 BT0358 Homo	1.28	1.06
30	418254	AA732511	Hs.86650	ESTs	1.28	2.38
	402474			NM_004079:Homo sapiens cathepsin S (CTSS	1.28	1.99
	448456	AI521830	Hs.171050	ESTs	1.28	2.18
	450098	W27249	Hs.8109	hypothetical protein FLJ21080	1.28	1.68
	405053			Target Exon	1.28	3.23
35	428915	AI041278	Hs.87908	Smf2-related CBP activator protein	1.28	4.25
	443721	AW450451	Hs.266355	ESTs	1.28	1.15
	452047	N35953	Hs.43510	ESTs, Weakly similar to BOX B BINDING FA	1.28	2.30
	440213	AW246253	Hs.7043	succinate-CoA ligase, GDP-forming, alpha	1.28	1.19
	452900	AA626794		prothymosin, alpha (gene sequence 28)	1.28	1.27
40	418721	NM_002731	Hs.87773	protein kinase, cAMP-dependent, catalyti	1.28	2.76
	458911	AA373131	Hs.24322	ATPase, H transporting, lysosomal (vacuo	1.28	1.21
	444250	R40815	Hs.12396	ESTs, Weakly similar to 2004399A chromos	1.28	2.43
	431831	AA548906	Hs.122244	ESTs	1.27	1.51
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	1.27	3.08
45	430316	NM_000875	Hs.235176	insulin-like growth factor 1 receptor	1.27	1.37
	416272	AA178882		gb:z38b09.r1 Stratagene muscle 937209 H	1.27	2.00
	437456	AL047045	Hs.60293	Homo sapiens clone 122482 unknown mRNA	1.27	3.18
	456327	H68741	Hs.38774	ESTs	1.27	2.35
	403349	NM_001406		ephrin-B3	1.27	2.28
50	428821	H91282	Hs.286232	Homo sapiens cDNA: FLJ23190 fis, clone L	1.27	2.13
	454555	AW807095		gb:MR4-ST0062-040100-024-e02 ST0062 Homo	1.27	2.05
	408872	AI760903		gb:wi09h08.x1 NCL_CGAP_CLL1 Homo sapiens	1.27	1.44
	401720			NM_014587:Homo sapiens SRY (sex determi	1.27	2.07
	400082			Eos Control	1.27	1.26
55	420183	W92885	Hs.143408	ESTs	1.27	2.24
	411579	AC006258	Hs.70830	U6 snRNA-associated Sm-like protein LSM7	1.27	1.17
	402191			NM_021733:Homo sapiens testis-specific	1.27	2.44
	457118	AI245525	Hs.182469	Homo sapiens mRNA; cDNA DKFZp564K1972 (f	1.27	2.17
	408576	NM_003542	Hs.46423	H4 histone family, member G	1.27	2.78
60	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	1.27	3.15
	414909	R80316	Hs.132569	PP2135 protein	1.27	1.37
	416114	AI695549	Hs.183868	glucuronidase, beta	1.26	2.48
	455476	AW948172		gb:RC0-MT0013-280300-021-b06 MT0013 Homo	1.26	2.18
	445926	AF054284	Hs.334826	splicing factor 3b, subunit 1, 155kD	1.26	1.35
65	432647	AI807481	Hs.278581	fibroblast growth factor receptor 2 (bac	1.26	1.16
	405436			Target Exon	1.26	2.38
	406140			Target Exon	1.26	3.20
	426201	AW182614	Hs.128499	ESTs	1.26	1.17
	433334	AJ927208	Hs.231958	matrix metalloproteinase 28	1.26	2.30
70	423262	NM_005479	Hs.126057	frequently rearranged in advanced T-cell	1.26	2.61
	422929	AA356694	Hs.94011	ESTs, Weakly similar to MGB4_HUMAN MELAN	1.26	2.11
	445605	AJ906088	Hs.67159	hypothetical protein FLJ12577	1.26	3.11
	425050	BE391854	Hs.7970	gb:601285394F1 NIH_MGC_44 Homo sapiens c	1.26	2.18
	420539	AA282735	Hs.44004	AD031 protein	1.26	2.03
75	437352	AL353957	Hs.284181	hypothetical protein DKFZp434P0531	1.25	1.19
	456535	AA305079	Hs.1342	cytochrome c oxidase subunit Vb	1.25	1.18
	434202	BE382411	Hs.3764	guanylate kinase 1	1.25	1.14
	439528	BE613180	Hs.288368	Homo sapiens cDNA: FLJ21314 fis, clone C	1.25	2.12
	400178			Eos Control	1.25	2.15
	430023	AA158243	Hs.227729	FK506-binding protein 2 (13kD)	1.25	1.20
	412841	AJ751157	Hs.101395	hypothetical protein MGC11352	1.25	1.39

5	425655	BE614551	Hs.738	ribosomal protein L14	1.25	1.22
	449636	AI656508	Hs.281328	ESTs, Weakly similar to T00378 KIAA0641	1.25	3.00
	418406	X73501	Hs.84905	cytokeratin 20	1.24	2.11
	414570	Y00285	Hs.76473	insulin-like growth factor 2 receptor	1.24	1.14
	436967	AA761729	Hs.136705	ESTs	1.24	2.53
10	457216	AA452554	Hs.283697	ESTs, Weakly similar to A41796 neural re	1.24	2.18
	418414	J04977	Hs.84981	X-ray repair complementing defective rep	1.24	1.35
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	1.24	0.92
	421733	AL119571	Hs.1420	fibroblast growth factor receptor 3 (ach	1.24	2.71
	402329			NM_006505*:Homo sapiens poliovirus recep	1.24	1.13
15	447525	AF151031	Hs.300631	hypothetical protein	1.24	1.07
	445939	BE018658	Hs.141003	Homo sapiens cDNA: FLJ21691 fis, clone C	1.24	2.23
	421936	AB040884	Hs.109694	KIAA1451 protein	1.24	2.15
	433681	AI004377	Hs.200350	Homo sapiens cDNA FLJ13027 fis, clone NT	1.24	2.15
	426717	N90977	Hs.49690	Homo sapiens mRNA: cDNA DKFZp434D2328 (f	1.24	2.14
20	404751	T70445		ribosomal protein L9	1.24	1.30
	411456	AW847588		gb:IL3-CT0213-161299-038-G09 CT0213 Homo	1.24	2.35
	425417	AF098948	Hs.157113	coenzyme Q, 7 (rat, yeast) homolog	1.24	2.88
	434508	AI648501	Hs.118012	ESTs	1.24	2.03
	428284	AA535762	Hs.183435	NM_004545:Homo sapiens NADH dehydrogenas	1.24	1.59
25	418597	AK001678	Hs.86337	similar to DNA-directed RNA polymerase I	1.24	2.27
	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	1.24	1.53
	449210	AI635363	Hs.345517	ESTs	1.24	2.18
	439551	W72062	Hs.11112	ESTs	1.24	2.13
	426244	AI064808	Hs.168289	succinate dehydrogenase complex, subunit	1.23	1.06
30	453635	BE148082	Hs.24724	MFH-amplified sequences with leucine-ric	1.23	1.34
	429617	X89984	Hs.211563	B-cell CLL/lymphoma 7A	1.23	2.27
	434943	AI929819	Hs.92909	chromosome 21 open reading frame 50	1.23	2.10
	417010	NM_006225	Hs.80776	phospholipase C, delta 1	1.23	1.21
	426508	W23184	Hs.170171	glutamate-ammonia ligase (glutamine synt	1.23	1.37
35	434055	AF168712	Hs.3726	x 003 protein	1.23	1.58
	438363	AI886351	Hs.22353	hypothetical protein FLJ21952	1.23	2.44
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	1.23	2.28
	407018	U49869		NM_018955:Homo sapiens ubiquitin B (UBB)	1.23	1.44
	444981	AW855398	Hs.12210	hypothetical protein FLJ13732 similar to	1.23	1.19
40	440112	AA099014	Hs.231029	Homo sapiens, clone MGC:15961, mRNA, com	1.22	2.07
	426672	AW270555	Hs.171774	hypothetical protein	1.22	1.16
	404956			C1003210*:g f6912582 ref NP_036524.1 pe	1.22	2.18
	435088	NM_000481	Hs.102	aminomethyltransferase (glycine cleavage	1.22	1.08
	438588	AW274454	Hs.6318	peroxisomal short-chain alcohol dehydrog	1.22	1.02
45	434454	AF217798	Hs.3850	LIS1-interacting protein NUDEL; endodig	1.22	1.27
	425689	W16480	Hs.24283	ESTs, Moderately similar to reduced expr	1.22	2.52
	428755	D87454	Hs.192968	KIAA0265 protein	1.22	1.16
	420685	AA279362		gb:zs84d04.r1 NCL_CGAP_GCB1 Homo sapiens	1.22	2.75
	458991	AI743502		gb:wf63h12.x2 Soares_NFL_T_GBC_S1 Homo s	1.22	2.39
50	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	1.22	1.00
	434023	AI277883	Hs.146141	ESTs	1.22	2.12
	430801	AI580935	Hs.105698	ESTs	1.22	2.53
	414880	AW247305	Hs.119140	eukaryotic translation initiation factor	1.21	1.16
	454144	BE280478	Hs.182695	hypothetical protein MGC3243	1.21	1.04
55	404790			C12001707*:g f7305215 ref NP_038599.1 k	1.21	2.05
	403943			C5000355:g f4503225 ref NP_000765.1 cyt	1.21	2.05
	400201			NM_006156*:Homo sapiens neural precursor	1.21	1.35
	421005	AW293089	Hs.33263	ESTs	1.21	2.02
	414774	X02419	Hs.77274	plasminogen activator, urokinase	1.21	1.11
60	400789			C11001367*:g f1076205 pir f550754 hypoth	1.21	1.06
	412853	M34175	Hs.74625	adaptor-related protein complex 2, beta	1.21	1.24
	449709	BE410592	Hs.23918	hypothetical protein PP5395	1.20	1.27
	413726	AJ278465	Hs.75510	annexin A11	1.20	1.14
	428485	NM_002950	Hs.2280	ribophorin I	1.20	1.24
65	405163			C5000561*:g f7513700 pir f14151 Inv pro	1.20	1.11
	415887	NM_003375	Hs.78902	voltage-dependent anion channel 2	1.20	1.16
	434468	N29309	Hs.39288	ESTs	1.20	3.20
	446843	AW135925	Hs.98798	hypothetical protein MGC11332	1.20	2.25
	432642	BE297835	Hs.3069	heat shock 70kD protein 9B (mortalin-2)	1.20	2.18
70	448242	R80648	Hs.20768	HSPC189 protein	1.20	1.22
	415753	U52819	Hs.78781	vascular endothelial growth factor B	1.20	1.05
	442156	AI690586	Hs.29403	hypothetical protein FLJ22060	1.20	1.18
	408824	L80005	Hs.48375	small nuclear ribonucleoprotein polypept	1.20	1.45
	430012	NM_015373	Hs.227637	chromosome 22 open reading frame 2	1.20	1.03
75	413392	AW021404	Hs.13021	ESTs	1.20	2.07
	401286			Target Exon	1.20	2.08
	415665	AI097276	Hs.274430	surfeit 6	1.20	2.53
	456562	AA306049	Hs.102659	DKFZP434O125 protein	1.20	2.40
	408988	AL119844	Hs.49476	Homo sapiens clone TUAB Cri-du-chat regi	1.20	3.45
	427818	AW511222	Hs.193765	ESTs	1.19	2.99
	406404			NM_002162*:Homo sapiens intercellular ad	1.19	1.17

	400124		Eos Control	1.19	2.12
	416023	AA173029	gb:zp05e01.r1 Stralagene ovarian cancer	1.19	2.45
	427751	AF000152	conserved gene amplified in osteosarcoma	1.19	1.07
5	401204		ENSP00000252232*-Sterol regulatory elama	1.19	2.40
	446771	AA128965	TATA box binding protein (TBP)-associate	1.19	2.03
	429673	AA884407	protein tyrosine phosphatase, non-recept	1.18	2.36
	400130		Eos Control	1.18	2.58
	405365		CX001212*gi 7861932 gb AAF70445.1 (AF2	1.18	2.38
	406181		Target Exon	1.18	2.18
10	422559	AW247696	hypothetical protein MGC12934	1.18	2.13
	409524	AW402151	tumor necrosis factor (ligand) superfam	1.18	1.07
	438446	AW137476	Homo sapiens cDNA FLJ13884 fis, clone TH	1.18	2.11
	447980	AI703397	ESTs	1.18	2.02
15	425503	W92517	actin binding LIM protein 1	1.18	1.29
	411469	T09997	cysteine-rich protein 2	1.18	0.99
	409162	H25530	solute carrier family 22 (organic cation	1.17	1.04
	429986	AF092047	sine oculis homeobox (Drosophila) homolo	1.17	1.00
	420869	X58964	regulatory factor X, 1 (influences HLA c	1.17	2.58
20	425943	H46986	ESTs	1.17	2.25
	415376	R35960	Homo sapiens, Similar to hypothetical pr	1.17	2.13
	420588	AF000982	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.17	2.38
	457205	AI905780	Target CAT	1.17	1.11
	407970	AW403814	BCL2-associated athanogene	1.16	3.60
25	440214	AA247118	hypothetical protein FLJ11305	1.16	2.15
	405646		C12000200:gi 4557225 ref NP_000005.1 al	1.16	1.11
	438438	AA257992	Janus kinase 1 (a protein tyrosine kinas	1.16	1.08
	431427	AK000401	Homo sapiens cDNA FLJ20394 fis, clone KA	1.16	2.08
	419885	AA251551	ESTs	1.16	2.07
30	427679	AA973904	ESTs, Moderately similar to MYPH_HUMAN M	1.16	2.15
	443865	AW296385	hypothetical protein FLJ12610	1.15	2.05
	415511	AI732617	ESTs	1.15	3.44
	417988	AA210878	ESTs, Moderately similar to ALU1_HUMAN A	1.15	2.09
	405058		Target Exon	1.15	1.16
35	446623	AF279865	kinesin family member 13B	1.15	1.21
	419754	H52299	Homo sapiens mRNA; cDNA DKFZp58610523 (f	1.15	1.15
	420003	AA256906	ESTs, Weakly similar to ubiquitous TPR m	1.15	2.06
	422988	AW673847	ESTs	1.15	1.00
	426371	M63967	aldehyde dehydrogenase 1 family, member	1.15	2.31
40	422895	NM_015958	CGI-30 protein	1.15	2.08
	426295	AW367283	zinc finger protein 6 (CMPX1)	1.15	2.13
	448323	AI492298	ESTs	1.14	2.54
	414244	AA287801	ESTs, Moderately similar to Z195_HUMAN Z	1.14	2.23
	442872	AI471987	ESTs	1.14	2.09
45	425318	AU076845	BCL2/adenovirus E1B 19kD-interacting pro	1.14	2.33
	415667	F11582	developmentally regulated GTP-binding pr	1.14	1.10
	401058		Target Exon	1.14	2.20
	409838	AW502928	gb:U1-HF-BP0p-ahw-e-10-0-U1.r1 NIH_MGC_5	1.14	2.15
50	438493	AI130740	phosphoinositide-3-kinase, regulatory su	1.14	1.00
	404392		C7001460:gi 12667420 gb AAK01436.1 AF332	1.14	2.82
	433220	AI076192	ESTs	1.14	2.78
	405166		Target Exon	1.14	2.23
	401038		C11000425:gi 4507721 ref NP_003310.1 ti	1.14	2.71
55	414052	AW578849	ESTs, Weakly similar to unnamed protein	1.14	2.08
	442043	BE567620	ESTs	1.13	2.17
	419727	AW180796	DKFZP564O243 protein	1.13	1.14
	425206	NM_002153	hydroxysteroid (17-beta) dehydrogenase 2	1.13	2.07
	414682	AL021154	inhibitor of DNA binding 3, dominant neg	1.13	1.47
	402712		C1003562*gi 10047177 db BAB13382.1 (A	1.13	1.18
60	452289	BE568205	mitogen-activated protein kinase kinase	1.12	2.16
	401496		Target Exon	1.12	1.10
	459249	AI970399	ESTs	1.12	2.67
	447495	AW401864	programmed cell death 8 (apoptosis-induc	1.12	2.03
	428422	AI557280	capping protein (actin filament) muscle	1.11	2.60
65	421762	AA297546	gb:EST113074 Fetal brain III Homo sapien	1.11	2.15
	405855		Target Exon	1.11	1.98
	428972	AK001470	cysteine desulfurase	1.11	2.19
	406761	AI241715	ATP synthase, H transporting, mitochondr	1.10	3.33
70	432425	AF070619	Homo sapiens clone 24481 mRNA sequence	1.10	2.30
	446241	AI004677	chromosome 14 open reading frame 4	1.10	2.28
	424454	AB011139	optic atrophy 1 (autosomal dominant)	1.10	2.18
	418242	AW976183	BTB and CNC homology 1, basic leucine zi	1.10	2.07
	437407	AI479332	ESTs	1.10	2.09
	447459	AI380255	ESTs	1.10	2.22
75	426682	AV660038	UDP glycosyltransferase 1 family, polype	1.09	2.33
	403655		NM_003071:Homo sapiens SWI/SNF related,	1.09	2.25
	433156	R59206	Homo sapiens cDNA: FLJ22539 fs, clone H	1.09	2.70
	403826		Target Exon	1.09	1.10

5	433333	AI016521	Hs.71816	v-akt murine thymoma viral oncogene homo	1.09	1.06
	451382	H86180	Hs.221513	ESTs	1.08	2.75
	454717	AW815123		gb:QV4-ST0212-261199-045-b01 ST0212 Homo	1.08	1.98
	422743	BE304678	Hs.119598	ribosomal protein L3	1.08	1.00
	411672	AJ275986	Hs.71414	transcription factor (SMIF gene)	1.08	1.00
	452748	AB011128	Hs.30512	Homo sapiens mRNA for KIAA0556 protein,	1.08	2.45
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	1.08	2.15
	447703	AI420277		gb:U06c12.x1 NC1 CGAP_P28 Homo sapiens	1.08	2.05
10	452420	BE564871	Hs.29463	centrin, EF-hand protein, 3 (CDC31 yeast	1.07	2.03
	455234	R41084		gb:Hk7634 Adult heart, Clontech Homo sa	1.07	2.08
	413945	NM_000591	Hs.75627	CD14 antigen	1.07	0.91
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	1.07	1.00
	434105	AW952124	Hs.13094	presenilins associated rhomboid-like pro	1.07	1.11
	455630	AV655701	Hs.75183	cytochrome P450, subfamily IIE (ethanol-	1.06	2.14
15	455424	AW937733		gb:QV3-DT0045-210100-063-d06 DT0045 Homo	1.05	2.03
	438324	AI792660	Hs.6162	KIAA0771 protein	1.05	2.27
	421604	AW293880	Hs.248367	MEGF11 protein	1.05	2.00
	422614	AI908006	Hs.295362	Homo sapiens cDNA FLJ14459 fis, clone HE	1.04	2.33
20	404058			Target Exon	1.04	2.10
	453085	AW954243		KIAA0251 protein	1.04	2.18
	417500	H59970		gb:yr16104.r1 Soares fetal liver spleen	1.04	2.40
	408653	AW410189	Hs.98074	itchy (mouse homolog) E3 ubiquitin prote	1.04	2.73
	440439	N92818	Hs.64754	ESTs, Weakly similar to potential CDS [H	1.04	2.05
25	409209	AA460160	Hs.73217	ESTs	1.04	2.73
	456107	AA160000	Hs.137396	ESTs, Weakly similar to JC5238 galactosy	1.03	2.18
	415403	F07923	Hs.26744	ESTs	1.02	2.43
	455591	BE008018		gb:QV0-BN0147-290400-214-c01 BN0147 Homo	1.02	2.08
	428491	AF091035	Hs.184627	KIAA0118 protein	1.02	2.81
30	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	1.02	2.11
	434540	NM_016045	Hs.3945	CGI-107 protein	1.02	2.78
	442174	AI690080	Hs.128907	ESTs, Weakly similar to ARUX homeodomain	1.02	2.05
	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	1.02	1.00
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-tin	1.02	2.25
35	454412	AW582568		gb:RC1-ST0278-080100-011-h04 ST0278 Homo	1.00	2.20
	426955	AA393669	Hs.238094	ESTs	1.00	2.18
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	1.00	2.10
	405710			CX000682-g112741327[refXP_008833.2] zi	1.00	2.00
40	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	1.00	1.00
	402001			Target Exon	1.00	1.00
	402812			NM_004930*:Homo sapiens capping protein	1.00	1.00
	402892			Target Exon	1.00	1.00
	403329			Target Exon	1.00	1.00
45	407202	N58172	Hs.109370	ESTs	1.00	1.00
	408684	R61377	Hs.12727	hypothetical protein FLJ21610	1.00	1.00
	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	1.00	1.00
	413573	AI733859	Hs.149089	ESTs	1.00	1.00
	414343	AL038166	Hs.323378	coated vesicle membrane protein	1.00	1.00
	414422	AA147224	Hs.249195	Homeo box A13	1.00	1.00
50	417006	AW673606	Hs.80758	aspartyl-tRNA synthetase	1.00	1.00
	421577	BE465451	Hs.105925	single-minded (Drosophila) homolog 1	1.00	1.00
	423349	AF010258	Hs.127428	homeo box A9	1.00	1.00
	424273	W40460	Hs.144442	phospholipase A2, group X	1.00	1.00
	424649	BE242035	Hs.151461	embryonic ectoderm development	1.00	1.00
55	426827	AW067805	Hs.172665	methyleneletrahydrofolate dehydrogenase	1.00	1.00
	427308	D26087	Hs.174905	KIAA0033 protein	1.00	1.00
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	1.00	1.00
	430261	AA305127	Hs.237225	hypothetical protein HT023	1.00	1.00
	431078	U82827	Hs.249195	homeo box A13	1.00	1.00
60	433222	AW514472	Hs.238415	dickkopf (Xenopus laevis) homolog 4	1.00	1.00
	434980	AW770553	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	1.00	1.00
	435974	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	1.00	1.00
	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	1.00	1.00
	443564	AI921685	Hs.199713	ESTs	1.00	1.00
65	444542	AI161293	Hs.280380	aminopeptidase	1.00	1.00
	445413	AA151342	Hs.12677	CGI-147 protein	1.00	1.00
	448706	AW291095	Hs.21814	interleukin 20 receptor, alpha	1.00	1.00
	448807	AI571940	Hs.7549	ESTs	1.00	1.00
	449448	D60730	Hs.57471	ESTs	1.00	1.00
70	449517	AW500106	Hs.23643	serine/threonine protein kinase MASK	1.00	1.00
	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	1.00	1.00
	451844	T61430		gb:yc06a03.s1 Stratagene lung (937210) H	1.00	1.00
	452039	AI922988	Hs.172510	ESTs	1.00	1.00
	452795	AW392555	Hs.18878	hypothetical protein FLJ21620	1.00	1.00
	453096	AW294631	Hs.11325	ESTs	1.00	1.00
75	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	1.00	1.00
	453966	BE148734	Hs.63325	transmembrane protease, serine 4	1.00	1.00
	405580			Target Exon	1.00	1.00

5	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	1.00	1.00
	450377	AB033091	Hs.74313	KIAA1265 protein	1.00	1.00
	433226	AW503733	Hs.9414	KIAA1488 protein	1.00	1.00
	412719	AW016610	Hs.816	ESTs	1.00	1.00
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	1.00	1.00
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	1.00	1.00
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	1.00	1.00
	438817	AI023799	Hs.163242	ESTs	1.00	1.00
10	455474	AW948094		gb:RC0-MT0012-290300-031-c10 MT0012 Homo	0.99	2.00
	420148	U34227	Hs.95361	myosin VIIA (Usher syndrome 1B (autosoma	0.99	2.33
	428466	AF151063	Hs.184456	hypothetical protein	0.98	2.20
	421594	R45689	Hs.21889	Homo sapiens cDNA FLJ12978 fis, clone NT	0.98	3.09
	444654	AV650572	Hs.23440	KIAA1105 protein	0.98	2.00
15	409759	N40285	Hs.81182	histamine N-methyltransferase	0.97	2.20
	401936			Target Exon	0.97	2.39
	403463			Target Exon	0.96	2.58
	434421	AI915927	Hs.34771	ESTs	0.96	2.15
	412636	NM_004415		desmoplakin (DPI, DPII)	0.95	2.01
20	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	0.93	2.55
	421938	AA405951		gb:zu66c01.r1 Soares_testis_NHT Homo sap	0.93	3.10
	447470	BE618324	Hs.263561	ESTs, Weakly similar to A53531 oncofetal	0.92	2.08
	448369	AW268962	Hs.111335	ESTs	0.91	2.35
	421710	AB007930	Hs.107088	KIAA0461 protein	0.91	2.63
25	406805	AI686003	Hs.296031	ESTs	0.91	2.21
	447475	AI380797	Hs.158992	ESTs	0.90	3.25
	428892	U82828	Hs.194382	ataxia telangiectasia mutated (includes	0.90	2.02
	450222	U75308	Hs.24644	TATA box binding protein (TBP)-associate	0.89	2.73
	401572			C15001384:gi12737057[refXP_012129.1]	0.88	2.00
30	429226	AA913330	Hs.53542	choreoacanthocytosis gene; KIAA0986 prot	0.88	2.37
	421979	AW062518	Hs.233150	hypothetical protein MGC5560	0.87	3.70
	407614	NM_001932	Hs.37144	membrane protein, palmitoylated 3 (MAGUK	0.86	2.02
	417912	R25269	Hs.50547	ESTs	0.86	2.00
	401654			NM_007242:Homo sapiens DEAD/H (Asp-Glu-A	0.86	2.11
35	403149			NM_001450:Homo sapiens four and a half L	0.86	2.19
	413000	BE046280		gb:dn43c09.x2 NC1_CGAP_RDF2 Homo sapiens	0.85	2.40
	425166	AK001456	Hs.154919	KIAA0625 protein	0.85	2.18
	447371	AA334274	Hs.18368	DKFZP564B0769 protein	0.84	2.13
40	452801	AB935587	Hs.34447	ESTs	0.84	2.55
	400957			Target Exon	0.83	2.15
	426420	BE383808	Hs.322430	NDRC family, member 4	0.83	2.14
	429354	AA451666	Hs.269363	ESTs	0.80	2.25
	417831	H16423	Hs.82685	CD47 antigen (R)-related antigen, integr	0.78	2.43
	443368	BE568891	Hs.199210	ESTs, Moderately similar to bK116F5.2 [H	0.78	2.00
45	441901	AB914445	Hs.128103	ESTs	0.76	2.06
	429462	AB90356	Hs.127804	Homo sapiens, clone IMAGE:3536432, mRNA,	0.76	2.03
	403010			C21000152:gi16226483[sp]Q52118[YM03_ERWS	0.75	2.43
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	0.75	2.42
	448332	AW293110	Hs.171068	ESTs	0.74	2.00
50	421674	T10707	Hs.296355	hypothetical protein FLJ23138	0.71	2.18
	450645	AL117441	Hs.301997	hypothetical protein FLJ13033	0.67	2.06
	448514	AB020626	Hs.301866	KIAA0819 protein	0.67	2.03
	431609	AW792792	Hs.264330	N-acylsphingosine amidohydrolase (acid c	0.60	2.54
	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	0.60	2.00
55	425960	AW410646	Hs.164649	hypothetical protein DKFZp434H247	0.57	2.15
	408077	AL133574	Hs.42458	Homo sapiens mRNA; cDNA DKFZp586C1817 [J	0.53	2.29

TABLE 9B

60	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers
<hr/>		
65	Pkey	CAT Number
	409345	112147_1
		AI949109 AW118631 AI833148 AW117891 R45932 R80970 AA733110 AW269428 T27024 R97693 AI149202 AI475492 H98845 AA609665
		AI125598 AW663742 AI140029 AW103164 AA126862 N68829 W55398 H94509 W65300 R07712 R36955 AA812477 AA609576 AI754304
		Z41075 AA970004 AW274661 AA923584 AI673108 AA070706 AA541812 T90938
	409540	1138613_1
	409806	1155259_1
70	409838	1155987_1
	409844	1156139_1
	409855	1156256_1
	409865	1156518_1
	410600	121108_1
75	410846	1223902_1
	410946	1227589_1
	411456	1246706_1
		AW409569 BE297044 BE295828
		AW500960 AW501280 AW500814
		AW502928 AW505606 AW501576 AW501577
		AW502336 AW502339 AW501736 AW501839
		AW502461 AW503000 AW502207 AW501862
		AW502208 AW502366 AW502148
		AW575742 BE549623 AI335824 BE463447 AA729043 AW408712 AW499616 AA086179 AW499617 AA191322
		AW807057 AW807054 AW807189 AW807193 AW807369 AW807429 AW807364 AW807365 AW807078 AW807258 AW807180 AW807331
		AW811502 AW811521 AW811548 AW811471 AW811511 AW811508
		AW847588 AW847716 AW847654 AW847592

5	411609 412210 412383 412560	1251530_1 1283615_1 1292509_1 130601_1	AW993680 AW853769 AW901492 AW947725 AW901448 AW947577 AW947574 AW947576 AW947734 AW947733 AW947732 R24601 R23657 AA194467 AI948584 AI678666 AA194383 AI765219 AA702993 AA813511 AA620965 AI990303 AI624682 AI003925 AI338670 AI004589 AI004590 AI127228 Z25302 F29302 BE044308 F32992 AA112966 T30825 F24958 F18071 C00537 T30841 R24502 AI934786 AI770075 AI144132 AA812597 AW203978 H82735 AI813349 AI142908 C04894 AI208243 AI208044 N89963 AI767866 AI290470 AI865963 H83611 BE463806 AI082639 AA507760
10	412636	13165_1	NM_004415 AL031058 M77830 BE149760 AW752599 AW848723 AW376697 AW376817 AW376699 AW848371 AW376782 AW848789 AW361413 AW849074 AW997139 AW799304 AW799309 BE077020 BE077017 BE185187 AW997196 BE156621 BE179915 BE006561 BE143155 AW890985 BE002107 AW103521 AA857316 AW383133 BE011378 AW170253 BE185750 AW886475 BE160433 J05211 BE082576 BE082584 BE004047 AW607238 AW377700 AW377699 BE082526 BE082505 BE082507 BE082514 AW178000 AW177933 AI905935 AW747877 AW748114 BE148516 AW265328 AW847678 AW847688 AW365151 AW365148 AW365153 AW365156 AW365175 AW365157 AW365154 AW058840 BE005272 AW365145 BE001925 BE182166 BE144243 BE001923 AI951766 AI434518 BE184920 BE184933 AI284090 BE184941 AW804674 BE184924 C04715 W39488 AW995615 BE184948 BE159646 AW606653 AA099891 AA131128 AA337270 AA340777 AW384371 AA852212 R58704 AW366566 AW364859 AA025851 AA025852 AA455100 AA179958 AW352220 AW996245 BE165351 BE073467 AA377127 AW890264 AW609750 AW391912 AW849690 T87267 AW853812 AA852213 W74149 BE009090 AA056401 H01011 AW368529 AW390272 C18457 AW674920 N57176 AA026480 AW576767 H93284 AA026863 AW177787 AA026654 AW177786 BE092134 BE092137 BE092136 AW177784 AI022862 BE091653 AW376811 AW848592 AA040018 BE185331 BE182164 AA368564 AW951576 T29918 AA131077 W95048 W25458 AW205789 H90899 N29754 W32490 R20904 BE167181 BE167165 N84767 H27408 H30146 AI190590 C03378 AI554403 AI205263 AA128470 AI392926 AF139065 AW370813 AW370827 AW798417 AW798780 AW798883 AW798569 R33557 AA149190 C03029 AW177783 AA088866 AW370829 AA247685 BE002273 AI760816 AI439101 AW879451 AI700953 AA451923 AI340326 AI590975 T48793 AI568096 AI142882 AA039975 AJ470146 AA946936 BE067737 BE067786 W19287 AA644381 AA702424 AI417612 AI306554 AI686869 AI568892 AW190555 AI571075 AI220573 AA056527 AI471874 AI304772 AW517828 AI915596 AI627383 AI270345 AW021347 AW166807 AW105614 AI346078 AA552300 W95070 AI494069 AI911702 AA149191 AA026864 AI830049 AI887258 AW780435 AI910434 AI819984 AI858282 AI078449 AI025932 AI860584 AI635878 AA026047 AA703232 D12062 AW192085 AA658154 AW514597 AW591892 T87181 AA782066 AW243815 AW150038 AW268383 AW004633 AI927207 AA782109 AW473233 AI804485 AW169216 AI572669 AA602182 AW015480 AW771865 AI270027 AA961816 AA283207 AI076962 AI498487 AI348053 AI783914 H44405 AW799118 AA128330 AA515500 AA918281 W02156 AI905927 AA022701 W38382 R20795 T7861 AW860878
30	412998 413000 413611 413709 413804 413895 415789 416023 416272 417500 419555 420685 421762 421938 422895	1343218_1 1343239_1 1380017_1 1384144_1 1390710_1 1397743_1 1555357_1 156696_1 158407_1 168443_1 185884_1 195591_1 206590_1 209376_1 22276_1	BE046254 BE046673 BE046253 BE046280 BE046763 BE046676 BE153275 BE153189 BE153329 BE153022 BE153030 BE152974 BE158687 BE158688 T64682 BE168190 BE168256 BE178160 BE177986 BE178330 BE178480 H01581 H12850 R65905 H13053 AA173029 BE467711 AA176710 AA178882 AA179898 AA178897 H59970 AA203382 R08822 AA244416 AA244401 AA279362 AA454496 AA584871 AA297546 AA297410 AA297401 AA297465 AA297268 AW966174 AA405851 AA300675 AA412243 AA412383 NM_015958 AF132964 AA088658 N28882 AI197842 AA338679 AA405666 W16871 AA385447 AI928315 AI928318 AW846613 AW960009 AI860687 AI206534 AI961336 T64873 AI735559 H58826 AA857710 AW337576 BE242131 AA339340 AA371380 AA334618 AA316398 R96579 AW771996 AA366110 W07461 H77948 W28514 W27435 AI983043 AA364395 AW572472 AW190386 AI129278 AI913081 AW473549 AA830713 AI982871 AI638547 AI828466 AW572486 N52853 N89687 AW075567 AI571047 AI887479 AI559469 AI685802 AA805256 AI458777 AA974369 AI866929 AI888032 AI823925 AI823566 AW198135 AI287510 AI5655910 AA765775 AI866019 AI263697 AI355825 R42668 AA894603 AW105585 AI824555 AW339175 D20479 AI017717 AA349998 AA350286 BE501310 R48207 AI372769 AJ003450 AA915976 AI261513 AI033019 AI222825 AW150983 AA420700 AA420570 AW884784 Z40157 AW182416 AA918195 AA778707 AA927922 AA888718 AA853991 AA609856 AA634398 AF153201 AW888811 AW888810 AW842970 AA383181 F35832 F26805 X78930 AF026094 N83362 AA206766 AW874294 AA284205 AI091885 AA206800 AW370684 AA904608 AA806352 AA894757 AW068376 AA807284 AA311341 AW958314 AW974687 AA649656 AA652145 AA778647 AW070999 R42302 H16902 AA814856 T65225 AI523569 F09869 F04737 AI538427 AI051714 AW172603 F02602 F01437 AI684417 AI801950 F02970 Z39367 F02882 T16704 H14597 AW952332 R52080 H10427 T06175 T31057 AI381431 R60918 R41255 R43059 R39905 H19330 R36988 BE535511 M62096 AA306787 AW891766 AA348998 AA338869 AA344013 AW956561 AW389343 AW403607 L40391 AW408435 AA121738 AI568978 H13317 R20373 AW948724 AW948744 AA335023 AA436722 AA448690 C21404 AW884390 AA345454 AA303292 AA174174 BE092290 T90614 AA035104 R76028 AA126924 AA741086 AW022056 AW118940 AA121656 AI832409 AA683475 AI140901 AI623576 AW519064 AW474125 AI953923 AI735349 AW150109 AI436154 AW118130 AW270782 AI804073 N27434 AA876543 AA937815 AI051166 AA505378 AI041975 AI335355 AI089540 AA662243 AI127912 AI925604 AI250880 AI366874 AI564386 AI815196 AI683526 AI435885 AI160934 H79030 AI801493 AA448691 AI673767 AI076042 AI804327 AA813438 AA680002 AI274492 T16177 AI287337 AI935050 AA907805 AA911493 AI589411 AI371358 AW576236 AI078866 AW516168 AA346372 AI560185 AA471009 R75857 AA296025 AA523155 AA853168 AI696593 AI658482 AI566601 AW072797 AA128047 AA035502 AW243274 AA992517 R43760 AW979062 AA848000 AA847968 AA829138 AA315805 AA376906 BE539395 AW579186 H44349 BE328145 BE041644 AW579187 AW366504 H28241 H25318 W37573 AW600919 AA528775 R75904 AW780125 AA149420 AI672414 AI122760 AA345675 AW172758 AI337912 AI961291 AW090300 AI090244 BE219837 AI623661 BE501576 AI742232 AW887496 BE501734 AI023964 AI288904 AA975373 AA890325 AI458424 AI984583 N32562 AI356102 AW241694 AI038448 AA576391 AI018389 AI672071 AA977874 W37448 AW189392 AA612894 AI373563 H89551 H89365 AI699774 AI277548 W27992 AF056988 BE566411 AL121194 AW976385 AW366882 AI767324 AW189787 AI215430 AW268499 AW205930 AI392907 BE093017 BE093019 BE093010 AI402277 AW747989 W26565
75	442473 442506 445182 447703	543413_1 54405_1 632151_1 733191_1	

448079	74834_1	R76981 AA101801 AA101722 AA122297 AA098802 BE006483 AA343200 AW963375 BE090425 AA213871 BE621402 AA309094 AW960171 AI275045 Z44230 AW243724 AI051487 AI376624 R68631 AW978550 C00116 AI984051 AA122265 AI379941 AW205843 AW205839 AW190219 AW129532 AI954133 AI668659 AI383948 AI537386 AA213788 AI088416 AI360826 AA101802 AI619505 AA101795 AA101723 AW614392 R64287 AA927599 AI251904 AI803003 AI675123 AW023079 AW134959 AI926156 AA831069 AI638324 F29901 R46085 F03383 C17731 R20584 T90131 AI033745 AI034133 AA844424 AW166024 AI831699 AJ971097 AA011685 H70852 H70851 T61430 AI820545 AI821336 AA626794 AA626779 AA071274 AA928041 AI954235 N71035 N70230 AW674412 AI871136 AI563955 AI954237 AA649543 AI340231 AI368586 AI868721 W44486 T83736 AA126250 AI343619 H94297 T47633 AI672897 AA496355 R23240 AI814680 AA902119 AA644262 N67040 AW074273 AI357512 AA865354 AI027942 R33837 H95828 N63928 AI418701 AI186469 AA693672 AA778429 AA128352 AW954072 C00015 AA861853 AW022016 AI955845 AI753118 AI755095 AA029523 T70086 AA029458 AW675640 N79506 AI659597 AI417119 AI804089 AI383091 AA128493 T83907 T47632 AA094118 AA496405 H94191 AW887759 N98454 AA512988 AI623761 AW028373 AW249740 AI187029 AA991733 AI683085 AI336036 D60550 D60466 D60009 D60248 AW262673 AI524080 AA205643 AI969141 AW674989 AA093704 R81248 R73069 W01019 R23316 C14688 W44485 AA093663 T70157 H57883 R94790 D81287 D81788 AA364340 AA383533 N41706 BE295144 D60973 D81466 D60551 R33836 D60249 AA354560 W01933 T71478 AA515461 F27984 BE084745 W19084 R81247 AI080252 AI382863 AA205542 AW954243 AA829930 AA412478 AA828434 AA814538 AI927418 AI192435 W52897 AA443666 AA031913 AI683306 AA918481 AI183314 D83907 AI206832 AA876122 D83836 D83838 D82533 AI761290 AI191125 AI143749 AW771909 AI241436 AI767257 W56507 AA847787 AA568692 T10502 AI247870 AA715017 AA643304 AA890233 AA811387 AA897470 AA907729 AI708679 AI078010 AA452830 AW419160 AI783713 N80205 W56778 AA676899 AI888718 N69930 AI338935 AI217580 AA639508 AA575836 BE046852 AI312651 AI038406 AA628649 AA643838 AI493761 AA032024 W38849 AA340178 AA447052 AA452969 W19369 AA296364 H44229 W58767 C05751 C05835 AI741989 N98532 AW102617 AA412583 AI922246 W38495 AA355375 AA928571 C06275 AA352500 N93132 AW582568 AW818656 AW818647 AW818655 AW818637 AW818234 AW807095 AW807022 AW845880 AW807096 AW807461 AW846116 AW807070 AW815123 AW815138 AW815259 R41084 AW875856 AW937733 AW937727 AW937883 AW948094 AW948118 AW948070 AW948093 AW948084 AW948088 AW948074 AW948079 AW948117 AW948085 AW948081 AW948096 AW948102 AW948087 AW948080 AW948061 AW948091 AW948098 AW948089 AW948104 AW948119 AW948089 AW948100 AW948112 AW948121 AW948068 AW948109 AW948105 AW948097 AW948120 AW948108 AW948111 AW948114 AW948115 AW948072 AW948083 AW948095 AW948116 AW948078 AW948077 AW948071 AW948067 AW948107 AW948122 AW948065 AW948064 AW948113 AW948063 AW948062 AW948172 AW948178 AW948169 AW948176 AW948191 AW948192 AW948186 AW948184 AW948187 AW948188 AW948189 AW948181 AW948177 AW948171 AW948183 AW948173 BE008018 BE008025 BE008026 BE007959 BE007994 BE008016 BE008019 BE008024 BE008022 BE008027 BE008029 BE008020 BE008015 BE008021 BE008028 BE008023 BE008030 BE008014 BE011183 BE011170 BE011333 BE011188 BE011181 BE011324 BE011161 BE011169 BE145837 BE145894 AW975000 AA658945 AA661558 AI743502 AI807438 AW176180 AW176212 AI909464 AW176218 AW176171 AW176203 AW176181 AW176213
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TABLE 9C

45	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham 1. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham 1. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
50	NL_position:	Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	NL_position
	400634	8567750	Minus	101102-101223,101886-102018
	400750	8119067	Plus	198991-199168,199316-199548
55	400752	7331445	Minus	36215-36461
	400772	8131629	Minus	34896-35021,41078-41197
	400773	8131629	Minus	44116-44238,48208-48321
	400788	7342055	Plus	184369-184715
	400789	8307741	Plus	82281-83693
60	400835	8954121	Plus	89366-89622
	400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,10634-10789,15254-15403,23827-23958
	400844	9188605	Plus	24746-24872,25035-25204
	400845	9188605	Plus	34428-34612
	400846	9188605	Plus	39310-39474
65	400847	9188605	Plus	44543-44835
	400957	7705148	Minus	66959-67241
	400967	7770682	Minus	32697-32999
	401038	7232177	Minus	4277-4469
	401041	7232177	Plus	44750-45076
70	401058	8117654	Minus	45226-45414
	401155	9438289	Plus	31381-31526
	401177	9438503	Minus	62773-63330
	401196	9719673	Plus	33138-33834
	401204	9743388	Minus	33694-33872
75	401286	9801342	Minus	147036-147318
	401346	9926605	Minus	12031-13032
	401371	9650602	Plus	80901-81283

	401383	6721135	Minus	155543-157381
	401496	7381769	Minus	82790-83002
	401512	7622346	Plus	136399-136557
	401563	8247910	Plus	91395-91763
5	401572	8570271	Minus	78651-78889
	401593	7230957	Plus	10368-10572, 11293-12356
	401600	4388746	Minus	27363-27518, 28727-28891, 29526-29731
	401603	7689953	Minus	116659-116780
	401613	4878062	Plus	22461-22831
10	401654	9097132	Minus	64695-64797
	401660	9100664	Minus	173662-174024
	401720	6468551	Plus	7783-8468
	401784	7249190	Plus	148362-148606, 149453-149535, 149731-149962
	401835	7139700	Plus	142257-142742
15	401886	7229913	Minus	79215-79393
	401936	3808091	Plus	46817-46943
	402001	9501818	Plus	68052-68223
	402087	8117546	Plus	137069-137213, 138678-138828, 138969-139050
20	402138	7704985	Plus	14173-15108
	402144	7242326	Plus	115425-115977
	402190	8576067	Minus	76488-76959
	402191	8576073	Minus	69410-69583
	402329	7798735	Plus	15833-16180, 18419-18715, 22507-22624
25	402368	9558577	Minus	47218-47330, 48052-48203
	402371	9558584	Plus	68736-68956
	402378	9625333	Minus	41312-41468, 48313-48720
	402449	9796674	Plus	59867-60039, 62588-62828, 63465-63623, 64923-65108
	402474	7547175	Minus	53526-53628, 55755-55920, 57530-57757
30	402517	9798106	Plus	17569-17721
	402599	7239666	Plus	5835-5987
	402617	9930797	Minus	69466-69945
	402712	8969253	Minus	10941-11138
	402731	9211639	Minus	117913-118004, 121110-121211, 121327-121457, 125478-125623, 126540-126663
35	402737	9212184	Minus	13358-13552
	402754	9213730	Plus	15345-15852
	402760	9213869	Plus	136829-136952, 137336-137521
	402812	6010110	Plus	25026-25091, 25844-25920
	402845	9369288	Plus	160451-160617, 160788-161009
40	402869	6434843	Minus	138639-139335
	402892	8086844	Minus	194384-194645
	403010	3132346	Plus	78385-79052
	403149	9799833	Plus	25034-25185
	403326	8440025	Minus	110959-111122
45	403329	8516120	Plus	96450-96598
	403342	7233487	Minus	42312-43750
	403349	8569773	Minus	167815-168374
	403381	9438267	Minus	26009-26178
	403463	9929538	Plus	102596-102879
50	403655	8736093	Plus	65668-65859
	403725	7534031	Plus	86737-86843
	403728	7534291	Minus	34481-34671
	403807	8439933	Minus	162963-165773
	403826	9838209	Plus	121197-121358
55	403885	7710403	Minus	53259-53524
	403943	7711864	Plus	100742-100904, 101322-101503
	403988	8575087	Plus	16251-16462
	404029	7671252	Plus	108716-111112
	404058	3548785	Plus	99397-101808
60	404059	3168619	Plus	47310-47450
	404178	7630978	Minus	178075-178383
	404204	3169112	Minus	79868-80321
	404231	8218035	Minus	61077-61322
	404250	9187145	Minus	36099-36212, 37928-38075
65	404273	9885189	Plus	97789-98285, 99601-99855
	404343	9838093	Plus	122664-122931
	404349	7630858	Minus	61006-61187
	404391	3135305	Minus	26030-26173, 27852-27997
	404392	3135305	Minus	29738-29857
70	404397	9558608	Minus	104042-104232
	404438	6984205	Plus	63413-63553
	404439	7139680	Plus	55316-55585
	404530	6479107	Plus	3157-3304
	404596	9958262	Minus	104807-105043
75	404649	9798926	Minus	100027-100399
	404666	7272179	Minus	18677-18993
	404687	9797554	Minus	128456-128565
	404744	9187237	Plus	71776-71852, 72885-73019, 73700-73822, 74692-74850

	404751	7630939	Plus	113799-114252,114393-114715
	404769	8099713	Minus	175801-176823
	404790	7230958	Plus	38611-38761
5	404906	7331453	Minus	100985-101126
	404956	7387343	Plus	55883-56203
	404977	3738341	Minus	43081-43229
	405000	6957544	Minus	88854-89993
	405022	7330304	Plus	217163-217439
10	405053	7651944	Minus	157134-157430
	405068	7655685	Plus	150740-151556
	405155	9966228	Plus	130469-130723
	405163	9966267	Minus	161171-161299
	405165	9966302	Plus	6461-6845
	405166	9966302	Plus	40526-40891
15	405172	9966752	Plus	153027-153262
	405180	7139743	Plus	65438-65740
	405193	7230072	Plus	128187-128383
	405194	7230072	Plus	190465-190645,193346-193610
20	405245	7249293	Minus	57560-58312
	405365	2275192	Minus	119867-120372,120481-120824,121029-121357
	405376	1552533	Plus	28875-29099
	405418	6997292	Plus	51839-51953
	405436	7408068	Minus	55716-55979
25	405443	7408143	Plus	90716-90887,101420-101577
	405474	8439781	Plus	172005-172175
	405602	9211311	Minus	50360-50584
	405580	4512267	Plus	169232-169647
	405595	7159256	Plus	47585-47688
30	405630	4508116	Minus	103218-103291,105858-105993,110051-110126
	405646	4914350	Plus	741-969
	405710	5531256	Minus	66203-66832
	405806	7274891	Minus	224961-226780
	405812	4775630	Minus	29424-29764
35	405855	7652031	Minus	60377-60795
	405879	6758747	Minus	54789-55457
	405891	6758795	Plus	41062-41861
	405902	6758795	Minus	82322-83110
	405932	7767812	Minus	123525-123713
40	406038	8389537	Plus	37764-37877
	406140	9168231	Minus	49887-50219
	406181	5923650	Plus	16586-16855
	406231	7417725	Plus	17206-17641,17772-17968
	406248	7417725	Plus	49711-50227
45	406274	7543787	Plus	932-1123
	406356	7107907	Plus	18761-18973
	406404	9256305	Minus	152569-152874
	406467	9795551	Plus	182212-182958
	406557	7711569	Minus	5446-5574,6170-6352
50	406575	7711679	Plus	142034-142473

TABLE 10A: Genes preferentially expressed in non-invasive bladder tumors

Pkey:	Unique Eos probeset identifier number			
ExAccn:	Exemplar Accession number, Genbank accession number			
UnigeneID:	Unigene number			
Unigene Title:	Unigene gene title			
R1	80th percentile of T4 tumor Als divided by the 80th percentile of T2-T4 tumor Als			
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TABLE 10B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

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Pkey	CAT Number	Accession
411880	1263110_1	AW872477 BE088101 T05990
413804	1390710_1	T64662 BE168190 BE168256

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TABLE 10C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

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20

Pkey	Ref	Strand	Nt_position
400752	7331445	Minus	36215-36461
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,10634-10789,15254-15403,23827-23958
400844	9188605	Plus	24746-24872,25035-25204
401093	8516137	Minus	22335-23166
401512	7622346	Plus	136399-136557
401929	3810670	Minus	3167-3286,4216-4310
402230	9966312	Minus	29782-29932
402844	9369286	Plus	54958-55313
403010	3132346	Plus	78385-79052
403381	9438267	Minus	26009-26178
403383	9438267	Minus	119837-121197
403818	8962065	Minus	138360-138512,144658-144796
404606	9212936	Minus	22310-23269
404977	3738341	Minus	43081-43229
405364	2281075	Minus	48325-48491,49136-49252
406081	9123861	Minus	38115-38691

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TABLE 11A: Genes preferentially expressed in muscle-invasive bladder tumors

5	Pkey: Unique Eos probeset identifier number ExAccn: Exemplar Accession number, Genbank accession number UnigenelD: Unigene number Unigene Title: Unigene gene title R1 80th percentile of T2-T4 tumor AIs divided by the 80th percentile of Ta tumor AIs			
	Pkey	ExAccn	UnigenelD	Unigene Title
10	423961	D13666	Hs.136348	periostin (OSF-2os)
	421948	L42583	Hs.334309	keratin 6A
	401780			NM_005557*:Homo sapiens keratin 16 (foca
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti
15	439926	AW014875	Hs.137007	ESTs
	408243	Y00787	Hs.624	Interleukin 8
	414183	AW957446	Hs.301711	ESTs
	411573	AB029000	Hs.70823	KIAA1077 protein
	414522	AW518944	Hs.76325	step II splicing factor SLU7
20	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote
	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1
	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIb, r
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias
25	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (tus
	401781			Target Exon
	421116	T19132	Hs.101850	retinol-binding protein 1, cellular
	448429	D17408	Hs.21223	calponin 1, basic, smooth muscle
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous
30	447526	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)
	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial
35	406663	U24683	Hs.293441	immunoglobulin heavy constant mu
	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule
	433336	AF017986	Hs.31386	secreted frizzled-related protein 2
	425118	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase
	415994	NM_002923	Hs.78944	regulator of G-protein signalling 2, 24k
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous
40	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL
	448921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy
	433470	AW960564		transmembrane 4 superfamily member 1
	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule
	446500	U78093	Hs.15154	sushi-repeat-containing protein, X chrom
45	413324	V00571	Hs.75294	corticotropin releasing hormone
	436729	BE621807		transmembrane 4 superfamily member 1
	450455	AL117424	Hs.25035	chloride intracellular channel 4
	413731	BE243845	Hs.75511	connective tissue growth factor
	412429	AV650262	Hs.75765	GRO2 oncogene
50	418283	S79895	Hs.83942	cathepsin K (pseudosclerosis)
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly
	420899	NM_001629	Hs.100194	arachidonate 5-lipoxygenase-activating p
	400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,
	437446	AA788946	Hs.101302	ESTs, Moderately similar to CATC RAT COL
55	413441	AJ929374	Hs.75367	Src-like-adaptor
	404854			Target Exon
	431319	AA873350	Hs.302232	ESTs
	452432	AW206008	Hs.283378	Homo sapiens cDNA: FLJ21778 fis, clone H
60	429679	NM_006290	Hs.211600	tumor necrosis factor, alpha-induced pro
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,
	408380	AF123050	Hs.44532	diubiquitin
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac
	422545	X02761	Hs.287820	fibronectin 1
	418203	X54942	Hs.83758	CDC28 protein kinase 2
65	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a
	406687	M31126		matrix metalloproteinase 11 (stromelysin
	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob
	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers
	417497	AW402482	Hs.82212	CD53 antigen
70	449335	AW150717	Hs.345728	STAT induced STAT inhibitor 3
	445033	AV652402	Hs.72901	mucln 13, epithelial transmembrane
	427274	NM_005211	Hs.174142	colony stimulating factor 1 receptor, fo
	427527	AI809057	Hs.293441	immunoglobulin heavy constant mu
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso
75	453331	AI240665		ESTs
	428036	AW068302		Homo sapiens mRNA for caldesmon, 3' UTR
	417366	BE185289	Hs.1076	small proline-rich protein 1B (corniflin)

5	414622	AI752666	Hs.76669	nicotinamide N-methyltransferase	3.07
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.02
	417771	AA804698	Hs.82547	retinoic acid receptor responder (Iazaro	2.77
	413936	AF113676	Hs.297681	serine (or cysteine) proteinase inhibito	2.75
	406755	N80129	Hs.94360	metallothionein 1L	2.75
	426653	AA530892	Hs.171695	dual specificity phosphatase 1	2.67
	443623	AA345519	Hs.9641	complement component 1, q subcomponent,	2.65
	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	2.64
10	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	2.51
	410204	AJ243425	Hs.326035	early growth response 1	2.46
	438973	AW959503	Hs.60440	ESTs, Weakly similar to serin protease w	2.46
	420202	AL036557	Hs.95910	putative lymphocyte G0/G1 switch gene	2.44
	422526	AA344932	Hs.118786	metallothionein 2A	2.44
15	442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	2.43
	413902	AU076743	Hs.75613	CD36 antigen (collagen type I receptor,	2.42
	434868	R50032	Hs.159263	collagen, type VI, alpha 2	2.42
	407207	T03651	Hs.336780	tubulin, beta polypeptide	2.30
	438855	AW946276	Hs.6441	Homo sapiens mRNA; cDNA DKFZp586J021 (fr	2.29
20	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	2.20
	424909	S78187	Hs.153752	cell division cycle 25B	2.18
	419938	AU076772	Hs.1279	complement component 1, r subcomponent	2.17
	416819	U77735	Hs.80205	p1m-2 oncogene	2.11
	422582	AI962060	Hs.118397	AE-binding protein 1	2.07
25	414081	AW969976	Hs.279009	matrix Gla protein	2.07
	426406	AI742501	Hs.169756	complement component 1, s subcomponent	2.03
	443950	NM_001425	Hs.9999	epithelial membrane protein 3	2.01
	418323	NM_002118	Hs.1162	major histocompatibility complex, class	1.94
	414420	AA043424	Hs.76095	Immediate early response 3	1.90
30	415149	X12451	Hs.78056	cathepsin L	1.72
	415213	NM_002933	Hs.78224	ribonuclease, RNase A family, 1 (pancrea	1.70
	421848	X15880	Hs.108885	collagen, type VI, alpha 1	1.69
	452516	AA058630	Hs.29759	RNA POLYMERASE I AND TRANSCRIPT RELEASE	1.64
	427676	AA394062	Hs.300772	tropomyosin 2 (beta)	1.64
35	415198	AW009480	Hs.943	natural killer cell transcript 4	1.60
	424390	AW815557	Hs.182241	interferon induced transmembrane protein	1.59
	426825	AL133415	Hs.297753	vimentin	1.51
	452363	AI582743	Hs.94953	Homo sapiens, Similar to complement comp	1.46
	407694	U77594	Hs.37682	retinoic acid receptor responder (Iazaro	1.44

TABLE 11B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
428036	28620_1	AW068302 AI754558 AI750727 AI752631 AA302174 AA327522 M64110 AW859944 AW859989 AI751995 AA769620 AI858829 AI924875 AI868636 AA864291 AI685060 AW088029 AI924908 AW466328 AI093800 AA991651 AI254501 BE004703 AA334442 AW938852 AA194330 AL046953 AA852866 AW391995 W30846 AW662928 W25261 AA042863 R99045 H97060 W03910 H94687 TB8984 AL048165 T29632 N31556 N36484 AI798879 AA989355 W23832 AA873789 AI743646 AA363587 AI814748 AW338990 N73740 N83666 AL047816 R24137 R63433 AA524984 AA234043 AA195131 N99903 AA453669 AI240302 AA370271 AI950026 AW771049 AA121476 AA569557 AI752632 AI355594 AI471993 AI159941 N94555 AI753138 N21537 H97881 N25769 AW068044 AA808425 R63380 AA384738 AA852352 AI073645 AA527960 AA525036 AA044414 AI752450 AA703064 RD1216 AA897183 AI751996 TB1078 H95047 AA573642 D58348 N20953 AA437143 N95439 AA579540 AW857056 AA770090 AI085180 AI806799 AA426421 AI572513 R24081 AA853189 AA295620 AA234044 AA371020 AW994984 H20896 AW964438 AA318516 AA318499 AA318727 AA318211 AA318478 AA318444 AA318307 AA318497 AA318448 AA318309 AA318496 AA318213 AA318435 AA318424 AA318217 AA318523 AA318438 AA318487 AA318724 AA593185 AW994985 T69842 AI251813 AA478174 AA447737 T68350 F07712 AA121145 H08973 AA345212 BE000667 AW068210 AW608407 R05674 H16712 N85426 N42354 H85516 BE147991 T28113 R32682 AA384578 AW239275 H82382 AW840700 D58229 C04082 W45394 AW795667 R73973 BE002409 AA042828 AA363555 AJ223812 AA344709 BE149590 R70995 W46881 W90778 N71242 AA534826 AL040676 R23797 H96450 AA062957 D79947 W46960 AW959278 AA295997 AA026215 AW579469 AW365135 AW365134 AW994353 AW972886 AW069166 AA343690 AW888731 AI751527 AA937490 AA937506 AI826715 BE465604 AI925532 AI858109 AW339097 AI858524 AI720571 BE046506 AW384981 AA043908 AA375983 AA525181 AW068366 AW070577 AW891837 N83985 AW182753 AI422979 AI679733 BE006555 AL048166 AI081401 AI888821 AI626043 N37087 AI824140 AI801298 AA600048 AI753947 H89615 N66424 AW069756 AI814880 AI982806 AI754287 AI971816 AW069022 AW069069 AW069454 AA342989 AI077712 AI311467 AI087381 AI801015 W46993 AI281324 AW191963 AI421675 AI300881 AI356670 AA873156 AI004219 AI189685 AA478018 AA076063 AI445222 AI753124 AI521569 AI925026 AI022368 AI475993 H20846 AI223234 AI635123 AA579170 N30442 AW117889 AA807935 AA558975 AI306636 AA888963 AI952591 AI935835 AI445293 H16713 AW139833 AA622122 AA972051 AI280828 H09543 AI453725 AW069613 AI865615 AI753921 AI368782 AI633208 AA46651 W46961 N22201 H82276 C16555 AA291477 AW440535 AW517755 AA669921 AI926777 AW662118 AA553369 N67873 AW023948 C15861 C16601 AI251455 AW079187 BE045090 AI273006 C16390 C16503 AI620823 F13661 N68864 Z21311 C16108 C16089 C16400 AA758273 AI287781 AA864676 AW608074 AW385583 AI589944 AA665817 AW192979 AW469065 AA564048 H84715 C16417 AA731072 AA661674 C16487 N29477 AW189997 AI370492 C16471 AA652809 AA936687 AA506512 C16306 AW028413 AI537935 AA528347 C16255 AW029046 C16202 AI868152 AI524662 T94414 AI567041 AI619654 AW008488 AI075624 AA577434 AA345104 T30105 AA932002 C16585 AI750390 AW294265 AI619552 AA669781 AA026678 AW132002 AW263919 C18562 AA759137 AA693351 Z40779 C16577 AA885045 AW073763 R45484 AI520895 U54708 T49285 AI568126 AW006569 AI093317 AL119781 T61046 AI053563 H51958 AF114144 AA305739 AW950394 AW793928 AW793910 AL047737 AV659047 AV659632 AI750389 AA092053 AA092798 H85367 T61597 R23745 Z20418 T78485 AI751528 AW068121 AA853188 AI752459 AA853711 AW950653 R78964 R36359 R21626 R21522

433470	3672_1	AW950564 AA092457 T55890 D56120 T92525 AI815987 BE182608 BE182595 AW080238 M90657 AA347236 AW961686 AW176446 AA304671 AW583735 T61714 AA316968 AI446615 AA343532 AA083489 AA488005 W52095 W39480 N57402 D82638 W25540 W52847 D82729 D58990 BE619182 AA315188 AA308636 AA112474 W76162 AA088544 H52265 AA301631 H80982 AA113786 BE620997 AW651691 AA343799 BE613669 BE547180 BE546656 F11933 AA376800 AW239185 AA376086 BE544387 BE619041 AA452515 AA001806 AA190873 AA180483 AA159546 F00242 AI940609 AI940602 AI189753 T97663 T66110 AW062896 AW062910 AW062902 AI051622 AI828930 AA102452 AI685095 AI819390 AA557597 AA383220 AI804422 AI633575 AW338147 AW603423 AW606800 AW750567 AW510672 AI250777 AA083510 AW629109 AW513200 AA921353 AI677934 AI148698 AI955858 AA173825 AA453027 AI027865 AW375542 AA454099 AA733014 AI591384 R79300 R80023 AA843108 AA626058 AA844898 AW375550 AA889018 AI474275 AW205937 AI052270 AW388117 AW388111 AA699452 AI242230 N47476 H38178 AA366621 AA113196 AA130023 H39740 T61629 AI885973 AW083671 AA179730 AA305757 AI285455 N83956 AA216013 AA336155 AW999959 T97525 AA345349 T91762 AA771981 AI285092 AI591386 BE392486 BE385852 AA682601 AI682684 AA345840 T85477 AA292949 AA932079 AA098791 D82607 T48574 AW752038 C06300 436729 42585_1 BE621807 AI445461 AI346835 AI453743 AI564644 AI928364 AW984527 BE156214 AI694111 AI591358 C17504 C17476 C17963 C18304 AW071625 AI678712 C17732 D57559 H61762 AI720939 AI262930 H27252 AA479712 AI927769 AA291465 AA155661 AI963432 AI567995 AA421678 AI925607 AA292956 AA192448 AW192593 AI865838 AI696905 AI871950 AI911921 BE619741 BE439796 AI161312 AI597801 AI424384 AI093510 AI240988 AW820230 AA92554 BE044033 AW262737 AW008570 AA043216 AW629505 AA136645 AA037772 AA706057 AA088439 AW806193 AW806183 AA479834 BE501957 AA129574 R38114 AA649494 AA524526 BE327120 AW572531 BE219784 BE349186 AW015724 AA043217 AW772000 AI799814 AI671727 AW779725 AA502832 AI470033 AA129575 W38161 AI972739 AA404570 AA627686 AA723200 AA147228 AA903050 AI990245 AI075878 T32487 C06123 AA157944 AI800106 W60075 AI859160 AA478328 AW673152 AA182640 AI990827 AW275048 AW103470 AI298935 AW471421 R79190 AW085158 W45410 AI333170 AW300456 AA662517 T55840 AI823466 AI692845 AA962397 AW191997 AA136658 AI251817 BE044134 AW339104 AW517762 AA724739 R79933 AA411108 AA191349 AA037696 AA190966 AA757735 AW772283 AA010631 H80983 AI769516 H64985 AI061065 AI950693 AA085492 AI245632 H28594 AW088968 BE156360 AI349390 AI621320 AI738844 AW194272 AA148284 AA953883 C06365 AA487893 AI927217 AI918523 AI453453 AI798502 AI189365 AI261359 AI032569 AW338678 AI972899 AI500576 AI872628 AI693030 Z28771 AI985583 AI363829 AW339301 AA581093 AI650338 W60032 AA603586 AI686240 AW242958 AA719173 AI745717 AW675302 AI582462 AI244845 AI565439 F09579 AI918453 AA035576 AI472527 AW351556 AA191414 AW674145 D57558 AI446740 D57845 AI589264 C05782 AA722206 AI432033 R21752 BE157510 AI829840 AI468237 AW384233 AA989662 AI865912 AW197954 AI344941 X75684 AI344943 AW583310 AA988297 AI334860 AI348877 AI798415 D11921 AI377596 AI983655 AI744233 C06111 AI248307 AA948565 AI224807 453331 96214_1 AI240665 T53681 N77468 H51833 AA147247 R75732 C18450 R73999 AI095755 T49904 H03868 AA411580 R33395 AA410586 T48869 D63292 R31981 H12498 H02668 AA035018 R75957 AI803329 R27528 R36203 AI809932 AI808765 R78948 AA411449 AA976929 AI378760 AI378620 T48870 R73906 R75632 H03612 AA909684 N50695 H02580 H12839 N58781 AA742532 AI360919 H03502 BE208298 R68588 AI350463 R31935 AW069127 AA411621 R25671 R36105 H12451 H03869 H51263 AA035486 R25109 R25110 AA147933
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TABLE 11C.

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Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

Nt_position: Indicates nucleotide positions of predicted exons.

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Pkey	Ref	Strand	Nt_position
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,85290-86814
404854	7143420	Plus	14260-14537

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TABLE 12A: Genes preferentially expressed in muscle-invasive bladder tumors

	Pkey:	Unique Eos probset identifier number		
	ExAccn:	Exemplar Accession number, Genbank accession number		
	UnigenelD:	Unigene number		
	Unigene Title:	Unigene gene title		
	Seq ID No.:	Sequence Identification Number linking Information in Table 12A to sequences in Table 13		
5				
10	Pkey	ExAccn	UnigenelD	Unigene Title
	424503	NM_002205	Hs.149509	Integrin, alpha 5 (fibronectin receptor,
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial
	418738	AW388633	Hs.6882	solute carrier family 7, (cationic amino
	406964	M21305		FGENES predicted novel secreted protein
	429276	AF056085	Hs.198612	G protein-coupled receptor 51
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 (Ciona savignyi)
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin
	424735	U13875	Hs.272499	short-chain alcohol dehydrogenase, clone
	420159	AJ572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fs, clone C
	415511	AJ732617	Hs.182362	ESTs
	452461	N78223	Hs.108106	transcription factor
	413324	V00571	Hs.75294	corticotropin releasing hormone
	443211	AJ128388	Hs.143655	ESTs
	439926	AW014875	Hs.137007	ESTs
	432222	AJ204995		gb:an03c03.x1 Stratagene schizo brain S1
	408908	BE296227	Hs.250822	serine/threonine kinase 15
	443171	BE281128	Hs.9030	TODNU
	432829	W60377	Hs.57772	ESTs
	410553	AW016824	Hs.272068	hypothetical protein MGC14128
	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin
	425721	AC002115	Hs.159309	uroplakin 1A
	420370	Y13645	Hs.97234	uropod 2
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365012.1 [H.s.a
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like
	456034	AW450979		gb:U1-H-B13-ala-a-12-0-U1.s1 NCL_CGAP_Su
	421110	AJ250717	Hs.1355	cathepsin E
	451668	Z43948	Hs.326444	cartilage acidic protein 1
	408243	Y00877	Hs.624	interleukin 8
	440304	BE159984	Hs.125395	ESTs
	414918	AJ219207	Hs.72222	hypothetical protein FLJ13459
	418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2
	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1
	450533			C1002652*:gij544327[sp][Q04799][FMO5_RABIT
	422282	AF019225	Hs.114309	apolipoprotein L
	425852	AK001504	Hs.159561	death receptor 6, TNF superfamily member
	400844			NM_003105*:Homo sapiens sorfin-related
	404875			NM_022819*:Homo sapiens phospholipase A2
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549
	431347	AJ133461	Hs.251664	Insulin-like growth factor 2 (somatomedin
	413804	T64682		gb:yc48b02.r1 Stratagene liver (377224)
	444163	AJ126098		FGENESH predicted RNaseH domain-containi
	444444	AJ149332	Hs.14855	ESTs
	427747	AW411425	Hs.180655	serine/threonine kinase 12
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C
	420281	AJ623693	Hs.323494	Predicted cation efflux pump
	402305			C19000735*:gij4508027[ref][NP_003414.1] z
	436608	AA628980		down syndrome critical region protein DS
	427239	BE270447		ubiquitin carrier protein
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa
	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding
	414907	X90725	Hs.77597	pole (Drosophila)-like kinase
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy
	426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase doma
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist
	401093			C12000686*:gij6330167[mbj][AA86477.1] (A
	422247	U18244	Hs.113602	solute carrier family 1 (high affinity a
	449722	BE280074	Hs.23960	cyclin B1
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me
	439606	W79123	Hs.58561	G protein-coupled receptor 87
	418543	NM_005329	Hs.85982	hyaluronan synthase 3
	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)
	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGCI_HUMAN G ANT
	427335	AA448542	Hs.251677	G antigen 7B
	409420	Z15008	Hs.54451	laminin, gamma 2 (lncin (100kD), kafini

404440			NM_021048:Homo sapiens melanoma antigen,	Seq ID No. 148 & 149
433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	Seq ID No. 150 & 151
408380	AF123050	Hs.44532	diubiquitin	Seq ID No. 152 & 153
409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	Seq ID No. 154 & 155
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	Seq ID No. 156 & 157
438817	AI023799		ESTs	Seq ID No. 158
421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	Seq ID No. 159 & 160
431515	NM_012152	Hs.258583	EDG-7 (endothelial differentiation, lys	Seq ID No. 161 & 162
433159	AB035898	Hs.150587	kinesin-like protein 2	Seq ID No. 163 & 164
432441	AW292425	Hs.163484	ESTs	Seq ID No. 165
425726	AF085808	Hs.159330	uroplakin 3	Seq ID No. 166 & 167
448045	AJ297436	Hs.20166	prostate stem cell antigen	Seq ID No. 168 & 169
431846	BE019924	Hs.271580	uroplakin 1B	Seq ID No. 170 & 171
437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	Seq ID No. 172 & 173
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	Seq ID No. 174 & 175
400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	Seq ID No. 176 & 177
452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	Seq ID No. 178 & 179
400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	Seq ID No. 180 & 181
428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	Seq ID No. 182 & 183
429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	Seq ID No. 184 & 185
417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	Seq ID No. 186 & 187
445537	AJ245671	Hs.12844	EGF-like domain, multipla 6	Seq ID No. 188 & 189
423961	D13666	Hs.136348	periostin (OSF-2os)	Seq ID No. 190 & 191
417433	BE270266	Hs.82128	ST4 oncofetal trophoblast glycoprotein	Seq ID No. 192 & 193
444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated protein homolog	Seq ID No. 194 & 195
430486	BE062109	Hs.241551	chloride channel, calcium activated, family member 2	Seq ID No. 196 & 197
425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen)	Seq ID No. 198 & 199
409103	AF251237	Hs.112208	XAGE-1 protein	Seq ID No. 200 & 201
129404	AI267700		ESTs	Seq ID No. 202
403047			NM_005656*:Homo sapiens transmembrane protease	Seq ID No. 203 & 204
439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig), transmem	Seq ID No. 205 & 206

TABLE 12B

35	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers

40	Pkey	CAT Number	Accession
	413804	1390710_1	T64682 BE168190 BE168256
	427239	27647_1	BE270447 AW409921 BE207288 BE207170 D56355 BE263223 BE408171 BE262243 BE392439 BE292738 BE261776 BE314300 BE267719
45			BE269715 BE513876 BE295291 BE297066 AA210923 BE407519 H51344 BE622905 AW248281 AW250313 T19021 AA355115 AA316879
			BE269633 BE621936 AA290724 AA380031 AA993616 BE301331 W79220 H73020 AW797850 BE274611 BE314315 BE542407 BE562063
			BE312868 BE278817 BE252503 AA426470 M91670 NM_014501 BE264533 AI884863 AI884942 AI678077 AA829937 AI869333 AW273060
			AA906924 AI571293 AW172642 AA582906 AW674596 AW300936 AW615753 AW615587 AW665495 AI859298 AA594105 AA928110
			AI038859 AI589898 AA828316 AA938955 AA283711 AW170665 BE047759 AW732128 AI015067 AW070748 AW248955 AA975490
			AA211097 AI826097 AA826730 AA994072 AI367867 W74508 AI086474 AA827720 AI922589 AW000868 W58033 AA991461 BE048131
50			M91218 AA876186 AA661759 AI123879 AI089508 AW272915 AI566244 AW245061 AA688299 AW250988 AI953468 AI891144 AW089131
			AJ471577 AA293354 AA464019 BE044549 T29587 AW956171 BE537716 BE269400 AA918328 AI538087 AA969243 AW075033 BE139361
			AI340589 AI250128 AI247038 BE138953 AW075177 AI307208 BE049086 AW302327 AI054335 AI345565 AI334881 AI252075 AI254494
			AW075006 AW302733 AW302738 AI054057 AI054217 AI054172 AI054302 AI053722 AI054060 AI054079 AW075181 AI307473 AI312145
			AI340734 AI334909 AW071374 BE138502 AW074809 AW301901 AI251662 AI307559 BE139228 AI254764 AW073049 AI251264 AI802837
55			AW271867 AI307442 AW075100 AW073456 AW072496 AI270787 AW271039 AW071307 AI610913 AW071289 AI251232 AI251262
			AW073656 AW072901 AI307493 AI255068 AI251289 AI252160 AI271495 AI252427 AW073469 AW071420 AI270156 AI252926 AI252839
			AI252868 AW072520 AW073433 AI340643 AI802854 AI334733 AI583896 AW071311 AI802853 AI289711 AI345036 AW072513 AI348921
			AI307478 AI305762 BE139315 AW271034 AI334886 AI340619 AW470478 BE139280 BE138965 AW302085 BE041872 AW268964
	432222	343347_1	AI204995 AW827539 AW969908 AW440776 AA528756
60	436608	42361_3	AA628980 AI126603 BE504035
	438817	465592_1	AI023799 AA826307 AI683094 AI307373 AI870547 AW979007
	444163	593658_1	AI126098 AI184746 AI148521
	456034	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367
			BE011368 BE011362 BE011215 BE011365 BE011363

TABLE 12C

70	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
	Nt_position:	Indicates nucleotide positions of predicted exons.

75	Pkey	Ref	Strand	Nt_position
	400844	9188605	Plus	24745-24872,25035-25204
	401093	8516137	Minus	22335-23166

402305	7328724	Plus	40832-41362
404440	7528051	Plus	80430-81581
404875	9801324	Plus	96588-96732,97722-97831
405033	7107731	Minus	142358-142546

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Table 13
Seq ID NO: 1 DNA sequence:
Nucleic Acid Accession #: NM_002205
Coding sequence: 24..3173

5

	1	11	21	31	41	51	
10	CAGGACAGGG	AAGAGCGGGC	GCTATGGGGA	GCCGGACGCC	AGAGTCCCCT	CTCCACGCCG	60
	TGCAGCTGCG	CTGGGGCCCC	CGGGCGCGAC	CCCCGCTCGT	GCCGCTGCTG	TTGCTGCTCG	120
	TGCCGCGCGC	ACCCAGGGTC	GGGGGCTTCA	ACTTAGACGC	GGAGGCCCCA	GCAGTACTCT	180
	CGGGGCCCCC	GGGCTCCTTC	TTCCGATTCT	CAGTGGAGTT	TTACCGGCCG	GGAACAGACG	240
	GGGTCAAGT	GCTGGTGGGA	GCACCCAGG	CTAATACCAG	CCAGCCAGGA	GTGCTGCAGG	300
	TTGGTGTCTG	CTACCTCTGT	CCTTGGGGTG	CCAGCCCCAC	ACAGTGCACC	CCCATTGAAT	360
15	TTGACAGCAA	AGGCTCTCGG	CTCCTGGAGT	CCTCACTGTC	CAGCTCAGAG	GGAGAGGAGC	420
	CTGTGGAGTA	CAAGTCTCTG	CAGTGGTTCT	GGGCAACAGT	TCGAGCCCAT	GGCTCTCTCA	480
	TCCTGGCATG	CGCTCCACTG	TACAGCTGGC	GCACAGAGAA	GGAGCCAATG	AGCGACCCCG	540
	TGGGCACCTG	CTACCTCTCC	ACAGATAACT	TCACCCGAAT	TCTGGAGTAT	GCACCTTGCC	600
	GCTCAGATTT	CAGCTGGGCA	GCAGGACAGG	GTTACTGCCA	AGGAGGCTTC	AGTGGCGAGT	660
20	TCACCAAGAC	TGGCCGTGTG	GTTTATGGTG	GACCAGGAAG	CTATTTCCTG	CAAGGCCAGA	720
	TCCTGTCTGC	CACCTCAGGAG	CAGATTGCAG	AATCTTATTA	CCCCGAGTAC	CTGATCAACC	780
	TGGTTCAGGG	GCAGCTGCAG	ACTGCCCAGG	CCAGTTCCTT	CTATGATGAC	AGCTACCTAG	840
	GATACTCTGT	GGCTGTGGGT	GAATTCAATG	GTGATGACAC	AGAAGACTTT	GTGCTGGTGT	900
	TGCCCAAAAG	GAACCTCACT	TACGGCTATG	TCACCATCCT	TAATGGCTCA	GACATTGAT	960
25	CCCTCTACAA	CTTCTCAGGG	GAACAGATGG	CCTCCTACTT	TGGCTATGCA	GTGGCCGCCA	1020
	CAGACCTCAA	TGGGGACGGG	CTGGATGACT	TGCTGGTGGG	GGCACCCTTG	CTCATGGATC	1080
	GGACCCCTGA	CGGGCGGCTC	CAGGAGGTGG	GCAGGGTCTA	CGTCTACCTG	CAGCACCCAG	1140
	CCGGCATAGA	GCCCAACGCC	ACCCCTTACC	TCACCTGGCA	TGATGAGTTT	GGCCGATTGT	1200
	GCAGCTCCTT	GACCCCTCTG	GGGGACCTGG	ACCAGGATGG	CTACAATGAT	GTGGCCATCG	1260
30	GGGCTCCCTT	TGGTGGGGAG	ACCCAGCAGG	GAGTAGTGTG	TGTATTTCCT	GGGGGCCCAG	1320
	GAGGGCTGGG	CTCTAAGCCT	TCCCAAGGTT	TGCAGCCCTT	GTGGGCAGCC	AGCCACACCC	1380
	CAGACTTCTT	TGGCTCTGCC	CTTCGAGGAG	GCCGAGACCT	GGATGGCAAT	GGATATCCTG	1440
	ATCTGATTGT	GGGTCTCTTT	GGTGTGGACA	AGGCTGTGGT	ATACAGGGGC	CGCCCATCTG	1500
	TGTCGCTAGT	TGCCTCCTCT	ACCATCTTCC	CCGCCATGTT	CAACCCAGAG	GAGCGGAGCT	1560
35	GCAGCTTAGA	GGGGAACCTT	GTGGCCTGCA	TCAACCTTAG	CTTCTGCCTC	AATGCTTCTG	1620
	GAAACACAGT	TGCTGACTCC	ATTGGTTTCA	CAGTGGAACT	TCAGCTGGAG	TGGCAGAAAG	1680
	AGAAGGGAGG	GGTACGGGCG	GCACGTCTTC	TGGCCTCCAG	GCAGGCCAAC	CTGACCCAGA	1740
	CCCTGTCTAT	CCAGAATGGG	GCTCGAGAGG	ATTGCAGAGA	GATGAAGATC	TACCTCAGGA	1800
	ACGAGTCAGA	ATTTCCGAGC	AAACTCTCGC	CGATTTCACAT	CGCTCTCAAC	TTCTCCTTGG	1860
40	ACCCCAAGC	CCCAAGTGAC	AGCCACGGCC	TCAAGCCAGC	CCTACATTAT	CAGAGCAAGA	1920
	GCCGGATAGA	GGACAAGGCT	CAGATCTTGC	TGGACTGTGG	AGAAGACAAC	ATCTGTGTGC	1980
	CTGACCTGCA	GCTGGAAGTG	TTTGGGGAGC	AGAACCATGT	GTACCTGGGT	GACAAGAAATG	2040
	CCCTGAACCT	CACITTTCCAT	GCCCAGAAAG	TGGGTGAGGG	TGGCGCCTAT	GAGGCTGAGC	2100
	TTCCGGTTCAC	CGCCCTCCCA	GAGGCTGAGT	ACTCAGGACT	CGTCAGACAC	CCAGGGAACT	2160
45	TTCTCAGCCT	GAGCTGTGAC	TACTTTGCCG	TGAACCAAGG	CCGCTGTGCT	GTGTGTGACC	2220
	TGGGCAACCC	CATGAAGGCA	GGAGCCAGTC	TGTGGGGTGG	CCTTCGGTTT	ACAGTCCCTC	2280
	ATCTCCGGGA	CACATAAGAA	ACCATCCAGT	TTGACTTCCA	GATCCTCAGC	AAGAATCTCA	2340
	ACAACCTCGCA	AAGCGAGCTG	GTTCCTTTTC	GGCTCTCCGT	GGAGGCTCAG	GCCCAGGTCA	2400
	CCCTGAACGG	TGCTCTCAAG	CCTGAGGCG	TGCTATTCCC	AGTAAGCGAC	TGGCATCCCC	2460
50	GAGACCAAGC	TCAGATGGAG	GAGGACCTGG	GACCTGCTGT	CCACCATGTC	TATGAGCTCA	2520
	TCAACCAAGG	CCCCAGCTCC	ATTAGCCAGG	GTGTGCTGGA	ACTCAGCTGT	CCCCAGGCTC	2580
	TGGAAGGTCA	GCAGCTCCTA	TATGTGACCA	GAGTTACGGG	ACTCAACTGC	ACCACCAATC	2640
	ACCCCATTA	CCCAAGGGCG	CTGGAGTTGG	ATCCCGAGGG	TTCCCTGCAC	CACCAAGCAA	2700
	AACGGGAAGC	TCCAAGCCGC	AGCTCTGCTT	CCTCGGGACC	TCAGATCCTG	AAATGCCCGG	2760
55	AGGCTGAGTG	TTTCAGGCTG	CGCTGTGAGC	TGGGGCCCTT	GCACCAACAA	GAGAGCCAAA	2820
	GTCTGCAGTT	GCAATTCCGA	GTCTGGGCCA	AGACTTTCTT	GCAGCGGGAG	CACCAAGCAT	2880
	TTAGCTGCA	GTGTGAGGCT	GTGTACAAAG	CCCTGAAGAT	GCCCTACCGA	ATCCTGCCTC	2940
	GGCAGCTGCC	CCAAAAGAG	CGTCAGGTGG	CCACAGCTGT	GCAATGGACC	AAGCAGAGAAG	3000
	GCAGCTATGG	CGTCCCACCT	TGGATCATCA	TCCTAGCCAT	CCTGTTTGCC	CTCCTGCTCC	3060
60	TAGGTCTACT	CATCTACATC	CTCTACAAGC	TTGGATTCTT	CAAAAGCTCC	CTCCCATATG	3120
	GCACCGCCAT	GGAAAAGCT	CAGCTCAAGC	CTCCAGCCAC	CTCTGATGCC	TGAGTCTCTC	3180
	CAATTTCAGA	CTCCCATTTCC	TGAAGAACCA	GTCCCCCCAC	CCTCATTCTA	CTGAAAAGGA	3240
	GGGGTCTGGG	TACTTCTTGA	AGGTGCTGAC	GGCCAGGGAG	AAGCTCCTCT	CCCCAGCCCA	3300
	GAGACATACT	TGAAGGGCCA	GAGCCAGGGG	GGTGAGGAGC	TGGGGATCCC	TCCCCCCCAT	3360
65	GCACTGTGAA	GGACCTTGT	TTACACATAC	CCTCTTCATG	GATGGGGGAA	CTCAGATCCA	3420
	GGGACAGAGG	CCCAGCCTCC	CTGAAGCCTT	TGCATTTTGG	AGAGTTTCCT	GAAACAACTG	3480
	GAAAGATAAC	TAGGAATATC	ATTACAGATT	CTTTGGGCCA	GACATGCCAC	AAGGACTTCC	3540
	TGTCCAGCTC	CAACCTGCAA	AGATCTGTCC	TGACCTTGGC	CAGAGATCCA	AAGCAAGCCC	3600
	CCAGTAAGAA	CCTGGAACCT	GGGGAGTTAA	GACCTGGCAG	CTCTGGACAG	CCCCACCTCG	3660
70	GTGGGCCAAC	AAGAACAACCT	AACTATGCAT	GGTGCCCCAG	GACCAAGCTCA	GGACAGATGC	3720
	CACAAGGATA	GATGCTGGCC	CAGGGCCAGA	GCCCAAGCTC	AAGGGGAATC	AGAACTCAA	3780
	TGGGGCCAGA	TCCAGCCTGG	GGTCTGGAGT	TGATCTGGAA	CCCAAGACTCA	GACATTGGCA	3840
	CCRAATCCAG	CAGATCCAGG	ACTATATTTG	GGCTGTGCTC	AGACCTGATC	CTGAGGGCCC	3900
	AGTTCAACCT	GATTTAGGAG	AAGCCAGGAA	TTTCCCAGGA	CCTGAAGGGG	CCATGATGGC	3960
75	AACAGATCTG	GAACCTCAGC	CTGGCCAGAC	ACAGGCCCTC	CCTGTTCCCC	AGAGAAAGGG	4020
	GAGCCCACTG	TCTTGGGCTC	GCAGAAATTT	GGTCTGCTCT	GCCAGCTGCA	CTGATGCTGC	4080
	CCCTCATCTC	TCTGCCCAAC	CCTTCCCTCA	CCTTGGCACC	AGACACCCAG	GACTTATTTA	4140
	AACTCTGTG	CAAGTGCAAT	AAATCTGACC	CAGTGCCCCC	ACTGACCAGA	ACTAGAAAAA	4200

AAAA

Seq ID NO: 2 Protein sequence:
Protein Accession #: NP_002196.1

5
10
15
20
25
1 11 21 31 41 51
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GFSVEFYRPG TDGVSVLVGA PKANTSQPGV LQGGAVYLCF WGASPTQCTP IEFDSKGSRL 120
LESSLSSEEG EEPVEYKSLQ WFGATVRAHG SSILACAPLY SWRTEKEPLS DPVGTCTYLS 180
DNFTRILEYA PCRSDFSWAA GQGYCQGGFS AEFTKTGRVV LGGPGSYFWQ GQILSATQEQ 240
IAESYYPEYL INLVQQLQLT RQASSIYDDS YLGYSVAVGE FSGDDTEDFV AGVPEKGNLTY 300
GYVTILNGSD IRSLYNFSGE QMASYFGYAV AATDVNGDGL DDLLVGAPLL MDRTPDGRPQ 360
EVGRVYVYLQ HPAGIEPTPT LTLTGHDEFG RFGSSLTPLG DLDQDGYNDV AIGAPFGGET 420
QQGVVVFVPG GPGGLGSKPS QVLQPLWAAS HTPDFFGSAL RGGRLDNGNG YPDLIVGSFG 480
VDKAVVYRGR PIVSASASLT IFPAMFNPEE RSCSLBGNPV ACINLSFCLN ASGKHVADSI 540
GPTVELQLDW QKQKGVVRR LFLASQATL TQTLILQNGA REDCREMKIY LRNESEFRDK 600
LSPHIALNF SLDPQAPVDS HGLRPAHYQ SKSRIEDKQ ILLDCGEDNI CVPDLQLEVF 660
GEQNHVYVLD KNALNLTFFA QNVGEGGAYE AELRVTAPE ABYSGLVRHP GNFSLSLSDY 720
FAVNSRLLV CDLGNPMKAS ASLWGLRFT VPHLRDTKKT IQPDFQILSK NLNNSQSDVV 780
SFRLSVEAQA PIVLNGVSKP EAVLPVPSDW HPRDQPKKEE DLGPAVHHVY ELINQGPSSI 840
SQGVLELSCP QALEGQQLLY VTRVTGLNCT TNHPINPKGL ELDPEGLSHH QOKREAPSR 900
SASSGPQILK CPEAEFCRLR CELGPLHQQE SQSLQLHFRV WAKTFLQREH QPFSLQCEAV 960
YKALKMPYRI LPRQLPQKER QVATAVQWTK AEGSYGVPLW IILAILFLGL LLLGLLIYIL 1020
YKLGFPKRLS PYGTAMEKAQ LKPPATSDA

Seq ID NO: 3 DNA sequence:
Nucleic Acid Accession #: NM_002425
Coding sequence: 23..1453

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45
50
55
60
65
1 11 21 31 41 51
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AGTCTGCTCT GCCTATCCTC TGAGTGGGGC AGCAAAAGAG GAGGACTCCA ACAAGGATCT 120
TGCCACGCAA TACCTAGAAA AGTACTACAA CCTCGAAAAG GATGTGAAAC AGTTTAGAAG 180
AAAGGACAGT AATCTCATTT TAAAAAAAT CCAAGGAATG CAGAAGTTCC TTGGGTTGGA 240
GGTGACAGGG AAGCTAGACA CTGACACTCT GGAGGTGATG CGCAAGCCCA GGTGTGGAGT 300
TCTGACGTT GGTCACTTCA GCTCCTTTC TGGCATGCCG AAGTGGAGGA AAACCCACCT 360
TACATACAGG ATTGTGAATT ATACACCAGA TTGCGCAAGA GATGCTGTTG ATTCTGCCAT 420
TGAGAAAGCT CTGAAAGTCT GGAAGAGGT GACTCCACTC ACATTCTCCA GGCTGTATGA 480
AGGAGAGGCT GATATAATGA TCTCTTTCG AGTTAAAGAA CATGGAGACT TTTACTCTTT 540
TGATGGCCCA GGACACAGTT TGGCTCATGC CTACCCACCT GGACCTGGGC TTTATGGAGA 600
TATTCACTTT GATGATGATG AAAAAATGGAC AGAAGATGCA TCAGGCACCA ATTTATTCCT 660
CGTTGCTGCT CATGAACCTG GCCACTCCCT GGGGCTCTTT CACTCAGCCA AACTGAAGC 720
TTTGATGTAC CCACCTTACA ACTCATTAC AGAGCTCGCC CAGTTCCGCC TTTGCAAGA 780
TGATGTGAAT GGCATTCACT CTCTCTACGG ACCTCCCCCT GCCTCTACTG AGGAACCCCT 840
GGTGCCCAAA AAATCTGTTT CTTCGGGATC TGAGATGCCA GCCAAGTGTG ATCCTGCTTT 900
GTCCTTCGAT GCCATCAGCA CTCTGAGGGG AGAATATCTG TTCTTTAAAG ACAGATATTT 960
TTGGCGAAGA TCCCACTGGA ACCCTGAACC TGAATTTTCA TTGATTTCTG CATTTTGGCC 1020
CTCTCTTCCA TCATATTTGG ATGCTGCATA TGAAGTTAAC AGCAGGGACA CCGTTTATAT 1080
TTTTAAAGGA AATGAGTTCT GGGCCATCAG AGGAAATGAG GTACAAGCAG GTTATCCAAG 1140
AGGCATCCAT ACCCTGGGTT TTCTCCCAAC CATAAGGAAA ATTGATGCAG CTGTTTCTGA 1200
CAAGGAAAAG AAGAAAACAT ACTTCTTTC AGCGGACAAA TACTGGAGAT TTGATGAAAA 1260
TAGCCAGTCC ATGGAGCAAG GCTTCCCTAG ACTAATAGCT GATGACTTTC CAGGAGTTGA 1320
GCCTAAGGTT GATGCTGTAT TACAGGCATT TGGATTTTTC TACTTCTTCA GTGATCATC 1380
ACAGTTTGAG TTTGACCCCA ATGCCAGGAT GGTGACACAC ATATTAAAGA GTACAGCTG 1440
GTTACATTGC TAGGCGAGAT AGGGGGAAGA CAGATATGGG TGTITTTAAT AAATCTAATA 1500
ATTATTCATC TAATGTATTA TGAGCCAAAA TGGTTAATTT TTCTGTCATG TTCTGTGACT 1560
GAAGAAGATG AGCCTTGCAG ATATCTGCAT GTGTCAATGA GAATGTTTCT GGAATCTTCT 1620
ACTTGTCTTT GAATTGCACT GAACAGAAAT AAGAAATACT CATGTGCAAT AGGTGAGAGA 1680
ATGTATTTTC ATAGATGTGT TATTACTTCC TCAATAAAAA GTTTTATTTT GGGCCTGTTC 1740
CTT

Seq ID NO: 4 Protein sequence:
Protein Accession #: NP_002416

70
75
1 11 21 31 41 51
MMHLAFLVLL CLPVC SAYPL SGAKEEDSN KDLAQQYLEK YYNLEKDVQK FRRKDSNLIV 60
KKIQGMQKPL GLEVTGKLDI DTLEVMRKPR CGVPDVGHFS SFPMPKWRK THLTIRIVNY 120
TFDLPDRAVD SAIEKALKVW EVTPLTFPSR LYEGEADIMI SFAVKEHGDF YSPDGPGLSL 180
AHAYPPGPGY YGDHFDDE KWTEDASGTN LFLVAHELO HSLGLFHSAN TEALMYPLYN 240
SPTELAQFRL SQDDVNGIQS LYGFPPASTE EPLVPTKSVS SGSEMPAKCD PALSFDAIST 300
LRGEYLFPKD RYFWRSHWN PEPEPHLISA FWPSLPSYLD AAYEVNSRDT VFIFKGNEFW 360
AIRGNEVQAG YPRGIHTLGF PPTIRKIDAA VSDKEKKKTY FFAADKYWRF DENQSMEQG 420

FPRLIADDFP GVEPKVDAVL QAFGFFYFFS GSSQFEFDPN ARMVTHILKS NSWLHC

Seq ID NO: 5 DNA sequence:

Nucleic Acid Accession #: NM_002421

Coding sequence: 72..1481

1 11 21 31 41 51
10 GGGATATTGG AGTAGCAAGA GGCTGGGAAG CCATCACTTA CCTTGCACCTG AGAAGAAGA 60
CAAAGGCCAG TATGCACAGC TTTCCTCCAC TGCTGCTGCT GCTGTCTCGG GGTGTGTGT 120
CTCAGAGCTT CCCAGCGACT CTAGAAACAC AAGAGCAAGA TGTGGACTTA GTCCAGAAAT 180
ACCTGGAAAA ATACTACAAC CTGAAGAATG ATGGGAGGCA AGTTGAAAAG CGGAGAAAAT 240
GTGGCCAGT GGTGAAAAA TTGAAGCAA TGCAGGAATT CTTTGGGCTG AAAGTGAAGT 300
15 GGAAACGAGA TGTGAAACC CTGAAGGTGA TGAAGCAGCC CAGATGTGGA GTGCCTGATG 360
TGGCTCAGTT TGTCTCACT GAGGGGAACC CTCGCTGGGA GCAACACAT CTGACCTACA 420
GGATTGAAAA TTACACGCCA GATTGGCCAA GAGCAGATGT GGACCATGCC ATTGAGAAAG 480
CCTTCCAACT CTGAGTAAT GTCAACCTC TGACATTAC CAAGGTCTCT GAGGTCAG 540
CAGACATCAT GATATCTTT GTGAGGGGAG ATCATCGGA CACTCTCTCT TTTGATGGAC 600
20 CTGGAGGAAA TCTTGCTCAT GCTTTTCAAC CAGGCCCAGG TATTGGAGGG GATGCTCATT 660
TTGATGAAGA TGAAGGTGG ACCAACAAAT TCAGAGAGTA CACTTACAT CGTGTTCGG 720
TTCATGAAGT CGGCATTCT CTGGACTCT CCCATTCTAC TGATATCGGG GCTTTGATGT 780
ACCTAGCTA CACCTTCACT GGTGATGTT AGCTAGCTCA GGATGACATT GATGGCATCC 840
AAGCCATATA TGGACGTTCC CAAAATCCTG TCCAGCCCAT CGGCCACAA ACCCAAAAG 900
25 CGTGTGACAG TAAGCTAAC TTTGATGCTA TAACTAGAT TCGGGGAGAA GTGATGTTCT 960
TTAAAGCAG ATTCTACAT CGCAAAATC CCTTCTACCC GGAAGTTGAG CTCAATTCA 1020
TTTCTGTTTT CTGGCCACAA CTGCCAAATG GGTCTGAAGC TGCTTACGAA TTTGCCGACA 1080
GAGATGAAGT CCGGTTTTTC AAAGGGAATA AGTACTGGGC TGTTCAGGGA CAGATGTGC 1140
TACACGATA CCCCAAGGAC ATCTACAGCT CCTTTGGCTT CCCTAGAACT GTGAAGCATA 1200
30 TCGATGCTGC TCTTCTGAG GAAACACTG GAAAAACCTA CTTCTTTGTT GCTAACAAAT 1260
ACTGGAGTGA TGATGAATAT AAACGATCTA TGGATCCAGG TTATCCCAAA ATGATAGCAC 1320
ATGACTTTCC TGGAAATTGC CACAAAGTTG ATGCAGTTT CATGAAAGAT GGATTTTCT 1380
ATTTCTTTCA TGGAAACAAG CAATACAAAT TTGATCCTAA AACGAAGAGA ATTTGACTC 1440
TCCAGAAAGC TAATAGCTGG TCAACTGCA GGAATAATG AACATTACTA ATTTGAATGG 1500
35 AAAACACATG GTGTGAGTCC AAAGAAGGTG TTTTCTGAA GAACGTCTA TTTTCTCAGT 1560
CATTTTAAAC CTCTAGAGTC ACTGATACAC AGAATATAAT CTTATTTATA CCTCAGTTT 1620
CATATTTTTC TACTATTAG AATGTAGCCC TTTTGTACT GATATAATTT AGTTCCCAA 1680
ATGGTGGGTA CAAAAGTCA AGTTTGTGGC TTATGGATTC ATATAGGCCA GAGTTGCAAA 1740
40 GATCTTTTCC AGAGTATGCA ACTCTGACGT TGATCCGAGA GAGCAGCTTC AGTGACAAAC 1800
ATATCCTTTC AAGACAGAAA GAGACAGGAG ACATGAGTCT TTGCGGAGG AAAAGCAGCT 1860
CAAGAACACA TGTGAGTCA CTGGTGTAC CCTGGATAGG CAAGGGATAA CTCTCTAAC 1920
ACAAATAAG TGTTTATGT TTGGAATAAA GTCAACCTTG TTTCTACTGT TTT

45 Seq ID NO: 6 Protein sequence:
Protein Accession #: NP_002412

1 11 21 31 41 51
50 MHSFPPLLLL LFWGVVSHSF PATLETOEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPFV 60
VEKLKQMQEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLYRIEN 120
YTPDLPRADV DHAIEKAPQL WSNVTPLTFT KVSEQQADIM ISFVRGDHRD NSPFDGPGGN 180
LAHAFQPGPG IGGDAHPDED ERWTNNFREY NLHRVAAREL GHSGLSHST DIGALMYPY 240
55 TFSGDVQLAQ DDIDGIQAIY GRSQNFVQPI GPQTPKACDS KLTFDAITTI RGEVMFFKDR 300
FYMRTNPFYP EVELNFIQSV WPQLPNGLEA AYEFAADRDEV RFFKGNKYNA VQGQNVLHGY 360
PKDIYSSPGF PRTVKHIDAA LSEENTGKTY FVANKYWRY DEYKRSMDPG YPKMIAHDFP 420
GIGHKVDVAF MKDGFYFFH GTRQYKFDPK TKRILTLQKA NSWFNCRKN

60 Seq ID NO: 7 DNA sequence:
Nucleic Acid Accession #: NM_014331
Coding sequence: 1..1506

1 11 21 31 41 51
65 ATGGTCAGAA AGCCTGTTGT GTCCACCATC TCCAAGGAG GTTACCTGCA GGGAATGTT 60
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AAGAGGAAAG TCACTTTACT GAGGGGAGTC TCCATTATCA TTGGCACCAT CATTCGAGCA 180
70 GGAATCTTCA TCTCTCTAA GGGGTGCTC CAGAACAAGG GCAGCGTGGG CATGCTCTG 240
ACCATCTGGA CGGTGTGTGG GGTCTGTCA CTATTGGAG CTTTGTCTTA TGCTGAATTG 300
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GTGATATCCC TGGCATTGG ACGCTACATT CTGGAACCAT TTTTATTCA ATGTGAAATC 480
75 CCGAACTTG CGATCAAGCT CATTACAGCT GTGGGCATAA CTGTAGTAT GGTCTCTAAT 540
AGCATGAGTG TCAGCTGGAG CGCCCGGATC CAGATTTTCT TAACCTTTTG CAAGCTCACA 600
GCAATTCTGA TAATTATAGT CCCTGGAGTT ATGCAGCTAA TTAAGGTCA AACGCAGAAC 660
TTTAAGACG CGTTTTCAGG AAGAGATTCA AGTATTACCG GGTGCCACT GCCTTTTAT 720

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TATGGAATGT ATGCATATGC TGGCTGGTTT TACCTCAACT TTGTTACTGA AGAAGTAGAA 780
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TATGTGCTGA CAAATGTGGC CTACTTTACG ACCATTAATG CTGAGGAGCT GCTGCTTCA 900
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TTATTCTATG TTGGCTCTCG AGAGGGGTAC CTCTCCAGAAA TCCTCTCCAT GATTCAATGTC 1080
CGCAAGCACA CTCTCTACG AGCTGTTATT GTTTTGCAACC CTTTGACAAT GATAATGCTC 1140
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GTCCCTGGCT ATTTATCTCT TATTATATGG GACAAGAAAC CCAGGTGGTT TAGAATAATG 1440
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TATATATGGG TTTGTAAAG ATGGTTTAC ACACTACAGA TGTCTTACT GTGAAAAGTG 1920
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GCACCTTGGG AGGCTGAGGG GGTGGATCAC CTGAGGTGCG GAGTTCTAGA CCAGCCTGAC 2940
CAACATGGAG AAACCCATC TCTACTAAA ATACAAAAT AGCTGGGCAT GGTGGCAGAT 3000
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45 Seq ID NO: 8 Protein sequence:
Protein Accession #: NP_055146

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55
60

1 11 21 31 41 51
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GIFISPKGVL QNTGVSQMSL TIWTVCGVLS LFGALSYAEL GTTIKKSQGH YTYILEVFGP 120
LPAPFVRVWE LLIRPAATA VISLAFGRYI LEFFIQCEI PELAIKLITA VGITVVMVLN 180
SMSVSWRSRI QIFLTFCKLT AILIIIVPGV MQLIKGQTON FKDAFSGRDS SITRLPLAFY 240
YGMVYAGWF YLNFVTEVEE NPEKTIPLAI CISMAIVTIG YVLTNVAYPT TINAERILLS 300
NAVAVTFSER LLGNFSLAVP IFVALSCFGS MNGGVFAVSR LFYVASREGH LPEILSMIHV 360
RKHTPLPAVI VLHPLTMIML FSGDLSLLN FLSFARWLF GLAVAGLIYL RYKCPDMHRP 420
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65 Seq ID NO: 9 DNA sequence
Nucleic Acid Accession #: FGENESH
Coding sequence: 1..546

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70
75

1 11 21 31 41 51
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CAGCTCGCG GTGCCCTCGA CCTGCCCGCT GGGTCTCTGT CTTTGAAGA GAGCACTTGC 240
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TTCGTGCTCT CAGGAGACAT GTCTGACTGG GACTACTGGG TTGGCTGGCG GAAGTTAATT 360
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CAGTTTGTCA AAGGCCAGAA CTTGGACGTA ACAGTGTACT GCAGGCTCCA GGGCAGTGAG 480
AAACCCCTTG AAACCTGGTC CATGGTTCCA TTCACCTTCA TGTACTGGAT CCACCATGGA 540
AAGTAG

Seq ID NO: 10 Protein Sequence
Protein Accession #: FGENESH

1 11 21 31 41 51
 5 MALGSSAPVA LQGNHFFPA FMAGIKLWL FQVPLGLPE LVQRLGGR TETRFVPAAL 60
 QLAGALDLP GSCAFESTC GFDSVLASLP WILNEEQQP FWSSGDMSDW DYVWGWKLI 120
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10 Seq ID NO: 11 DNA sequence
 Nucleic Acid Accession #: EOS sequence
 Coding sequence: 461-3286

15 1 11 21 31 41 51
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 20 GCGGCGGTTT TGAGCCGAGC CGGAACCTTA GCCCGAGACG GAGCCGGGGC CCGGCGCGGC 360
 GCCATTGCGC GGGCGCGCG GGAAGACCTT GCGCGGGGGC GCGCGCGCGC GCCAGGCCAT 420
 GCGGCGCGAG TGAGCGGGC CCGCGAGCCC CCGCGCGGCG ATGGCTTCCC CCGGAGCTC 480
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 45 ATTTACTCAA TTTCAGACA GCAGGAGGAT GAAGGTGGGA GAGTACAAGC CTGTGGCCGA 1800
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 60 CATCATCTTC TGACGACCA TCACTCTCTG CCTGGTATTC GTGCGAAGC TCATCACCTT 2700
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 65 ACAGAACCAAC TACCAAGAGC TCAATGACAT CCTCAACCTG GGAACCTTCA CTGAGAGCAC 3000
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Seq ID NO: 12 Protein sequence:
 Protein Accession #: EOS sequence

1 11 21 31 41 51
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 IMPLTKEVAK GSIGRGVLPA VELAIEQIRN ESLLRPYFLD LRLYDTECDN AKGLKAPYDA 120
 IKYGNHLMV FGVCPSVTS IIAESLQGNW LVQLSFAATT PVLADKKKYP YFFRTVPSDN 180
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 KKLKGNLVRI ILGQFDQNMMA AKVFCCAYEE NMYGSKYQWI IPGWYEPSWV EQVHTEANSS 300
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 GIWVIATLQ RAMETLHASS RHQRIQDFNY TDHTLGRIL NAMNETNFFG VTGQVVRNG 420
 ERMGTIKFTQ FQDSREVKVG EYNAVADTLE IINDTIRPOG SEPPKDKTII LEQLRKISLP 480
 LYSILSALTI LGMIMASAPL FPNIKNRNQK LIKMSSPYMN NLIILGGLMS YASIFLPLGLD 540
 GSFVSEKTFE TLCTVRTWIL TVGYTTAFGA MFAKTWRVHA IFKNVKKKKK IIKDQKLLVI 600
 VGGMLLDLC ILICQAVDP LRRTVEKYSM EPDPAGRDIS IRPLLEHCEN THMTIWLIV 660
 YAYKGLMLF GCFLAWETRN VSPALNDSK YIGMSVYVNG IMCIIGAAVS FLTRDQPNVQ 720
 FCIVALVIF CSTITLCLVP VPKLITLRTN PDAATQNRFF QFTONQKKED SKTSTSVTSV 780
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Seq ID NO: 13 DNA sequence
 Nucleic Acid Accession #: NM_001565.1
 Coding sequence: 67-363

1 11 21 31 41 51
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 TCGAAGGCCA TCAAGAAATT ACTGAAAGCA GTTAGCAAGG AAATGTCTAA AAGATCTCTC 360
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5 Seq ID NO: 14 Protein sequence:
 Protein Accession #: NP_001556.1

1 11 21 31 41 51
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15 Seq ID NO: 15 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 241..1272

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 40 TGCGAGAGCA CGGACCCAGA GTGTCCCGTC TGCCACATCA CAGCCACGCA AGCCATCCGA 1260
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Seq ID NO: 16 Protein Sequence
 Protein Accession #: XP_044166

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 YNNENDFLAG SPDAIDSRY SDAWRVHPG CKPLSTFRQN SLGICIGECV DSGFEPRLG 180
 EQGDFGYGG YLFPYGVGK QDVYVGAET SPPLWAGQEN ATPSTVLFSS ASSSSSSSAK 240
 ARAGPPGAHR SPATSAGPEL AGLPRRPGE PLQGFSLGG GGLRSPGGGR DCMVCFESEV 300
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Seq ID NO: 17 DNA sequence
 Nucleic Acid Accession #: NM_005940
 Coding sequence: 23-1489

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 TCTGCGCGCG GAGCTCCACC ACCTCCATGC CGAGAGGAGG GGGCCACAGC CCTGGCATGC 180
 AGCCCTGCCC AGTAGCCCGG CACCTGCCCC TGCCACCGAG GAAGCCCCCC GGCCTGCCAG 240
 CAGCCTCAGG CCTCCCCGCT GTGGCGTGCC CGACCATCT GATGGGCTGA GTGCCGCCAA 300
 CCGACAGAAG AGGTTCGTGC TTTCTGGCGG GCGCTGGGAG AAGACGGACC TCACCTACAG 360
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 CGACTATGAT GAGACCTGGA CTATCGGGGA TGACCAAGGC ACAGACCTGC TGCAGGTGGC 660
 AGCCCATGAA TTTGGCCAGC TGCTGGGGCT GCAGCACACA ACAGCAGCCA AGGCCCTGAT 720
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 TCGCCTCTGG CAGGACTGCG CCAGCCCTGT GAGCGCTGCC TTCGAGGATG CCGAGGGCCA 1080
 CATTGTGTTT TTCCAAGGTG CTCAGTACTG GGTGTACGAC GGTGAAAAGC CAGTCTGGG 1140

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CCTCTACTGG AAGTTTGACC CTGTGAAGGT GAAGGCTCTG GAAGGCTTCC CCCGCTCGT 1440
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GTAGACCAT GGCAGGACTG GGGGAACTGG AGTGTCTTGT CTGTATCCCT GTTGTGAGGT 1860
TCCTCCAGG GGTGGGACT GAAGCAAGGG TGCTGGGGCC CCATGGCCCT CAGCCCTGGC 1920
TGAGCAACTG GGTGTAGGG CAGGGCCACT TCCTGAGGTC AGGTCTTGGT AGGTGCTGTC 1980
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GTTACAGTGC AAATGGGGAG GGGTATTCTT CATGCAGGAG ACCCCAGGCC CTGGAGGCTG 2100
CAACATACCT CAATCTGTGC CCAGGCCGGA TCCTCTGAA GCCCTTTTTC CAGCACTGCT 2160
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TTTTAAACT GAGGATTGTC ATTAACACA GTTGTTTTCT
  
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Seq ID NO: 18 Protein sequence:
 Protein Accession #: NP_005931.1

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LVQEQVQRTM AEALKVMSDV TPLTFTEVHE GRADIMIDFA RYWHGDDLPF DPGGILAHA 180
FFPKTHREGD VHFDDYDETWT IGDDQGTDL LQVAHEFGHV LGLQHTTAAK ALMSAFYTFR 240
YPLSLSPDDC RGVQHLYGQP WPTVTSRTPA LGPQAGIDTN EIAPLEPDAP PDACEASFDA 300
VSTIRGELFF FKAGFVWLRL GGQLQPGYPA LASRHWQGLP SPVDAAPEDA QGHINFPQGA 360
QYVVYDGEKP VLGPAPLTEL GLVRFPVHAA LVWGPEKNKI YFFRGRDYWR FHPSTRRVD 420
FVPRRATDWR GVPSEIDAAF QDADGYAYFL RGRLYWKFPD VKVKALEGFP RLVGPDFFGC 480
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Seq ID NO: 19 DNA sequence
 Nucleic Acid Accession #: NM_005794.1
 Coding sequence: 434-1276

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CTTCACTCCT GGGGCCAGCA AGACCACGAA TGCACCGAGA GGAATGAACA ACTCTGACA 180
CACCATCTTT AAGAACCCTA ATACTCACCG CAAGGCTCTG CAACCTCATT CTTGAAGTCA 240
GTGAGGCCAA GAACCCATCA ATTCCGTACA CATTTTGGTG ACTTTGAAGA GACTGTACCC 300
TATCACCAAG TGGTGAGACT ATTGCCAAGC AGTGAGACTA TTGCCAAGTG GTGAGACCAT 360
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GCTGCCCTAC ATGGAGAACA GGAGGGGTGC TGTATCCTG GTCTCTTCCA TTGACGTTA 960
TAATCCAGTA GTGGCGCTGG GTGTCTACAA TGTACAGCA ACAGCGCTGC TGGGTCTCAC 1020
TAGAACACTG GCATTGGAGC TGGCCCCCAA GGACATCCCG GTAAACTGCG TGGTTCAGG 1080
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CAAGGAACAT CATCAGCTGC AGAGGATTGG GGAGTCAGAG GACTGTGCGA GAATCGTGT 1200
CTTCTGTGTC TCTCCAGATG CCAGCTACGT CAACGGGGAG AACATTGCGG TGGCAGGCTA 1260
CTCACTCGG CTCTGAGAGG AGTGGGGGGC GCTGCGTAGC TGTGTTCCCA GCCCAGGAGC 1320
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Seq ID NO: 20 Protein sequence:
 Protein Accession #: NP_005785.1

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1 11 21 31 41 51
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AGVNPVVGST LGTSEQIWDK ILSVNVKSPA LLLSQLLPYM ENRRGAVILV SSIAAYNPVV 180
ALGVYVNSKT ALLGLRTRTL LELAPKDIRV NCVVPGIIKT DPSKVPHGNE SLWKNFKEHH 240
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Seq ID NO: 21 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 77-904

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10     CACGATCAGC AATGTCCTAT TTTTCATTT ACCGCCATC TGCGATGTGCT TGTTCGTCA 240
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20     CTCAGAGATT CCTGAGCAAG GCCCTGTCTT CAAGTCTTGG CCCAATGAGA AATGGGCTTT 840
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25     CATATGGTAC AAATATTCCC TGCCCCCTG CAGTTTCCCA TTGTCTTTC AGTATGTTAA 1140
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40     GAAGAATTAT GGCATGAACA TTCCCAAGA CCCACCATCT TTAAGACTTG ACCTCTGTAA 1980
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Seq ID NO: 22 Protein sequence:
Protein Accession #: E0S sequence

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Seq ID NO: 23 DNA sequence
Nucleic Acid Accession #: CAT cluster

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CACAGAGTCA ATCAGATTCA AAATGTTAAA ATCCTTCCCTG CTTGGAGTTT TCCGCTTCCA 840
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Seq ID NO: 24 DNA sequence
Nucleic Acid Accession #: E0S sequence

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ACTACTTGGC CTCTGGGACT CAGATTCTCT CTCTTTAAAA TGGTGCTAAT AATAGCACCC 240
ACCTCTGTG AGGAGGATGC TGTGAGGACA AAATGAGATC ATCCACATAA GCCGTGAACC 300
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CCAACAGTCC CCATTCTACT TGCAGAAAGG TTGCTTACAC TGAATAACAG TTTATTTTCC 480
CCTGGTGCAA AGAACAGTCG TTTCTCCAAA ACTGAAGCTG GAAATTATCT GAAATATCAG 540
GTCTCCGGA AAAGGGACGT GAAGCCCTCT TTGTAATTTT TGCATTAGCG TGCTCTCCTG 600
GCAAGCAGGA AACCTCATCA GAGAAGTCAG CCAAGGAAAG TCTTTAAATG GAAATGTGTC 660
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Seq ID NO: 25 DNA sequence
Nucleic Acid Accession #: E0S sequence

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ACCTCTGTG AGGAGGATGC TGTGAGGACA AAATGAGATC ATCCACATAA GCCGTGAACC 300
CTGTTCCTGG TAAGGAAATG AATAACATGA AGTGAAGTCT TCATCTCCAT TCCCAACAGT 360
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5 GAAAAGGGAC GTGAAGCCCC CTTTGTAAAT TCTGCATTAG CGTGCTCTCC TGGCAAGCAG 540
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20 Seq ID NO: 26 DNA sequence
 Nucleic Acid Accession #: NM_013282.2
 Coding sequence: 85..2466

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Protein Accession #: NP_037414.2

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PECRNDASEV VLAGERLRES KKKAKMASAT SSSQDWDGKG MACVGRTEKC TIVPSNHYGP 420
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SGGRDLGSKN RTABQSCDQK LNTNRLALAL NCFAPINDQE GAEAKDWRSG KPRVVRNVK 540
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SPRRTSKKTK VEPYSLTAQQ SSLIREDKSN AKLWNEVLAS LKDRPASGSP FQLFLSKVEE 720
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Coding sequence:186..776

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10 Seq ID NO: 31 DNA sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 134..1917

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70 Seq ID NO: 32 Protein Sequence
Protein Accession #: XP_054631.1

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LGSCLDLVAP AQHGEPGLA QETALMSDN LLRVLDPLCL YRRLSAADRE RILSLRTGRG 180
RAVLGLVLVLP SLVQGGRRSL PRGPRGSEPP AAAPVSLPLP AHLHVFNPFE NTRPLTQVP 240
EEAPLRGCGL CTMNYLFLA GGIRGSGAKA VCSNEVFCYN PLTNISQVR PMQARAQLK 300
LVALDGLLYA IGGECLYSME CYDPRDAWT PRAPLPAGTF PVAHEAVACR GDIYVTGGHL 360
FYRLRLRSPV KDAWDECPYS ASHRRSSDIV ALGGFLYRFD LLRGVGAAMV RYNTVTGSWS 420

RAASLELPAP APLHCTTLGN TIYCLNPQVT ATFTVSGGTA QFQAKELQPF PLGSTGVLSF 480
FILTLPPEDR LQTSL

Seq ID NO: 33 DNA sequence
Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
CCTCTGTCTA ACCTTACATG AAAAAACCG TTTCCAACGA AGGCCTCTAA AAGCCAAGA 60
AATCCCCCTG CAGACTTTAC AAACAGAGTG TTTCTTAAC GCTCTATGAA CAGAAAGGTT 120
AAACTCTGTG AGTTGAACCA ACACATCACA ACGCAGTTTG TGGGAATGAT TCTGTCTAGT 180
TTTGAACCGA AGATATTTC TTTCTGCGG TTGACCTTAA AGCGCTTGAA ATCTACACTT 240
GCAAAATTGCA CAAATAGAGT GTTTCAAATC TGCTCTGTCT AAGGGAACGT TCAACTCTGT 300
GAGTTGAATG CACACAACAC AAGGAAGTTA CTGGGAATTC TTCTGTCTAG CCTTACATGA 360
AAGAAAACCC GTTTCACACG AAGGCCTCTA AGTGGTCAAA ATATCCACGT GCAGACTTTA 420
CAACAGAGAG GTTTCACAAAC TGCTGAATGA AAAGAAAAGT AAACCTCTAG AGTTGAACGC 480
ACACATCGCA GAGCAGTTTC TGAGAATGAT TCTGTCTAGT TTTTATACGA AGATATTTC 540
TTTTCTGCCT TTGGCCTCAA AGCGCTTGAA ATCTCCACTT GCAAAATCCA CAAAAAGAGT 600
GTTTCAAAATC TGCTCTGTCT AAAGGAAGGT TCAACTCTGT GAGTTGAATA CACACAACAC 660
AAAGAAGTTA CTGAGAAATC TTCTGTCTAG CATATATGTA AGAAATCCCG TTTCCAACGA 720
AGGCATCTAA GAGGTCCAAA TATCCACTTG CAGACTTTAC AAACAGAGGG TTTCCAGAAT 780
GGCTGTATGA AAAGAAAGGT TAAACTCTGT GAGTTAAACA CACA

Seq ID NO: 34 DNA sequence
Nucleic Acid Accession #: AF011468.1
Coding sequence: 257..1468

1 11 21 31 41 51
GGAAGACTTG GGTCTTGGG TCGCAGGTGG GAGCCGACGG GTGGGTAGAC CGTGGGGGAT 60
ATCTCAGTGG CGGACGAGGA CGGCGGGGAC AAGGGGCGGC TGTCGAGAGT GCGGAGCGT 120
CAAGTCCCTT GTCGGTTCTT CCGTCCCTGA GTGTCTTGG CGCTGCCTTG TGCCCGCCCA 180
GCGCCTTTGC ATCCGCTCCT GGGCACCAGG GCGCCCTGTA GGATAGTCTT TGTACTTAT 240
TACAGCTAGA GGCATCATGG ACCGATCTAA AGAAAACTGC ATTTCAAGAC CTGTTAAGGC 300
TACAGCTCCA GTTGGAGGTC CAAAACGTGT TCTCGTGAAT CAGCAAAATC CTGTGTCAGAA 360
TCCATTACCT GTAATAGTGT GCCAGGCTCA GCGGGTCTTG TGTCCTTCAA ATTCTTCCA 420
GCGGTTCTCT TTGCAAGCAC AAAAGCTTGT CTCCAGTCAC AAGCGGTTTC AGAATCAGAA 480
GCAGAAGCAA TTGCAAGCAA CCAAGTGTACC TCATCCTGTC TCCAGGCCAC TGAATAACAC 540
CCAAAAGAGC AAGCAGCCCC TGCCATCGGC ACCTGAAAAA AATCCTGAGG AGGAACCTGGC 600
ATCAAAACAG AAAAATGAAG AATCAAAAAA GAGGCAGTGG GCTTTGGAAG ACTTTGAAAT 660
TGCTCGCCCT CTGGGTAAAG GAAAGTTTGG TAATGTTTAT TTGGCAAGAG AAAAGCAAAG 720
CAAGTTTATT CTGGCTCTTA AAGTGTATT TAAAGCTCAG CTGGAGAAAG CCGGAGTGA 780
GCATCAGCTC AGAAGAGAAG TAGAAATACA GTCCACCTT CCGCATCCTA ATATTCTTAG 840
ACTGTATGGT TATTTCCATG ATGCTACCAG AGTCTACCTA ATCTGGAAT ATGCACCACT 900
TGGAACAGTT TATAGAGAAC TTCAGAAACT TTCAAAGTTT GATGAGCAGA GAACTGCTAC 960
TTATATAACA GAATTTGGCA ATGCCCTGTC TTACTGTCTT TCGAAGAGAG TTATTGATAG 1020
AGACATTAAAG CCAGAGAACT TACTTCTTGG ATCAGCTGGA GAGCTTAAAA TTGCAGATTT 1080
TGGTGTGCTA GTACATGCTC CATCTTCCAG GAGGACCACT CTCTGTGGCA CCGTGGACTA 1140
CCTGCCCCCT GAAATGATTG AAGTCTGGAT GCATGATGAG AAGGTGGATC TCTGGAGCCT 1200
TGGAGTTCTT TGCTATGAAT TTTTAGTTGG GAAGCCTCCT TTTGAGGCAA ACACATAACA 1260
AGAGACCTAC AAAAGAATAT CACGGTGTGA ATTCACATTC CCTGACTTTG TAACAGAGGG 1320
AGCCAGGGAC CTCATTTCAG GACTGTGTA GCATAATCCC AGCCAGAGGC CAATGCTCAG 1380
AGAAGTACTT GAACACCCCT GGATCACAGC AAATTCATCA AAACCATCAA ATTGCCAAAA 1440
CAAAGAATCA GCTAGCAAAC AGTCTTAGGA ATCGTGACGG GGGAGAAATC CTTGAGCCAG 1500
GGCTGCCATA TAACCTGACA GGAACATGCT ACTGAAGTTT ATTTTACCAT TGAATGCTGC 1560
CCTCAATCTA GAACGCTACA CAAGAAATAT TTGTTTTACT CAGCAGGTGT GCCTTAACT 1620
CCCTATTTCAG AAAGCTCCAC ATCAATAAAC ATGACACTCT GAAGTGAAAG TAGCCACGAG 1680
AATTGTGCTA CTTATACTGG TTCAATATCT GGAGGCAAGG TTCAGATGCA GCCGCCCGGT 1740
CAGCCTGTGC TAGGCATGCT GTCTTACAG GAGGCAAAATC CAGAGCCTGG CTGTGGGGAA 1800
AGTGACCACT CTGCCCTGAC CCGGATCAGT TAAGGAGCTG TGCAATAACC TTCTAGTAC 1860
CTGAGTGAGT GTGTAACCTA TTGGGTTGGC GAAGCCTGTT AAAGCTGTTG GAATGAGTAT 1920
GTGATTCTTT TTAAGTATGA AAATAAAGAT ATATGTACAG ACTTGATATT TTTCTCTGTT 1980
GGCATTCTCT TAGGAATGCT GTGTGTCTGT CCGGCACCCC GGTAGGCTGT ATTGGGTTTC 2040
TAGTCTCTCT TAACCACTTA TCTCCATAT GAGAGTGTGA AAAATAGGAA CACGTGCTCT 2100
ACCTCCATTT AGGGATTTCG TTGGGATACA GAAGAGGCCA TGTGTCTCAG AGCTGTTAAG 2160
GGCTTATTTT TTTAAACAT TGGAGTCATA GCATGTGTGT AAACCTTAAA TATGCAATA 2220
AATAAGTATC TATGTCTAAA AAAAAAAAAA AAA

Seq ID NO: 35 Protein Sequence
Protein Accession #: AAC63902.1

1 11 21 31 41 51
MDRSKENCIS GPVKATAPVG GPKRVLVTQO IPCQNPLFVN SGQAQRVLCF SNSSQVRVPLQ 60
AQKLVSSEHKP VQNKQKQLQ ATSVPHVPSR PLNNTQKSKQ PLPSAPENNP EELASKQKN 120
EESKKRWAL EDPEIGRPLG KKGKFNVYLA REKQSKFILA LKVLFPKALE KAGVEHQLRR 180
EVEIQSHLRH PNILRLYGYF HDATRVYLIL EYAPLGTVYR ELQKLSRPFDE QRTATYITEL 240
ANALSYCHSK RVIHRIKPE NLLGSGAGEL KIADEFGSVH APSSRRRTLC GTLDYLPPEM 300

IEGRMHDEKV DLNSLGLVLCY EFLVGKPPFE ANTYQETYKR ISRVEFTFPD FVTEGARDLI 360
 SRLLLKHNFSQ RPNMLREVLEH PWITANSSKP SNCQNKESAS KQS

Seq ID NO: 36 DNA sequence
 Nucleic Acid Accession #: NM_016267
 Coding sequence: 67..843

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1      11      21      31      41      51
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10 CGGCACGAGG ACAGAATCAG GTGATGGTCC AGAATTAAGA GCTGTCACTT GTGTCAATTCA 60
    CTCACAATGG AAGAAATGAA GAAGACTGCC ATCCGGCTGC CCAAAGGCCA ACAGAAGCCT 120
    ATAAAGACGG AATGGAATTC CCGGTGTGTC CTTTTCACTT ACTTCCAAGG GGACATCAGC 180
    AGCGTAGTGG ATGAACACTT CTCCAGAGCT CTGAGCAATA TCAAGAGCCC CCAGGAATTG 240
    ACCCCCTCGA GTCAGAGTGA AGGTGTGATG CTGAAAAACG ATGATAGCAT GTCTCCAAAT 300
15 CAGTGGCGTT ACTCGTCTCC ATGGACAAAG CCACAACCAG AAGTACCTGT CACAAACCGT 360
    GCGGCCAACT GCAACTTGCA TGTGCCTGGT CCCATGGCTG TGAATCAGTT CTCACCGTCC 420
    CTGGCTAGGA GGGCCTCTGT TCGGCCTGGG GAGCTGTGGC ATTTCTCTCT CCTGGCGGGC 480
    ACCAGCTCCT TAGAGCCTGG CTACTCTCAT CCCTTCCCGG CTCGGCACCT GGTTCACAGAG 540
    CCCAGCCTG ATGGGAAACG TGAGCCTCTC CTAAGTCTCC TCAGCAAGA CAGATGCCTA 600
20 GCCCGTCCTC AGGAATCTGC CGCCAGGGAG AATGGCAACC CTGGCCAGAT AGCTGGAAGC 660
    ACAGGGTTCG TCTTCAACCT GCCTCCCGCG GAAACTCTTT CAGAGTTAGA GACACCTGGG 720
    CGTGGATCTG CCAGTACCCG CCTTCCAAAT GAAACTCTTT CAGAGTTAGA GACACCTGGG 780
    AAATACCTAC TTACACACCC AAACCACTGG GGCCACCCAC ATCGATACCT GCAGCATCTT 840
    TAGTCAAGTT GAGGAGAGAA GACAACACTT GGTCTAAGAC ACGGCAGCAA GACATCCCTG 900
25 CATATTGTTT CAGATAAAAA TGAAAGCTGC TCACACCCAC TTGCTCTCCC AATCTGTTAA 960
    ACAGCTTCGT GTCTAGTATG AGCTCAGTAC TTGCTCTGTG AAAATCCGAG AAGCCCCGCG 1020
    TGTCAATGTT CCCATCCAC ACCCTGCTTG CTCCTGTGTA ACAGCTCAGA TGATGAATAA 1080
    TAATAAACT GTACTTTTTT GGAAAAAATA AAAAAAATA AAAAAA 1080
  
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Seq ID NO: 37 Protein Sequence
 Protein Accession #: NP_057351.1

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1      11      21      31      41      51
|      |      |      |      |      |
35 MEEMKKTAIR LPKGKQKPIK TEWNSRCVLF TYPQGDISSV VDEHFSRALS NIKSPQELTP 60
    PSSQSEGVML KNDDSMSPNQ WRYSSPWTKP QPEVPVTNRA ANCNLHVPGP MAVNQFSPSL 120
    AARRASVRPG ELWHFSSLAG TSSLEPGYSH PFPARHLVPE PQPDGKREPL LSLLLQDRCL 180
    ARRPQESAAR ENGNFGQIAG STGLLPNLPP GSVHYKLYV SRGSASTSLP NETLSELETP 240
40 GKYYSLTPPN HWGHPRYLQ HL
  
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Seq ID NO: 38 DNA sequence
 Nucleic Acid Accession #: AK058088.1
 Coding sequence: 252..1772

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45 1      11      21      31      41      51
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    AGGAAACCAA GGCAAGCTCC CCTGTCAAA GCACCTTGGC CCATAAGAAG AAAAGGGGGA 60
    GCCCAGATG TGATGAGCGC TTCCAGGCTT CAGGCTCAGA AGGCGCCCCC AGCTCTCCTG 120
    TAATCTCAGG GCGAGTGTGA TGGAGTTCC TCCACTCAGC ACACTTCCCC TGTAAACACG 180
50 CCTGTGTGGG GCAAAGGGG TTTGGAACGG TTGCTTGTCT TTTCTCTCCT GCGTAATTTC 240
    CACTTTCAAT CATGATAATG TCGAACAACG ACAAGCTCG GCTGGAACGC CGGTCACCTG 300
    GCTCAACCAA CCGGTGGCGT TTGCCCAAAC AGCCTTTCTC TGGGACCTG CTCTCACTTT 360
    CCCAGATGTG CAAGGCTCTG AGCATAGACT TTGAGGAAGC TTTGAGGAAC CCAGACAGGT 420
    TATGCATTTT ACAAATCCAG AAGTTTTTCT TTGAGAATTT CAAGAACAAG GACATCCAAA 480
55 GTGGGAAGC AGATGTGATT CTCGAGTCCC TGGGCTTCAA ATGGGAGCTC CATCAGCCCC 540
    GGCTTTTTCA GTCTGAGACC TTGGCCAAGC TCTACCTGAA AGCCCTGGCG CAGGGCACCA 600
    CACACCCCTT GAGGGAGCTG GAGGAGCTTC TGCGAGCTCA ATCACCCTAG AAGACCAAAG 660
    AAAAATCCCC TGCAAGAGG ATCATCATTT CCTTGAAGAT CAATGACCCA CTGGTCACTA 720
    AAGTGCCTTT CGCCACGGCC CTGAAGAACC TCTACATGAG TGAGGTGGAG ATTAACTTGG 780
60 AAGACCTACT GGGAGTGTG GCTTCCGCCC ACATCTCCCA GTTCAGTGGC CTGTTTCAAA 840
    GGTGCGTGGG TGTGATGATA GCCAGACTCA AGCCAAGCAC CATCAAGAAA TTCTACGAGG 900
    CCGGCTGCAA GTACAAGGAA GAGCAGCTCA CCACCGGCTG CGAGAAGTGG CTGGAATGA 960
    ACTTGGTTCC TCTAGGGGGG ACGCAGATCC ACCTCCACAA AATCCACAG GACTGTCTCC 1020
    ACAAAGTGCT GAAGTCCCCC AGGTTATTTA CCTTTAGTGA ATTCCATCTT CTGAAAACAA 1080
65 TGCTTTTGTG GGTCTTCTTG CAACTGAAC ACAAAGTTCA GGCAATTCCG ACTTATGAAA 1140
    CGTGATGAC ATTTTAAAG AGCTTTCTCT AGAAGTGTG CTCTCTGGAC CGGACATAG 1200
    GACGGAGCTT GAGGCGCTC TTCTCTGCT TGCGTCTGCA CGGCTCAGC AAAGGCAAGG 1260
    ATCTGGAGGT GCTGCGGCAC CTTAACCTCT TCCAGAGTC ATGGCTCGAC CAGGTACAG 1320
    TCAACCATTA CCACGACTG GAGATGGGG GCGACATGGT CCACCTGAAA GATCTTAACA 1380
70 CCCAGGCTGT GAGATTGGG CTGCTCTTTA ACCAGGAGAA TACAATTAT TCGAAAAACA 1440
    TGCTCTATA TGGATTCTTC TTTAAGATAA AGGAGTCAA ACATGATACT ACCTCTTATA 1500
    GTTTTACAT GCAGAGAATA AAGCACACAG ACCTGGAATC TCCTCTGCG GTCTACGAGC 1560
    ACAACACGT CAGCCTGCGA GCGCACGCC TGGTGAAGTA TGAGATCAGA GCAGAGGCC 1620
    TGGTTGACGG CAAGTGGCAG GAGTTCAGGA CAAACAGAT CAAGCAGAAG TTTGGGTGA 1680
75 CCACGTCATC CTGCAAAAGC CATACCTTGA AAATCCAAC TGTGGGCAT CCAATCTATG 1740
    TAAGTTTTCG ATTCATCTTC CCAGCATCTT GACAGTTTCC AGAAGATCT ATGGGATTTT 1800
    CCCCCACTG GTCTGCATAA AAGAAATAA AATGACATAA AAGGGAGC
  
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Seq ID NO: 39 Protein Sequence
Protein Accession #: BAB71658.1

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5 1 11 21 31 41 51
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MIMSNTHKAR LERRVTGSTN RWRLPKQPF S DLLSLSQMC KALSIDFEEA LRNPDRLCIS 60
QIQKFFFFNF KNKDIQSSEA DVILECLGPK NELHQPRLFQ SBTAKLYLK ALAQGTTTHPL 120
RELEELLRAQ SPKTKYKESP AKRIIISLKI NDPLVTKVAF ATALKNLYMS EVEINLEDLL 180
GVLASAHILQ FSQLPQRCVD VMIA RLKPST IKKPYEAGCK YKEEQLTTGC EKWLEMLNVP 240
10 LGGTQIHLHK IPQDLLHKVL KSPRLFTFSE FHLLKTMLLW VFLQLNYKIQ AIPTYETVMT 300
FFKSFPFENC FLDRDIGRSL RPLFLCLRHL GITKGKOLEV LRHLNFPFES WLDQVTVNHY 360
HALENGGDMV HLKDLNTQAV RFGLLFNQEN TTYSKTIALY GFFFKIKGLK HDTTSYSFYM 420
QRIKHTDLES PSAYVEHNVH SLRAARLVKY EIRAEALVDG KWQEFRTNQI KQKFGTTSS 480
15 CKSHTLKIQT VGPIYVSFA FIFPAS
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Seq ID NO: 40 DNA sequence
Nucleic Acid Accession #: NM_032899.1
Coding sequence: 186..1070

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20 1 11 21 31 41 51
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GGCACGAGGA TTGCTCAGGA CAGCGGTAAA TCACTTCTTG GAGGTGCCCT GCACGCCGGT 60
CCTGGGAGCA GCGCGCTCC CCGGGGTGCG GGAGCCCCAC TCCTCCGTGG TGTGTTCCAT 120
TTGCTTCCCA CATCTGGAGG AGCTGACGTG CCAGCTCCCC CCAGCACCA CAGGGACGCG 180
25 GAGGCATGAG CCGGTCAAGG CACCTGGGCA AAATCCGGAA GCGTCTGGAA GATGTCAAGA 240
CCGAGTGGGT CCGGCCAGCC AGGGCTGACT TTAGTGACAA CGAGAGTGCC CGGCTGGCCA 300
CGGACGCCCT CTTGATGGG GGTCTGAAG CCTACTGGCG GGTGCTCAGC CAGGAAGGCG 360
AGGTGGACTT CTGTCTCTCG GTGGAGGCC AGTACATCCA GGCCAGGCC AGGGAGCCCC 420
CGTGTCCCCC AGACACCTCT GGAGGGGCGG AAGCAGGCC TAAGGGACTG GACTCCAGCT 480
30 CCTACAGTC CGGCACCTAC TTCCCTGTGG CCTCAGAGGG CAGCGAGCCG GCCCTACTGC 540
ACAGCTGGGC CTAGCTGAG AAGCCCTACC TGAAGGAAA ATCCAGGCC ACTGTGTACT 600
TCCAGACCTG CAGACCAAC AACATCAGAG ACCTCGTCC CCGCTGCATC ACCCGGACTA 660
GCCAGAACAT TTCCATCCCG AGTGTGGAAG GAGAGATATA CTGTGCCAAG TCAGGCAGGA 720
AATTCACCTG CCAAATCCCG GAGAAGTTCA TCATCTCGGA CTGGAGATT GTCTGTCTG 780
35 GATCTTACAG CTTCACCTGG CTCTGCGAC ACGTGACCG GAAACATCCT TCCAAGTTCA 840
CAGGCCAGGC GGTGAGCTG TTGACGAGG AGTTCCGCCA CCTCTACGCC TCCTCCAAGC 900
CTGTGATGGG CCTGAAGTCC CCGCGCTGG TCGCCCCGT CCGGCCCGGA GCAGCCCCGG 960
CCAATGGCCG CCTTAGCAGC AGCAGTGGCT CCGCCAGTGA CCGCACGTCC TCCAACCCCT 1020
40 TCAGCGCCCG CTCGGCAGGC AGCCACCCCG GTACCCGAAC TGACGGGTGA GATGAGGTTA 1080
GAATGACTGG GCCCGGCTGA ACATTCCAAA TTGGATTTC CCATCTGCTG AGAAAGTTA 1140
AGGAAGCAAA AGCTTGCCAG GTACAGAAAG CTCCTAAGCC CAGCTTTCCA AAGGCTCAG 1200
CCTGTGCTGG TGTCGAGCTC AGTCTGGGA GATAGGGGAG AACCTGCAGG CAGGAACAAG 1260
CTGTGCTGGT TGTCGAGCTC AGTCTCCCT CCGTGGTCTG CTTTGTGAG 1320
45 CCCCCTACT CTGACCAACC CTCCATCAGC AGTCTCCCT CCGTGGTCTG CTTTGTGAG 1380
AAAGGTGAGC TTTCTCTCTC CTGGGCACC TGTAACATGT GATGCGCTGC CTGCTGGGAG 1440
GTTAGTTCGG GCTGCGCCCG GCGAGTGGAG CATGAGCAGA ACCGCGAGG GTCACTTCTG 1500
GGCAGAGCTC TTGAGAGCTT GGGTCCAGGT TGCCACATAG AAGCAGCTCT CCAGTTGAAA 1560
CCCTCTCTG CCAGCTGGG GTCTTAAGC ATGAGCAGAA TCCCCACTC CCACCCACC 1620
50 AACCACAAT GGATATGTAG TGAGCAAGAA ATAAACCTTT GTTGTTTAAA AAAAAAAAAA
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Seq ID NO: 41 Protein Sequence
Protein Accession #: NP_116288.1

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55 1 11 21 31 41 51
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MSRSRHLGKI RKRLDVDKSO WVRPARDFS DNESARLATD ALLDGGSEAY WRVLSQEGEV 60
DFLSSVEAQY IQAQAREPPC PPDTLGGAEA GPKGLDSSSL QSGTYFFVAS EGSEPALHLS 120
WASAEKPYLK EKSSATVYFQ TVKHNIRDL VRRCITRTSQ NISIRSVEGE IYCAKSGRKF 180
60 TGQIREKPII SDWRPVLSSG YSPTWLCGHV HRNLSKFTG QAVELFDEEF RHLVASSKPV 240
MGLKSPRLVA PVPPGAAPAN GRLSSSSGSA SDRSSSNPFS GRSAGSHPGT RTDG
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Seq ID NO: 42 DNA sequence
Nucleic Acid Accession #: NM_000782.2
Coding sequence: 405..1946

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65 1 11 21 31 41 51
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70 TTTCCCTTTT CAAGAGGTAC CCAGACACC GGCCACCTTC TTCCAGCCCC TGCGGCCAGT 180
GCAAGGAGGC ACCAATGCTC TGAGGCTGTC GCGTGTGTGA GCGTCGAGCA TCCTCGCGGA 240
GTCTCTCTGC TGCTGTCTCC AGCCCCGACT CCCACTAGCA CCTCGTACCA ACCTCGCCCC 300
TCTTTTCCC AGAATGTTA AGCCCCGACT CCCACTAGCA CCTCGTACCA ACCTCGCCCC 360
75 ACCCCATCCT CTGCTCTGCC CGCGCTCCGG TGTCCCCCGC TGCCATGAGC TCCCCCATCA 420
GCAAGAGCCG CTGCTTGCC GCCTTCTGCG AGCAGCTGCG CAGTCCGAGG CAGCCCCGA 480
GACTGTGTAC ATCTACGGCG TACACGTCCC CTCAGCGCGG AAGAGGTGCA GTCTGCCCCG 540
TGACAGCTGG TGGCGAGACT CAGAACGCGG CCGCCTGCCC GGGCCCCACC AGCTGGCCAC 600
TGCTGGCGAG CCTGCTGCAG ATTCTCTGGA AAGGGGTCT CAAGAAACAG CACGACACCC 660
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5	TGGTGGAGTA	CCACAAGAAG	TATGGCAAGA	TTTCCGCGAT	GAAAGTTGGGT	TCCTTTGAGT	720
	CGGTGCACCT	GGGCTCGCCA	TGCCTGCTGG	AAGCGCTGTA	CCGCACOGAG	AGCGTACCCC	780
	AGCGGCTGGA	GATCAAAACG	TGGAAGGCCT	ATCGCGACTA	CCGCAAGAGAA	GGCTACGGGC	840
	TGCTGATCCT	GGAGGGGGAA	GACTGGCAGC	GGGTCCGGAG	TGCCTTTCAA	AAGAACTAA	900
	TGAAACCAGG	GGAGGTGATG	AAGCTGGACA	ACAAATCAA	TGAGGTCTTG	GCCGATTTTA	960
	TGGGCAGAAT	AGATGAGCTC	TGTGATGAAA	GAGGCCACGT	CGAAGACTTG	TACAGCGAAC	1020
	TGAACAAATG	GTCTTTTGAA	AGTATCTGCC	TCGTGTTGTA	TGAGAAGAGA	TTTGGGCTTC	1080
	TCCAGAAAGAA	TGCAGGGGAT	GAAGCTGTGA	ACTTCATCAT	GGCCATCAAA	ACAATGATGA	1140
	GACGCTTTGG	GAGGATGATG	GTCACCTCCAG	TCGAGCTGCA	CAAGAGCCTC	AACACCAAGG	1200
10	TCGCGCAGGG	ACACACTCTG	GCCTGGGACA	CCATTTTCAA	ATCAGTCAAA	GCTTGTATCG	1260
	ACAACCGGTT	AGAGAAGTAT	TCTCAGCAGC	CTAGTGCAGA	TTTCCTTTGT	GACATTTATC	1320
	ACCAGAATCG	GCTTTCAAAG	AAAGAATTGT	ATGCTGCTGT	CACAGAGCTC	CAGCTGGCTG	1380
	CGGTGGAAC	GACAGCAAA	AGTCTAATGT	GGATTCTCTA	CAATTTATCC	CGTAATCCCC	1440
	AAGTGCACCA	AAAGCTTCTT	AAGSAAATTC	AAAGTGTATT	ACCTGAGAAT	CAGAGGCCAC	1500
15	GGGAGGAAGA	TTTGAGGAAT	ATGCGGTATT	TAAAGCCCTG	TCTGAAAGAA	TCTATGAGGC	1560
	TTACCCGGGG	TGTACCATTT	ACAACCTCGA	CTCTTGACAA	GGCAACAGTT	CTGGGTGAAT	1620
	ATGCTTTACC	CAAAGGAACA	GTGCTCATGC	TAAATACCCA	GGTGTGGGA	TCCAGTGAAG	1680
	ACAATTTTGA	AGATTCAAGT	CAGTTTAGAC	CTGAACGTTG	GCTTCAGGAG	AAGGAAAAAA	1740
	TTAATCCTTT	TGCGCATCTT	CCATTTGGCG	TTGSAAAAAG	AATGTGCATT	GGTGGCCGAT	1800
20	TAGCAGAGCT	TCAACTGCAT	TTGGCTCTTT	GTGGAATTGT	CCGCAATAC	GACATCCAGG	1860
	CCACAGACAA	TGAGCTGTGT	GAGATGCTAC	ACTCAGGCAC	CCTGGTGCCC	AGCCGGGAAC	1920
	TCGCCATCGC	GTTTTGCCAG	CGATAATACG	CCTCAGATGG	TGGTATTTGC	TAACATCATA	1980
	TCCAACCTCAG	GGAGGGGAC	TGAGTGCTGG	GATCCAAGGC	ATTCTACAGG	GTTCACCTGT	2040
	GGTTTACACT	TCACCTGTGT	CAGCACCATC	TTCAAGTGCT	TAGAAATGGC	TGGGAGCCTG	2100
25	TTCTGTCTTG	CATCTCCAT	GACATGAAAG	GGAGGCTGGC	ACTTGTCACT	CAGGTAGAGG	2160
	TTACAAACCG	TTTCAGGCCC	TGCTACCACA	TTCACTGTTT	GAATCTTTAA	TTCCCAAGAA	2220
	TAAGTTTACA	TGTCACAATG	AATGACCTAC	AACAGCTAAA	TTTTCTGGGG	CTGGGAGTAA	2280
	TACTGACAA	CCATTACTGT	TAGCTCTGCT	TAATGTACTA	CTTAGGAAAA	TGTCCTGTCT	2340
	TAATAATGTA	AGCCAGCTTA	AATGATGGTT	AAAGTTATCA	GGCCTCCCAT	GAATTTGGGT	2400
30	TCTTCTGCA	TTGAAATAAA	AACATTATTG	GGAACTAGA	GAAACCTCT	ATTTTAAAA	2460
	GGACTTTAAC	GAACTCAAA	AACCTCTAAG	ACTAGTGATT	CAGTGGGGCA	TTATTTGTTA	2520
	GAGGACCTTA	AAATTTGTTA	TTTTTTAAAT	GTGATTCCTT	TATGGCATT	GGGTAAAGAT	2580
	GAAGCAATAA	TTTTTAAAT	GTGTATGTGC	ATATGAAGCA	CAGACATGCA	TGTGTGTGTG	2640
35	TGTCTGTGTG	TGTGTGTCG	TGTATGTGTG	TGTGGGTTCT	AATGGTAATT	TGCCTCAGTC	2700
	ATTTTFTTAA	TATTTGTCAGT	ACTTGATTTA	GGATCTGTGG	TGCAGGGCAT	GTTCCAAAGT	2760
	TTAGTCACAG	CTTAAAAACA	TTCACTGTGA	CTTTAATATT	ATAAAATGAT	TTCCCATGCC	2820
	ATAATTTTTC	TGTCCTATTAA	ATGGGACAAG	TGTAAAGCAT	GCAAAAGTTA	GAGATCTGTT	2880
	ATATAACATT	TGTTTTGTGA	TTTGAATCC	TAGGAAAAAT	ATGATTTTCA	AAATGTAAAA	2940
40	TGCACAGAAA	TGCATGCAAT	ACTTATAAGA	CTTAAAAATT	GTGTTTACAG	ATGGTTTATT	3000
	TGTGCATATT	TTTACTACTG	CTTTTCTTAA	ATGCATACCT	TATATAATTC	TGTGTATTGT	3060
	ATAAATATTT	CTTCTCATAT	TATATTTTAA	GAATATTTCA	GAAATATACA	TTTATGTCTT	3120
	TATATTGTAA	TAAATATGTA	CATATCTAGG	TATATGCTTT	CTCTCTGCTG	TGAAATTTAT	3180
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45	GTAAAAATAA	AAGTTTTTAA	ATATT				

Seq ID NO: 43 Protein Sequence
Protein Accession #: NP_000773.1

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	MSSPISKSR	LAFLQQLRS	PRQPPRLVTS	TAYTSPQPRE	VPVCPITAGG	ETQNAALPG	60
	PTSWPLLASL	LQILNKGLK	KQHDTLVEYH	KRYKIFRMK	LGSFBSVHLG	SPCLLEALYR	120
	TESVPQRL	KPWKAYRDYR	KEGYGLLILE	GEDWQVRSA	FQKMLMPKPE	VMKLDNKINE	180
	VLADEFMGRID	ELCDEHGHVE	DLYSELNKKWS	FESICLVLYE	KRFGLLQKNA	GDEAVNFIMA	240
55	IKTMMSTFGR	MMVTPVELHK	SLNTKVMQGH	TLAWDTIFKS	VKACIDNRLE	KYSQQPSADF	300
	LCDIYHQNRL	SKKELYAAVT	ELQLAAVETT	ANSLMWILYN	LSRNPQVQQK	LLKBIQSVLP	360
	ENQRPREDL	RNMPYLKACL	KESMRLTPGV	PFTTRTLDKA	TVLGEYALPK	GTVLMMLTQV	420
	LGSSDNEFED	SSQFRPERWL	QEKEKINPFA	HLFPVGVKRM	CIGRRLEALQ	LHLALCWIVR	480
60	KYDIQATDNE	PVEMLHSGTL	VPSRELPIAF	CQR			

Seq ID NO: 44 DNA sequence
Nucleic Acid Accession #: NM_007000.2
Coding sequence: 1-777

65	1	11	21	31	41	51	
	ATGGCGTCTG	CGGCAGCAGC	GGAGGCCGAG	AAGGGATCTC	CAGTTGTGGT	GGGCCTGCTA	60
	GTGTGGGCA	ATATCATTAT	TCTGCTGTCA	GGCCTGTCCC	TGTTTGCTGA	GACCATATGG	120
	GTGACAGCCG	ACCAGTACCG	TGTATACCCA	CTGATGGGAG	TCTCAGGCAA	GGATGACGTC	180
70	TTGCTGGTGG	CCTGGATTGC	CATCTTCTG	GGCTTCTCCT	TCTTCATGGT	AGCCAGTTTT	240
	GGTGTGGGTT	CCGCACTCTG	CCGCCGCCGG	TCCATGGTCC	TCACTACCT	GGTGCTCATG	300
	CTCATGTCCT	ACATCTTCTG	GTGCGCCTCC	TGCATCACTG	CCTACACCCA	CGTGACTAC	360
	ATGGTGTCCA	ACCCATCCCT	GATCACCAG	CAGATGCTGA	CCTTCTACAG	CGCGGACACC	420
	GACCAGGGCC	AGGAGCTGAC	CCGCCCTCGG	GACCGGTC	TGATTGAGCA	AGAATGCTGT	480
75	GGCACATCTG	GTCCCATGGA	CTGGGTGAAC	TTACGCTCAG	CCTTCCGGGC	GGCCACTCCG	540
	GAGGTGGTGT	TCCCTGGCC	CCCACTGTGC	TGTGCGCGGA	CGGGAACTT	CATCCCCCTC	600
	AACGAGGAGG	GCTGCCCTCT	GGGGCACATG	GACTACCTGT	TCACCAAGGG	CTGCTTCGAA	660
	CACATCGGCC	ACGCCATOGA	CAGCTACAG	TGGGGTATCT	CGTGGTTTGG	GTTTGCCATC	720

5 CTGATGTGGA CGCTCCCGGT CATGCTGATA GCCATGTATT TCTACACCAT GCTCTGAGGG 780
 ACAGGAGGGG AAGGCAACAT ACACACCCCG GACTCCTCCG CATCCTCCTC CTGCTTCCTC 840
 CGCTGGGCTT GGATGGCTGC CTCACCTCTC ACCTCCCAAC GTCCCTAGCC CTACGCTCCT 900
 TCCACTTCCA AGATCTTTT CCAGGTTCTT GAGCCCTACT GTGTCTCAGG TGTGCCCTGA 960
 AACCCACGGG CTGTGTGTGA CATATCCTTA GCCCATCTTT CAAGGGACCT CTCCATGATC 1020
 CCACCTCCCA TTCACAGATA CCTCTCTGT AGCTCTCTGA CCTCCTCCTT CATGGCAGGC 1080
 ATGCCCATTC TTGCTGAACC GTTTGTGATT GCCATTGAG CTCTGGAAGC CTCTATTGCC 1140
 ATGAGAGTTC TGTACGGTTC ACTTTACTGT CCCCATCATC ACCCAGCAGC GGGCTAAGCA 1200
 TATACATAGAT AGTCAATAAA TAA

Seq ID NO: 45 Protein sequence:
 Protein Accession #: NP_008931.1

15 1 11 21 31 41 51
 MASAAAAEAE KGSFVVVGLL VVGNIIILLS GLSLFAETIW VTADQYRVYP LMVSGVKDDV 60
 FAGAWIAIFC GFSFFMVASF GVGAALCRRR SMVLTYLVLM LIVIYIPECAS CITSYTHRDY 120
 MVSNPSLITK QMLTFYSADT DQGQELTRLW DRVMIEQECC GTSGPMDWVN FTSAFRAATP 180
 20 EVVFPWPLLC CRRTGNFIPL NEEGCRLGHM DYLFTKGCFE HIGHAIDSYT WGISWFGFAI 240
 LMWTLFVMLI AMYFYITML

Seq ID NO: 46 DNA sequence
 Nucleic Acid Accession #: NM_006760.1
 Coding sequence: 39..593

25 1 11 21 31 41 51
 GAAAGCCTGC CAGCACCTAT TCCACCTCCC AGCCACGAT GGCACCCCTG CTGCCCATCC 60
 30 GGACCTTGCC CTGTGATCCTG ATTTCTGCTGG CTCTGCTGTC CCCAGGGGCT GCAGACTTCA 120
 ACATCTCAAG CCTCTCTGGT CTGCTGTCTCC CGGCGCTAAC GGAGAGCCTG CTGGTTGCCT 180
 TGCCCCCCTG TCACCTCACA GGAGGCAATG CCACACTGAT GGTCCGAGGA GCCAATGACA 240
 GCAAAGTGGT GAGTCCAGC TTTGTGGTGC CTCGCTGCCG TGGGCGCAGG GAACTGGTGA 300
 GTGTGGTGA CAGTGTGTCT GGCTTACAG TCACTCGGCT CAGTGCATAC CAGGTGACAA 360
 35 ACCTCGTGCC AGGAACCAAA TTCTACATT CCTACCTAGT GAAGAAGGGG ACAGCCACTG 420
 AGTCCAGCAG AGAGATCCCA ATGTCCACAC TCCCTCGAAG GAACATGGA TCCATTGGGC 480
 TGGGTATGGC CCGCACAGGG GGCATGGTGG TCATCACGGT GCTGCTCTCT GTCGCCATGT 540
 TCCTGCTGGT GCTGGGCTTC ATCATTGCC TGGCACTGGG CTCGCGCAAG TAAGGAGGTC 600
 TGCCCGGAGC AGCAGCTTCT CCAGGAAGCC CAGGCGACCA TCCAGTCCC CAGCCACCT 660
 40 GCTCCAGGC CCCAGGCTG TGGCTCCCTT GGTGCCCTCG CCTCCTCCTC CTGCCCTCCT 720
 CTCGCCCTAGA GCCCTCTCCT CCTCTGTCC CTCTCCTTTC CCCAGTGCC TCACCTTCCA 780
 ACATCCATT ATTCTCTCA CCCCACTCCT GTCCAGATTG ACTTCTCTCC CATTTTACCA 840
 CTTTAAACAC CCCATAACA ATCCCCCAT CCTTCAGTGA ACTAAGTCCC TATAATAAAG 900
 GCTGAGGCTG CATCTGCCAA AAAAAAAAAA AA

45 Seq ID NO: 47 Protein Sequence
 Protein Accession #: NP_006751.1

50 1 11 21 31 41 51
 MAPLLPIRTL PLILILLALL SPGAADFNIS SLSGLLSPAL TESLLVALPP CHLTGNGATL 60
 MVRRANDSKV VTSFVVPVPP RGRRELVSUV DSGAGFTVTR LSAYQVTNLV PGTKFYISYL 120
 VKKGATBESS REIPMSTLPR RNMESIGLGM ARTGGMVVIT VLLSVAMFLI VLGFIIALAL 180
 GSRK

55 Seq ID NO: 48 DNA sequence
 Nucleic Acid Accession #: EOS sequence
 Coding sequence: 200-2932

60 1 11 21 31 41 51
 ATTGCTGATG GATCAGTGAG CCTGTGTTCA TGCCAGTGAG CTGCTGTGGC TCAGATACTG 60
 ATACITTTCTT TCCAAACAGC ATAAGAAGTG ATTGAGCCAC AAGTATACTG AAGGAAGGGC 120
 TCCCTCGAGT TCTGGTGTGA AGAGATAAAT CACCAGTCAAC AGACTATGCA CCCGACTGCT 180
 65 GCTGTTCAGT CCAGGGAATA TGAAAGTTGG AGTGCTGTGG CTCAITTTCTT TCTTCACTT 240
 CACTGACGGC CACGGTGGCT TCCTGGGGAA AAATGATGGC ATCAAAACAA AAAAAGAACT 300
 CATTGTGAAT AAGAAAAAAC ATCTAGGCC AGTCGAAGAA TATCAGTGC TGCTTCAGGT 360
 GACCTATAGA GATTCCAAGG AGAAAAGAGA TTTGAGAAAT TTTCTGAAGC TCTTGAAGCC 420
 TCCATTATTA TGGTCAATG GGCTAATTAG AATTATCAGA GCAAAGGCTA CCACAGACTG 480
 70 CAACAGCCTG AATGGAGTCC TGCAAGTGTAC CTGTGAAGAC AGCTACACCT GGTTCCTCC 540
 CTCATGCCCTT GATCCCCAGA ACTGCTACCT TCACACGGCT GGAGCACTCC CAAGCTGTGA 600
 ATGTCTCTC AACAACTCA GCCAGAGTGT CAATTTCTGT GAGAGAACAA AGATTGGGG 660
 75 CACTTTCAAA ATTAATGAAA GTTTACAAA TGACCTTTTG AATTCATCTT CTGCTATATA 720
 CTCCAAATAT GCAAATGGA TGAATTTCA ACTTAAAAA GCATATGAAA GAATTCAGG 780
 TTTTGAAGTC GTTCAGGTCA CCCAATTTG AAAATGGAAGC ATCGTGTCTG GGTATGAAGT 840
 TGTGTGCTCC AGCAGTGCAT CTGAAGTCT GTCAAGCAAT GAACATGTTG CCGAGAAGGC 900
 TAAGACAGCC CTTCACAAGC TGTTCCTAT AGAAGACGGC TCTTTCAGAG TGTTCGGAAG 960
 AGCCAGTGT AATGACATTG TCTTTGATT TGGGTCCAAG GATGATGAAT ATACCTGCC 1020
 CTGCAGCAGT GGCTACAGG GAAACATCAC AGCCAAGTGT GAGTCTCTG GGTGGCAGGT 1080

	CATCAGGAG	ACTTGTGTG	TCTCTGTCT	TGAAGAACTG	AACAAGAATT	TCAGTATGAT	1140
	TGTAGGCAAT	GCCACTGAG	CAGCTGTGT	ATCCTTCTGT	CAAAATCTTT	CTGTCAATCAT	1200
	TCGGCAAAAC	CCATCAACCA	CAGTGGGGAA	TCTGGCTTCG	GTGGTGTGCA	TTCTGAGCAA	1260
5	TATTTTCATCT	CTGTCACTGG	CCAGCCATTT	CAGGGTGTCC	AATTCAACAA	TGGAGGATGT	1320
	CATCAGTATA	GCTGACAATA	TCCTTAATTC	AGCCTCAGTA	ACCAACTGGA	CAGTCTTACT	1380
	GGGGGAAGAA	AAGTATGCCA	GCTCAGGTT	ACTAGAGACA	TTAGAAAACA	TCAGCACTCT	1440
	GGTGTCTCG	ACAGCTCTTC	CTCTGAATTT	TTCTCGGAAA	TTCAATTGACT	GGAAAGGGAT	1500
	TCCAGTGAAC	AAAAGCCAA	TCAAAAGGGG	TTACAGCTAT	CAGATTAAAA	TGTGTCCCCA	1560
10	AAATACATCT	ATTCCCATCA	GAGGCCGTGT	GTTAATTGGG	TCAGACCAAT	TCCAGAGATC	1620
	CCTTCCAGAA	ACTATTATCA	GCATGGCCTC	GTGACTCTG	GGGAACATTC	TACCCGTTTC	1680
	CAAAAATGGA	AATGCTCAGG	TCAATGGACC	TGTGATATCC	ACGTTTATTC	AAAACCTATTC	1740
	CATAAATGAA	GTTTTCCTAT	TTTTTCCAA	GATAGAGTCA	AACCTGAGCC	AGCCTCATTTG	1800
	TGTGTTTTGG	GATTTCAGTC	ATTGTCAGTG	GAACGATGCA	GGCTGCCACC	TAGTGAATGA	1860
	AACTCAAGAC	ATCGTGAGCT	GCCAATGTAC	TCACTTGACC	TCCTTCTCCA	TATTGATGTC	1920
15	ACCTTTTGTG	CCTCTACAAA	TCCTCCCGT	TGTAAAATGG	ATCACCTATG	TGGGACTGGG	1980
	TATCTCCATT	GGAAGTCTCA	TTTTATGCTT	GATCATOGAG	GCTTTGTTTT	GGAAGCAGAT	2040
	TAAAAAAGC	CAAACTCTTC	ACACAGCTCG	TATTTGCATG	GTGAACATAG	CCCTGTCCCT	2100
	CTTGATTGCT	GATGTCGTGT	TTATTGTTGG	TGCCACAGTG	GACACCAACG	TGAACCCCTC	2160
20	TGGAGTCTGC	ACAGCTGTCT	TGTTCTTTAC	ACACTTCTTC	TACCTCTCTT	TGTTCTCTCT	2220
	GATGCTCATG	CTTGGCATCC	TGCTGGCTTA	CCGGATCATC	CTCGTGTTC	ATCACATGGC	2280
	CCAGCATTTG	ATGATGGCTG	TGGGATTTTG	CCTGGGTTAT	GGGTGCCCTC	TCATTATATC	2340
	TGTCATTACC	ATTGCTGTCA	CGCAACCTAG	CAATACCTAC	AAAAGGAAAG	ATGTGTTTGG	2400
	GCTTAACTGG	TCCAATGGAA	GCAAACTACT	CCTGGCTTTT	GTTGTCCTTG	CACTGGCTAT	2460
25	TGTGGCTGTG	AACTTGTGTT	TGTTGCTGCT	AGTTCCTACA	AAGCTCTGGA	GGCCGACTGT	2520
	TGGGGAAGAA	CTGAGTCGGG	ATGACAAGGC	CACCATCATC	CGCGTGGGGA	AGAGCCCTCT	2580
	CATTCTGACC	CCTCTGCTAG	GGCTCACCTG	GGGCTTTGGA	ATAGGAACAA	TAGTGGACAG	2640
	CCAGAATCTG	GCTTGGCATG	TTATTTTGTG	TTTACTCAAT	GCATTCCAGG	GATTTTITAT	2700
	CTTATGCTTT	GGAATACTCT	TGGACAGTAA	GCTGCGACAA	CTTCTGTTC	ACAAGTTGTC	2760
30	TGCCTTAAGT	TCTTGGGAAG	AAACAGAAAA	GCAAACTACA	TCAGATTITAT	CTGCCAAACC	2820
	CAAAATCTCA	AAGCCTTTCA	ACCCACTGCA	AAACAAAGGC	CATTATGCAT	TTTCTCATAC	2880
	TGGAGATTCC	TCCGACAAAC	TCATGTAAAC	TCAGTTTGTG	TCAAATGAAT	AAGGCAAGGA	2940
	ATCATAAAAT	CAAGAAAAAA	TTTCCAGAAC	AACTTGACAT	TTAGAGACAA	ATGTCAATGA	3000
	AGAAATTATG	CTCAGTATTC	GATCGGGTTT	TCTGATTTAG	GGGTCTGGGA	ATAAAACAAG	3060
35	AATGTCTCAG	TGGCTTCA					

Seq ID NO: 49 Protein sequence:
Protein Accession #: EOS sequence

	1	11	21	31	41	51	
40	MKVGVLLWIS	PFTPTDGHGG	FLGKNDGIKT	KKELIVNKKK	HLGPVEEYQL	LLQVTYRDSK	60
	EKRDLRNLFLK	LLKPPLLWSH	GLIRIIRAKA	TTDCNSLNGV	LQCTCEDSYT	WFFPSCLDPQ	120
	NCYLHTAGAL	PSCECHLNLI	SQSVNFCERT	KIWGTFKINE	RFTNDLLNSS	SAIYSKYANG	180
45	IEIQLKKAYE	RIQGFESVQV	TQFRNGSIVA	GYEVVGSSEA	SELLSAIBHV	AEKAKTALHK	240
	LFPLEDGSFR	VFGKAQCNDI	VFGFGSKDDE	YTLPCSSGYR	GNITAKCESS	GWQVIRETCV	300
	LSLLEELNKN	FSMIVGNATE	AAVSSFVQNL	SVIIRQNPST	TVGNLASVVS	ILSNISLSL	360
	ASHFRVSNST	MEDVISIADN	ILNSASVTNW	TVLLREEEKYA	SRRLLETLEN	ISTLVPPTAL	420
	PLNFSRKPID	WKGIPVNKSG	LKRGYSYQIK	MCPQNTSIPI	RGRVLIGSDQ	FORSLPETII	480
50	SMASLTGLNI	LPVSKNGNAQ	VNGPVISTVI	QNYISINEVFL	FFSKIESNLS	QPHCVFWDPS	540
	HLOWNDAGCH	LVNETQDIDT	CQCTHLTSFS	ILMSPFVPST	IPFVVKWITY	VGLGISIGSL	600
	ILCLIIIBALF	WKQIKKQSIS	HTRRICMVNI	ALSLLIADVW	PIVGATVDTT	VNPSGVCTAA	660
	VFFTHFPYLS	LFWMMLMGI	LLAYRIILVF	HHMAQHLMMA	VGFCLGYGCP	LIISVITIAV	720
	TQPSNTYKRR	DVCWLNWSNG	SKPLAFVVP	ALAIVAVNPF	VVLLVLTKLW	RPTVGERLSR	780
55	DDKATIIIRVG	KSLLILTPLL	GLTWGFGIGT	IVDSQNLAWH	VIFALLNAFO	GPFILCFGLL	840
	LDKLRQLLF	NKLSALSSWK	QTEKGNSSDL	SAKPKFSKPF	NPLQNKGHYA	FSHTGDSSEN	900
	IMLTQFVSNE						

Seq ID NO: 50 DNA sequence
Nucleic Acid Accession #: EOS sequence
Coding sequence: 63-3224

	1	11	21	31	41	51	
65	CAGGAATTGG	TGGCGGAGAG	GGCAATAAAC	TGCGGCTCTC	CCGGCGCCCC	GATGCTCGCA	60
	CCATGTGCGAG	GCGCAAGCAG	GCGAAACCCC	AGCACATCAA	CTCGGAGGAG	GACCAGGGGG	120
	AGCAGCAGCC	GCAGCAGCAG	ACCCCGGAGT	TTGCAGATGC	GGCCCCAGCG	GCGCCCGGGG	180
	CGGGGGAGCT	GGGTGCTCCA	GTGAACCAAC	CAGGGAATGA	CGAGGTGGCG	AGTGAGGATG	240
	AAGCCACAGT	AAAGCGGCTT	CGTCGGGAGG	AGACGCACGT	CTGTGAGAAA	TGCTGTGCGG	300
70	AGTTCTTCAG	CATCTCTGAG	TTCTTGGAAC	ATAAGAAAAA	TTGCATAAAA	AATCCACCTG	360
	TCCTCATCAT	GAATGACAGC	GAGGGGCTTG	TGCCTTCAGA	AGACTTCTCT	GGAGCTGTAC	420
	TGAGCCACCA	GCCACCAAGT	CCCGGAGTGA	AGGACTGTCA	CAGGGAGAAAT	GGCGGCACGT	480
	CAGAGGACAT	GAAGGAGAG	CCGGATGCGG	AGTCTGTGGT	GTACCTAAAG	ACAGAGACAG	540
	CCCTGCCACC	CACCCCGGAG	GACATAAGCT	ATTTAGCCAA	AGGCCAAGTG	GCCAACTACT	600
	ATGTCACCTT	GCAGGCACCT	CGGGGCACCA	AGGTGGGGGT	GAATCAGCGG	AGCGCGGATG	660
75	CATCTCCCTG	CCCGTGTGCT	GGTGCCAACA	GCATCCCGTG	GGTCTCTGAG	CAGATCTTGT	720
	GTCTGCAGCA	GCAGCAGCTA	CAGCAGATCC	AGCTCACCGA	GCAGATCCCG	ATCCAGGTGA	780
	ACATGTGGGC	CTCCACGCGC	CTCCACTCAA	GCGGGGCAGG	GGCCGACACT	CTGAAGACCT	840
	TGGGCAGCCA	CATGTCTCAG	CAGGTTTCTG	CAGCTGTGGC	TTTGCTCAGC	CAGAAAGCTG	900

GAAGCCAAGG TCTGTCCTG GATGCCCTGA AACAAAGCCAA GCTACCTCAC GCCAACATCC 960
 CTTCTGCCAC CAGCTCCCTG TCCCCAGGGC TGGCACCCCT CACTCTGAAG CCGGATGGGA 1020
 CCGGGTGCT CCGGAAGCTC ATGTCCCGCC TCCCGAGCGC TTTGCTTCTC CAGGCCCCCG 1080
 5 GCTCGGTGCT CTTCCAGAGC CTTTCTCCA CTGTGGCGCT AGACACATCC AAGAAAGGGA 1140
 AGGGGAAGCC ACGGAACATC TCCGCGGTGG ATGTCAAACC CAAAGACGAG GCGGCCCTCT 1200
 ACAAGCACAA GTGTAAGTAC TGTAAGCAAG TTTTGGGAC TGATAGCTCC TTGCAGATCC 1260
 ACCTCCGCTC CCACACTGGA GAGAGACCCCT TCGTGTGCTC TGTCTGTGGT CATCGCTTCA 1320
 CCACCAAGGG CAACCTCAAG GTGCACCTTC ACCGACATCC CCAGGTGAAG GCAAAACCCC 1380
 10 AGCTGTTTGC CGAGTTCAG GACAAAGTGG CGGCCGCGAA TGGCATCCCC TATGCACTCT 1440
 CTGTACTGTA CCCCATAGAT GAACCGAGTC TTTCTTTAGA CAGCAAACCT GTCTTGTGTA 1500
 CCACCTCTGT AGGGCTACCT CAGAATCTTT CTTCGGGGAC TAATCCCAAG GACCTCACGG 1560
 GTGGCTCCTT GCCCGGTGAC CTGCAGCCTG GGCCTTCTCC AGAAAGTGAG GGTGGACCCA 1620
 CACTCCCTGG GGTGGGACCA AACTATAATT CCCCAGGGC TGGTGGCTTC CAAGGGAGTG 1680
 GGACCCCTGA GCCAGGCTCA GAGACCTTGA AATTGCAGCA GTTGGTGGAG AACATTGACA 1740
 15 AGGCCACCA C TGATCCCAAC GAATGTCTCA TTTGCCACCG AGTCTTAAGC TGTGAGAGCT 1800
 CCCTCAAGAT GCATTATCGC ACCCAACCG GGGAGAGACC GTTCCAGTGT AAGATCTGTG 1860
 GCGGAGCCTT TTCTACCAAA GGTAACCTGA AGACACACCT TGGGGTTCAC CGAACCAACA 1920
 CATCCATTAA GAGCAGCAT TCGTGCCCA TCTGCCAGAA GAAGTTCAT AATGCCGTGA 1980
 TGCTGCAGCA ACATATTCGG ATGCACATGG GCGGTCAGAT TCCCAACAG CCCCTGCCAG 2040
 20 AGAATCCCTG TGACTTTAGC GGTTCTGAGC CAATGACCGT GGGTGAGAAC GGCAGCACCG 2100
 GCGCTATCTG CCATGATGAT GTCATCGAAA GCATCGATGT AGAGGAAGTC AGCTCCACGG 2160
 AGGCTCCAG CAGCTCTCC AAGGTCCCA CCGCTTCTCC CAGCATCCAC TCGGCATCAC 2220
 CCACGCTAGG GTTGGCATG ATGGCTTCT TAGATGCCCG AGGGAAGTG GGTCTGCCCC 2280
 25 CTTTAACTT GCAGCGCCAG GGCAGCAGAG AAAACGGTTC CGTGGAGAGC GATGGCTTGA 2340
 CCAACGACTC ATCTCGCTG ATGGGAGACC AGGAGTATCA GAGCCGAAGC CCAGATATCC 2400
 TGAAGACCA ATCTCTCCAG GCATCTCCCC CGGCCAATAG TCAAGCCGAA AGCATCAAGT 2460
 CAAAGTCTCC GAGTGTGGG AGCAAGCAG AGAGTCCGA GAACAGCCGC ACTGAGATGG 2520
 AAGTTCGAG CAGTCTCCCT TCCACGTTA TCCGAGCCCC GCGCACTAT GTCAAGGTTG 2580
 30 AAGTTCCTGG CACATTTGTG GGACCTCGA CATTGTCCCC AGGGATGACC CCTTTGTAG 2640
 CAGCCAGCC AGCCGACAG GCCAAGCAAC ATGGCTGCAC ACGGTGTGGG AAGAACTTCT 2700
 CGTCTGCTAG CGCTCTTCAG ATCCACGAGC GGACTCACAC TGGAGAGAAG CCTTTTGTGT 2760
 GCAACATTG TGGCGAGCT TTTACCAACA AAGGCACTT AAAGGTTTAC TACATGACAC 2820
 ACGGGCGAA CAATAACTCA GCCCGCCGTG GAAGGAAGTT GGCCATCGAG AACACCATGG 2880
 35 CTCTGTAGG TACGGACGGA AAAAGAGTCT CAGAAATCTT TCCCAAGGAA ATCCTGGCCC 2940
 CTTCAAGTAA TGTGGACCTT GTTGTGTGGA ACCAGTACAC CAGCATGCTC AATGGCGGTC 3000
 TGGCCGTGAA GACCAATGAG ATCTCTGTGA TCCAGAGTGG GGGGGTCTCT ACCCTCCCGG 3060
 TTTCTTCTGG GCGCACCTCC GTTGTGAATA ACGCACTGT CTCCAAGATG GATGGCTCCC 3120
 AGTCGGGTAT CAGTGCAGAT GTGGAAAAAC CAAGTGCTAC TGACGGCGTT CCAAAACACC 3180
 40 AGTTTCTCTA CTCTCTGGAA GAAAACAAGA TTGCGGTCTG CTAAGGAGAA ACTTGCCTGG 3240
 AAGGAGCAAT GCAGACACAG TGAAATCTCT AGAATCTGCT TTGTTTGTGA AGAACTCATC 3300
 TCTCCTGTT TTCTTTTCT TACTGATATG CAAATGATGT TTACTACGTT GGTGTGTGAC 3360
 ACAACCTCAG GCAAGTGCTA CAATCACGAT TGTGTCTATG CTGCTTTGCA AAAAGTTG

Seq ID NO: 51 Protein sequence:
 Protein Accession #: NP_065169.1

1 11 21 31 41 51
 MSRRKQAKPQ HINSEEDQGE QPQQQTPEF ADAAPAAPAA GELGAPVNHV GNDEVASEDE 60
 50 ATVKLRREE THVCEKCAE FFSISEFLEH KKNCTKNPPV LIMNDSGVPV PSEDFSGAVL 120
 SHOPTSPGSK DCHRENGGSS EDMKEKPDAA SVVYLKTETA LPPTPDISY LAKGKVANTN 180
 VTLQALRGTK VAVNRSDADA LPAPVPGANS IPWVLEQILC LQQQLQQIQI LTEQIRIQVN 240
 MWASHALHSS GAGADTLKTL GSHMSQVSA AVALLSQKAG SQGLSLDALK OAKLPHANIP 300
 55 SATSSLSPLG APFTLKPDGT RVLPNVMSRL PSALLPQAPG SVLFQSPFST VALDTSKKGK 360
 GKPPNISAVD VKPKDEAALY KHKCKYCSKV FGTDSLQIH LRSHTGERPF VCSVCGHRFT 420
 TKGNLKVHFE RHPQVKANPQ LFAEFQDKVA AGNGIPYALS VPDPIDEPSL SLDSKPLVLT 480
 TSVGLPQNLN SGTNPDKLTG GSLPGDLQPG PSPSEGGPT LPGAAGPNVNS PRAGGFQSGG 540
 TPEPGSETLK LQQLVENIDK ATTDPNELCI CHRVLSCQSS LQMHYRTHTG ERPFQCKICG 600
 60 RAFSTGNLTK THLGVHRTNT SIKTQHSCTP CQKQFTNAVW LQGHIRMHMG QIPNTPLPE 660
 NPCTFTGSEP MTVGENGSTG AICHDDVIES IDVEEVSSQE APSSSSKVPT PLPSIHSASP 720
 TLGFAMMASL DAPGKVGPAF FNLQRQGSRE NGVESDGLT NDSSSLMGDQ EYQSRSPDIL 780
 ETTSFQALSP ANSQAESIKS KSPDAGSKAE SSENSRTEME GRSSLPTPI RAPPTYVKVE 840
 VPGTFVGPST LSPGMTPLLA AQPRRQAKQH GCTRCGNFNS SASALQIHER THTGKFPFVC 900
 65 NICGRAFTTK GNLVKHYMTH GANNNSARRG RKLAIENYMA LLGTGDKRVS EIFPKEILAP 960
 SVNVDPVVWN QYTSMLNGLL AVKTNBISVI QSGGVPTLPV SLGATSVVNN ATVKMDGDSQ 1020
 SGISADVEKP SATDGVKPKHQ PPHFLEENKI AVS

Seq ID NO: 52 DNA sequence
 Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
 TCTAGCATTAA AAGGAAGAAA CCCCCTCTTG CAACGAAGGC CTCAAAGAGG TCCAAATATC 60
 70 AACTTGCGAGA CATAACAAGC AGAGTGTTC TAAACTGCTC TAAGAAAAGA AAGTTAAAC 120
 TCTGTGAGTT GAAGGCACAC ATCACAAGT AGTTTCTGAG AATGATTCTG TCTAGTTTTT 180
 75 ATTTGAAGAT ATTTCTCTTT CTACTGTGAG CATCAATCG CTTGAAATCT CCACCTTGCAA 240
 ATTCCACAAA AAGAGTGTCT CAAATCTGCT CTGTGTAAAG GGACGTTCCA CTCTGTGAGT 300
 TGAATACACA CAACACAAGG AAGTTACTGA GAATCTCTCT GTCTAGCATG ATATGAAGAA 360

ATCCCGTTTC CAACGAAGGC CTCAATGAGG TCTATATATC CACTTGCAGA CTTTACAAAC 420
AGAGTGTTC CTAAGTCTCT TATGAAAAGA AAGGTTAAAC TCTGTGGAGT TGAACGCACA 480
CATCACAAAA GGAGTTTCTG AGAATCATTC TGTCTAGTTT TTTTAGGAAG ATATTTCCTT 540
TTCTACCGTT GACTTCAAAG CGGCTGAAAT

Seq ID NO: 53 DNA sequence
Nucleic Acid Accession #: NM_001910.1
Coding sequence: 50..1240

10 1 11 21 31 41 51
GGAGAGAAGA AAGGAGGGGG CAAGGGAGAA GCTGCTGGTC GGACTCACAA TGAACACGCT 60
CCTTCTTTTG CTGCTGGTGC TCCTGGAGCT GGGAGAGGCC CAAGGATCCC TTCACAGGGT 120
GCCCCTCAGG AGGCATCCGT CCCTCAAGAA GAAGCTGCGG GCACGGAGCC AGCTCTCTGA 180
15 GTTCTGAAA TCCATAATT TGGACATGAT CCAGTTCACC GAGTCTGTCT CAATGGACCA 240
GAGTGCCAAAG GAACCCCTCA TCAACTACTT GGATATGGAA TACTTCGGCA CTATCTCCAT 300
TGGCTCCCCA CCACAGAACT TCACTGTCTT CTTGACACT GGCTCTCTCA ACCTCTGGGT 360
CCCTCTGTGT TACTGCACCT GCCAGCCCTG CAAGACGCAC AGCAGGTTC ACCTCTCCCA 420
GTCCAGCACA TACAGCCAGC CAGGTCAATC TTTCTCCATT CAGTATGGAA CCGGGAGCTT 480
20 GTCCGGGATC ATTGGAGCCG ACCAAGTCTC TGTGGAAGGA CTAACCGTGG TTGGCCAGCA 540
GTTTGGAGAA AGTGTACAG AGCCAGGCCA GACCTTTGTG GATGCAGAGT TTGATGGAAT 600
TCTGGGCGCTG GGATACCCCTT CCTTGGCTGT GGGAGGAGTG ACTCCAGTAT TTGACAACT 660
GATGGCTCAG AACCTGGTGG ACTTGGCCGAT GTTTTCTGTC TACATGAGCA GTAACCCAGA 720
AGGTGTGTGG GGGAGGAGCG TGATTTTGGG AGGCTACGAC CACTCCCAT TCTCTGGGAG 780
25 CCTGAATTGG GTCCAGTCA CCAAGCAAGC TTAAGTGGAG ATTGCACTGG ATACATCCA 840
GGTGGGAGGC ACTGTATATG TCTGCTCCGA GGGCTGCCAG GCCATTGTGG ACACAGGGAC 900
TTCCCTCATC ACTGGCCCTT CCGACAAAGT TAAGCAGCTG CAAACGCCCA TTGGGGCAGC 960
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30 CTTACACATT AAGCGAGTCC CCTATACCTT CAGCCCAACT GCCTACACCC TACTGGACTT 1080
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35 GTTATTTTCC AGAGATGTA GCTGTTTCCA GGGTTGCAAC TTGAATTAAG ACCAAACAGA 1380
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40 CACACCGCCA GCGCTGTTA TCTACACTGC TGCCCACTCC TCTCTCCAGC TCCACATGCT 1680
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Seq ID NO: 54 Protein Sequence
Protein Accession #: NP_001901.1

50 1 11 21 31 41 51
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75 CTCAGAGATG TGGCTGTCTG GCTTGGGGTC AGCAATATA CAGGGGGCCG AGGCGTCAGC 420
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5	ACCCATGGGA	AGGTCGGCTT	CCGGGACATC	GCCTCACCCA	AGTTCTCCAT	GCCCTCCCCT	720
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	GGAGACCCCC	TGATCGAGGA	GCTCAATCCC	GGCGACGCCT	TGGAGCCTGA	GGGCCGGGGC	900
	ACAGGGGGTG	TGGTGACCGA	CTTCGACCGA	GACGGGATGC	TGGACCTCAT	CTTGTCCCAT	960
	GGAGAGTCCA	TGGCTCAGCC	GCTGTCCGTC	TTCCGGGGCA	ATCAGGGCTT	CAACAACAAC	1020
	TGGCTGCGAG	TGGTGCCACG	CACCCGGGTT	GGGGCCTTTG	CCAGGGGAGC	TAAGTCCGTG	1080
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	GTGCTGGAGA	TCCTCTACCC	CCGGGATGAG	GACACACTTC	AGGACCCAGC	CCCACTGGAG	1320
	ACACCAATGA	ATGCATCCAG	TTCCCATTCG	TGTGCCCTCG	AGACAAGCCC	GTATGTGTCA	1380
	ACACCTATGG	AAGCTACAGG	TGCCGGACCA	ACAAGAAGTG	CAGTCGGGGC	TACGAGCCCA	1440
	ACGAGGATGG	ACCGCGTGGC	GTGGGGACTC	TCGGCCAGTC	ACCGGGCCCC	CGCCCCACCA	1500
15	CCCCCACCGC	TGCTGCTGCC	ACTGCCGCTG	CTGCTGCCGC	TGCTGGAGCT	GCCACTGCTG	1560
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	ATTCCAGTGG	GTCTAATGAC	CATATCTTAG	GACACAGATG	TGCCCAAGGA	GGTGGTGTCA	1920
	CTGCACAGGA	AGTATGAGGA	CTTTAGTGTG	CTGAGTTCAA	ATCCTGATTG	AGGAACTCAC	1980
	AAAGCTATGT	GACCTTACAC	CAGTCACTTA	ACTTGTTAGC	CATCCATTAT	CGCATCTGCA	2040
25	AAATGGGGAT	TAAGAATAGA	ATCTTGGGGT	TAGTGTGGAG	ATTAGATTAA	ATGTATGTAA	2100
	GACACTTGGC	ACAAAACCTG	GCACATAGTA	AAGGCTCAAT	AAAAACAAGT	GCCTCTCACT	2160
	GGGCTTTGTC	AACACGTG					

Seq ID NO: 56 Protein Sequence
Protein Accession #: NP_060528.1

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35	FRDIASPKFS	MPSPVRTVIT	ADFDNDQELE	IFPNNIAYRS	SSANRLFRVI	RREHGDFLIE	180
	ELNPGDALEP	EGRGTGGVVT	DFDGDGMLDL	ILSHGESMAQ	PLSVFRGNQ	FNNNWLVRVP	240
	RTRVGAFARG	AKVLYTKKS	GAHLRIIDGG	SGYLCEMEPV	AHFGLGKDEA	SSVEVTWPDG	300
	KWVSRNVASG	EMNSVLEILY	PRDEDTLQDP	APLETFMNAS	SSHSCALET	PYVSTPMET	360
40	GAGPTRSAVG	ATSPTRMAQP	AWGLSASHRA	PAPPPFPLLL	PLPLLLPLLE	LPLLRHRS	

Seq ID NO: 57 DNA sequence
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Coding sequence: 1..1962

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	AGTAATCCCA	CCGAGCTCAA	CTATGGTGTG	GCAGTTACTG	ATGTGGACCA	TGATGGGGAC	180
50	TTTGAGATCG	TCTGTGGCGG	GTACAATGGA	CCCAACCTGG	TTCTGAAGTA	TGACCGGGCC	240
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	GACCGGCAGG	GGAAACGCTC	CGGGGTCA	GCCTGCGACA	TGCGCGGGGA	CGCGCGGGAG	360
	GAGATCTACT	TCCTCAACAC	CAATAATGCC	TTCTCGGGGG	TGGCCACGTA	CACCGACAAG	420
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55	CGTGGTGTGG	CCAGCCTCTT	TGCCGAGCGC	TCTGTGGCCT	GTGTGGACAG	AAAGGGCTCT	540
	GGACGCTACT	CTATCTACAT	TGCCAATTAC	GCCTACGGTA	ATGTGGGGCC	TGATGCCCTC	600
	ATTGAAATGG	ACCCTGAGGC	CAGTGACCTC	TCCCGGGGCA	TTCTGGCGCT	CAGAGATGTG	660
	GCTGCTGAGG	CTGGGTGAG	CAATATACA	GGGGGCGGAG	GCGTCAGCGT	GGGCCCCATC	720
	CTCAGCAGCA	GTGCTCGGA	TATCTCTG	GACAATGAGA	ATGGGCTTAA	CTTCTTTTC	780
60	CACAAACCGG	CGATGGCAC	CTTTGTGGAC	GCTGCGGCCA	GTGCTGGTGT	GGACGACCCC	840
	CACCAGCATG	GGCGAGGTGT	CGCCCTGGCT	GACTTCAACC	GTGATGGCAA	AGTGGACATC	900
	GTCTATGGCA	ACTGGAATGG	CCCCCACCGC	CTCTATCTGC	AAATGAGCAC	CCATGGGAAG	960
	GTCGCTTCC	GGGACATCGC	CTACCCCAAG	TTCTCCATGC	CCTCCCTCTG	CCGCAACGTC	1020
	ATCACCGCGG	ACTTTGACAA	TGACCAGGAG	CTGGAGATCT	TCTTCAACAA	CATTGCTTAC	1080
65	CGCAGCTCCT	CAGCCAACCG	CCTCTTCCGC	GTATCCGTA	GAGAGCACGG	AGACCCCTC	1140
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	GCTCAGCGCG	TGTCGCTCTT	CGGGGCAAT	CAGGGCTTCA	ACAACAACCTG	GCTGCGAGTG	1320
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70	AAGAGTGGGG	CCACCTGAG	GATCATCGAC	GGGGGCTCAG	GCTACCTGTG	TGAGATGGAG	1440
	CCCGTGGCAC	ACTTTGGCCT	GGGGAAGGAT	GAAGCCAGCA	GTGTGGAGGT	GACGTGGCCA	1500
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	CTCTACCCCC	GGGATGAGGA	CACACTTCAG	GACCCAGCCC	CAGTGGAGTG	TGSCCAAGGA	1620
	TTCTCCCGAG	AGGAAATGG	CCATTGCATG	GACACCAATG	AATGCATCCA	GTTCCTATTC	1680
75	GTGTGCCCTC	GAGACAAGCC	CGTATGTGTC	AACACTATG	GAAGCTACAG	GTGCGGAGC	1740
	AACAGAAAGT	GCAGTCGGGG	CTACGAGCCC	AACGAGGATG	GCACAGCCTG	CGTGGGGACT	1800
	CTGGGCAAGT	CAACGGGGCC	CCGCCCAACC	ACCCCAACCG	CTGCTGCTGC	CAGTGCCTG	1860
	GCTGCTGCGG	CTGCTGGAGC	TGCCACTGCT	GCACCGGTCC	TGCTAGATGG	AGATCTCAAT	1920

5 CTGGGGTGGG TGGTTAAGGA GAGCTGCGAG CCCAGCTGCT GAGCAGGGGT GGGACATGAA 1980
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Seq ID NO: 58 Protein Sequence
 Protein Accession #: CAC08451.1

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 20 EYPLANTNNA FSGVATYTDK LFKFRNNRWE DILSDEVNVA RGVASLFAGR SVACVDRKGS 180
 GRYSIYIANY AYGNVGPDAL IEMDPEASDL SRGILALRDV AAEAGVSKYT GGRGVSVGPI 240
 LSSASDIFC DNENGNPFLF HNRGDGTFVD AAASAGVDDP HQHGRGVALA DFNRDGKVDI 300
 VYGNWNGPHR LYLQMSHKG VRFRDIASPK FSPSPVVRTV ITADFDNDQE LEIPFNNIAY 360
 RSSANRLFR VIRREHGDPL IEELNPGDAL EPEGRGTGGV VTDFOGDGML DLILSHGESM 420
 25 AQPLSVFRGN QGFNNWLRV VPRTRFGAFA RGAKVLYTK KSGAHLRIID GSGGYLCME 480
 PVAHFLGKD EASSVEVTWP DGKMVSRNVA SGEMNSVLEI LYPRDEDTLQ DPAPLECGQG 540
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 40 ATCGACGGGG ACGGCGGGGA GGAGATCTAC TTCTCAACA CCAATAATGC CTTCTCGGGC 300
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 Seq ID NO: 60 Protein Sequence
 Protein Accession #: FGENESH

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 Seq ID NO: 61 DNA sequence
 Nucleic Acid Accession #: NM_000584.1
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5 CACTGTGTGT AAACATGACT TCCAAGCTGG CCGTGGCTCT CTTGGCAGCC TTCCTGATTT 120
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Seq ID NO: 62 Protein Sequence
 Protein Accession #: NP_000575.1

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Seq ID NO: 64 Protein sequence:
 Protein Accession #: NP_036338.1

40 1 11 21 31 41 51
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 45 SLEIVPKVT TPIVTVPT VTVRTSTTV PTTTVPPTT VPTTMSIPTT TIVPTMTVS 180
 TTSVPTTTS IPTTSVPVT TTVSTFVPPM PLPRQNHBPV ATSPSSPQPA ETHPTTLQGA 240
 IRREPTSSPL VSYITDGNDF VTESDGLWN NNQTLFLEH SLTANTTKG IYAGVCISVL 300
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50 Seq ID NO: 65 DNA sequence
 Nucleic Acid Accession #: E08 sequence
 Coding sequence: 2932-4764

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GAGGCGGAGT TCCGGCAGCC TGCAGTGTCTG GTCCTGCAGG ATCCCTGGAG TTGCAGCTAC 6180
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 GGGCGGGGCC GAGGTGCAAT CTGTTTCGCT GCCCGCCCT GAGGGGCTGG TGGCGGTAG 6300
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 AGAAGCGAAA GCAGAGGAGG AGGAAGGGCC GGCCAGAAGA CCTGGAGTTC ACAGACATGG 6420
 GTGGCAATGT GTACATCTCT ACGGGCAAGG TGGAGGAGCA GTTTGAGCTG CTGACTGTGG 6480
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 CCAGCGCCCC CAAACTTCC TTCAACTGGT TTGTGAACCC GCTGAAGACC TTTGCTTCT 6600
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 TCCTCTCTCT GGTCTTCTAC ACCATCCCTG GCCAGATCAG CCAGGTCTATC TTCCGTCCCC 6720
 TCCACAAGTG ACTCTCGCTG ACCTTGGACA CTCACCCAGG GTGCCAACCC TTCAATGCCT 6780
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 AAACCTATCA CAGCC

Seq ID NO: 66 Protein sequence:

Protein Accession #: EOS sequence

1 11 21 31 41 51

1 MCKRRWHWPR SSWQNCAFWL RRHPGQPLVR SVPSWSSSCG HAWASKPRPA PLSCPRICCP 60
 20 SPQPGPPAY TGTVLBQTL PLWDELLVPE QLIVDGRREH LQEEPLVII NVFDHNKFGP 120
 PVFLGRALAA PRVKLMEDPY QRPELQFFPL RKGPAWAGEL IAAFQLIELD YSGRLEPSVP 180
 SEVEPDLLAP LVEPHSGRLS LPPHVCEVLR EFRVEVLFWG LRGRLRVHLL EVEQPQVLE 240
 VAGQGVSEV LASVRESNPF TELVRHLTVV FKDTAPLFHP QDLPEQPYLQ PPLSILVIER 300
 RAPGHTVLVG SHIVPHMLRF TFRGHEDPPE EGEEMEETGD MPRGPGQK SLDPLAEAG 360
 25 ISRQLLKHNF DEDEMDPDG SDGVNLISMV GEIQDQGEAE VKGTVSPKKA VATLKIYNRS 420
 LKSEFNHNFED WLVNFPFLYRG QGGQDGGGEE EGSGHLVKGK KGSFLIYPES EAVLFSEPI 480
 SRGIPQNPRI KLLVRVYVVK ATNLAPADPN GKADPYVVSV AGRBRQDTKE RYIPKQLNPI 540
 FGEILELSIS LPAETELTVA VFDHDLVGS DLIGETHIDL ENRFYSHHRA NGLASQYEV 600
 30 WVGQGPQEPF

Seq ID NO: 67 DNA sequence

Nucleic Acid Accession #: NM_002449.2

Coding sequence: 223..1026

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1 11 21 31 41 51

1 GGGGGGGGGG GGCAGCTCTT CGGGAAGAGC CAATCAGGGG CGAGCGTCTT CTGTCGCAC 60
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 TCCAGCGCGC CCCCTCCCGT CTCCGAGACA AAAAAGTTTG AGTCGCGCTC GCCGGTTGC 180
 40 CAGCGGAGTC GCGGTCGCGG AGCTACGTAG GGCAGAGAAG TCATGGCTTC TCCGTCCAAA 240
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 GGGCTGGGGG GCGCGCGCGG GCGCGCGGAG GAGCGCGCG TCAAGGTCTC CAGCCTGCC 360
 TTACGCTGG AGCGCTCAT GTCCGACAAG AAGCGCGCCA AGGAGTCGCC CGCTGTGCC 420
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 45 CGGGAAGCGC ACAGCCCGG GCGGCTGGT AAGCCCTTC AGACCGCTTC GGTCAAGTCG 540
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 50 CTCTCCATTG CAGAGCGTGC AGAGTTCTCC AGCTCTCTGA ACCTCACAGA GACCCAGTTC 780
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 55 TCCTAAGGAA GACCAATCCA ATAGACTCCA TGATGGATGC TTGTTTCAAA GGGTTTCTC 1080
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 70 TCCCGCCAC GCCCACACAT ATTTTAAAG TTTTAAAGAA CCGGCGGAT ATTCGCGCC 1980
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 TGAACATTA GTAGATCCAG AAAGAAAAAA AAAATATGCT TCTCTGTGTG TGTACTGT 2520

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Seq ID NO: 68 Protein Sequence
 Protein Accession #: NP_002440.1

1 11 21 31 41 51
 MASPSKGNL FSPDEEGPAV VAGPGFGLGG AAGAAEERRV KVSSLPFSVE ALMSDKKPPK 60
 ESPAVPPEGA SAGAHRLPLL LSGHRAREAH SPGFLVKPFE TASVKSGNSE DGAAMWQEPG 120
 RYSPPPRHMS PTTCTLRKHK TNKRPRTPTF TSQLLALERK FRQKQYLSIA ERAEPSSSLN 180
 LTETQVKIWF QNRSKAKRKL QEAELEKLM AAKPMLPSSP SLPPFPISSPL QAASIYAASY 240
 PFHRPVLPIP FVGLYATPVG YGMYHLS

Seq ID NO: 69 DNA sequence
 Nucleic Acid Accession #: NM_005603.1
 Coding sequence: 1..3756

1 11 21 31 41 51
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 GAACCAAGAA AAGACCGAGT CAACAGGGAA GCAGAGGAGA ACCGGGAGCC ATTCAGAAAA 180
 GAATGTACAT GGCAAGTCAA AGCAAAACGAT CGCAAGTACC ACGAACCAAC TCACCTTTATG 240
 AACACAAAAT TCTTGTGTAT TAAGGAGAGT AAAATATGCGA ATAATGCAAT TAAAAATAC 300
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 AATTATATTT TCCTGGCTCT TCTTATCTTA CAGGCAGTTC CTCAAATCTC TACCCTGGCT 420
 TGGTACACCA CACTAGTGCC CCTGCTTGTG GTGCTGGGCG TCACTGCAAT CAAAGACCTG 480
 GTGGACGATG TGGCTCGCCA TAAAATGGAT AAGGAAATCA ACAATAGGAC GTGTGAAGTC 540
 ATTAAGGATG GCAGGTTCAA AGTTGTCTAAG TGGAAAGAAA TTCAGTTGG AGACGTCATT 600
 CGTCTGAAAA AAAATGATTT TGTTCAGCT GACATTCTCC TGCTGTCTAG CTCTGAGCCT 660
 AACAGCCTCT GCTATGTGGA AACAGCAGAA CTGGACGGAG AAACCAATTT AAAATTTAAG 720
 ATGTCACTTG AAATCAGACA CCAGTACCTC CAAAGAGAAG ATACATTGGC TACATTTGAT 780
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 TGGAGAAACA CAAGTTTTC TTTGGATGCT GATAAAATTT TGTTACGTGG CTGTGTAATT 900
 AGGAACACCG ATTTCTGCCA CGGCTTAGTC ATTTTTCAG GTGCTGACAC TAAATAATG 960
 AAGAATAGTG GGAAGACAG ATTTAAAGA ACTAAATTTG ATTACTTGAT GAACTACATG 1020
 GTTTACACGA TCTTTGTGT TCTTATTCTG CTTTCTGCTG GTCTTGCCAT CGGCCATGCT 1080
 TATTGGGAAG CACAGGTGGG CAATTCCTCT TGGTACCTCT ATGATGGAGA AGACGATACA 1140
 CCCTCCTACC GTGGATTCTT CATTTCTGCG GGCTATATCA TTGTCTCAA CACCATGGTA 1200
 CCCATCTCTC TCTATGTCAG CGTGGAAAGT ATTCGTCTTG GACAGAGTCA CTTTATCAAC 1260
 TGGGACCTGC AAATGTACTA TGCTGAGAAG GACACACCGG CAAAGCTAG AACCAACACA 1320
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 CAAAATATCA TGACCTTTAA AAGTGTCTGT ATCAACGGGC AGATATATGG GGACCATCGG 1440
 GATGCTCTC AACACAACCA CAACAAAATA GAGCAAGTTG ATTTTAGCTG GAATACATAT 1500
 GCTGATGGGA AGCTTGCAAT TTATGACCAC TATCTTATTG AGCAAAATCCA GTCAGGAAAA 1560
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 AAGCGAATGT CTATCATTTG AAGAACCCCA GAAGGCAATA TCAAGCTTTA CTGTAAGGT 1860
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 GTGGGACAAA GAGACTTACT ATTCAACTAT AAGAGATTCT TTGTAAGCTT GTTGCATGGG 3120
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 CAGGATGGAG AGGCACCTTC CGACTACCAG TCTTTTGGCC TCACCATGTC CTCTGCTCTT 3240

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GTAATAACAG TCAATTTCCT GATTGGCTTG GATACTTCTT ATTGGACTTT TGTGAATGCT 3300
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GGAATACATG TTCTCTTTCC ATCTGCATTT CAATTTACAG GCACAGCTTC AAACGCTCTG 3420
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GGCGTGTCAA CGCGGCGCTC GGCCTACGCC TTCTCGCACC AGCGGGGCTA CGCGGACCTC 3660
ATCTCTCCGG GCGCAGCAT CCGCAAGAAG CGCTCGCCGC TTGATGCCAT CGTGGCGGAT 3720
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Seq ID NO: 70 Protein Sequence
Protein Accession #: NP_005594.1

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1 11 21 31 41 51
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NLYFLALLIL QAVPOISTLA WYTLVPLLV VLGVTAIKDL VDDVARHKMD KEINNRTCEV 180
IKDGRFKVAK WKEIQVGDVI RLKKNDFVPA DILLSSSEF NSLCYVETAE LDGETNLKFK 240
MSLEITDQVL QREDTLATFD GFIECEPNRN RLDKFTGTLF WRNTPFLDA DKILLRGCVI 300
RNTDFCHGLV IFAGADTKIM KNSGKTRPKR TKIDYLMNYM VYTIFVVLIL LSAGLAIGHA 360
YWEAQVGNSS WYLVGDGDDT PSYRGFLIFW GYIIVLNTMV PISLYVSVEV IRLGQSHFIN 420
WDLQMYAEK DTPAKARTTT LNEQLGQIHY IFSDKTGTLT QNIMTFKKCC INGQIYGDHR 480
DASQHNHNI EQVDFSWNTY ADGKLAFYDH YLIEQIQSGK EPEVRQPFPL LAVCHTMVD 540
RTDQQLNYQA ASPDEGALVN AARNFGFAPL ARTQNTITIS ELGTERTYNV LAILDPNSTR 600
KRMSIIVRTP EGNIKLYCKG ADTVIYERLH RMNPTKQETQ DALDIFANET LRTLCLCYKE 660
IEEKEFTFEN KKFMAASVAS TNRDEALDKV YSEIEKDLIL LGATAIEDKL QGVFPETISK 720
LAKADIKIWV LTGDKKETAE NIGFACELLT EDTTICYGED INSLHARME NQRNRGGVYA 780
KFPAPPVQESF PPGGNRALI ITGSWNLBIL LEKKTNRNKI LKLKFPRTBE ERRMRQSKR 840
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IKTAHIGVGI SQEGMQAVM SSDYSFAQFR YLQRLLLVHG RWSYIRMCKF LRYFFYKNFA 960
PTLVHVPYSE FNGYSAQTAY EDWFITLYNV LYTSLPVLLM GLLDQDVSDK LSLRFPGLYI 1020
VGQRDLLFNY KRPFVSLHNG VLTSMILFPI PLGAYLQTVG QDGEAPSDYQ SFAVTIASAL 1080
VITVNFQIGL DTSYMTFVNA FSIFGSIALY FGIMFDFHSA GIHVLFPSPAF QFTGTASNAL 1140
RQPYINLTII LTVAVCLLPV VAIRFLSMTI WSESDEKIQK HRKRLKAEQ WQRQVQVFR 1200
GVSTRRSAYA FSHQRGYADL ISSGRSIRKK RSPDLAIVAD GTAERYRTGD S

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Seq ID NO: 71 DNA sequence
Nucleic Acid Accession #: NM_138784.1
Coding sequence: 334-816

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1 11 21 31 41 51
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CTACTTTTAT TAAGAAGCTG AAATTAATTT TGGATTTCCT TCCTTCCAAA GCTGAGACAC 180
GATGGCCAAA AAGCGATTGC TGTGATTGGA GCTGGAATTA GCGGACTGGG GGCATCAAG 240
TGCTGCCTGG ATGAAGATCT GGAGCCCACC TGCTTTGAAA GAAATGATGA TATTGGACAT 300
CTCTGGAAAT TTCAAAAAAA TACTTCAGAG AAAATGCCTA GTATCTACAA ATCTGTGACC 360
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CTTCTAAATT TAAATCTTFA TTTATATATG AAGCATAGCT ATGTCAATGT CCAGGGAAGC 1140
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Seq ID NO: 72 Protein sequence:
Protein Accession #: NP_620139.1

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1 11 21 31 41 51
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Seq ID NO: 73 DNA sequence
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Coding sequence: 1..1152

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10	CGTGCTGCAG	CCATGGAGCC	AGAGAGAGCT	ATCTTTATTA	AGGATGCCAT	TAAGTATTCT	180
	AAGGAAAAG	TGAGCACACA	GAATCTGTGA	CTCTGCTGTA	CTGATAATGA	GGCCCTGAAAC	240
	GGATTCTGGT	CTGCTGCTGA	ACTGCCCCAG	AATGAGGCAG	ATGAGCTCCG	TAAGGCTCTG	300
	GACAACTTTG	CAAGACAATA	GATCTAGAA	GACAAAAACT	GGCACGATAA	AGGCCAGCAG	360
	TACAGAAACT	GGTTCCTGA	AGAGTTTCTC	CGGTGAAAA	GTGAGCTTGA	GGATACACATA	420
15	AGAAAGCTCC	AGTCCCTTGC	AGATGGGGTG	CAGAAGGTC	CAAAAGGCCA	CACCATCGCC	480
	AATGTGGTGT	CTGGCTCTCT	CAGCATTTC	TCTGGCATCT	TGACCTCTGT	CGGCAATGGT	540
	CTGGCAGCC	CCACAGAGTG	AGGAGCCGCT	GTACTCTTGG	AACTCGGGAT	GAGAGTTGGGA	600
	ATCACAGCCG	CTTTGACCGG	GATTACACG	AGTACCATGT	ACTACGGAAA	GAGGTGGTGT	660
	ACACAGACCC	AGGCCCCACA	CCTGGTCATC	AAATGGCCCT	CAAAATTTGA	GGAGGTGAGG	720
	GAGTTTTTGG	GTGAGAACAT	ATCCAACATT	TTTCTCTTAG	CTGGCAATAC	TTACCAACTC	780
20	ACACAGAGCCA	TTGGGAAGGA	CATCGCTGCC	CTCAGACGAG	CCAGAGGCCA	TCTTCAGTCA	840
	ATACCGCATG	CCTCAGCCTC	ACGCCCCCGG	GTCAGTGAGC	CAATCTCAGC	TGAAGAGCGGT	900
	GAGCAGGCTG	AGAGGCGTTAA	TGAACCCAGC	ATCTGGGAA	TGAGCAGAGG	AGTCAAGCTC	960
	ACGAGTTGGG	CCCTCTGAAG	CTTCTTTCTT	GTGCTGGATG	TAGTCTACCT	CGTGTACGAA	1020
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	CAGGAGCTCG	AGGAGAAGCT	AAACATTCTC	AAACAATAATT	ATAAGATTCT	GCAGGCCGAC	1140
	CAGAAGCTGT	GA					

Seq ID NO: 74 Protein Sequence
Protein Accession #: NP_003652.1

Protein Accession #: NP_003622.1

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	KEKYSTQNLL	LLLTDNDAWN	GFVAANELPR	NDEADLRKAL	DNLARQMIMK	DKNWHDQKQQ	120
35	YRNFLKEKPP	RLKSELEDNI	RLRLALDAGV	QKVVHGKTII	NVVSGLSIS	SGILTLVGMG	180
	LAPFTEGGSL	VLLEPGMELG	ITTAALTGTS	STMDYGKKW	TQAQAHDLVI	KSLLDKLKEVR	240
	EFLGENISNF	LISLAGNTYQL	TRGIGKDIRA	LRRARANLQS	VPHASASRPR	VTEPISAESG	300
	EQVERVNEPS	LIEMSRGVKL	TDVAPVSFFL	VLDVVYLVE	SKHLEHGAKS	ETAELKKKVA	360
40	QELEEKLNIL	NNNYKILQAD	QEL				

Seq ID NO: 75 DNA sequence
Nucleic Acid Accession #: NM_014452.1
Coding sequence: 1..1968

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	GCTCAGGCAG	AACGAAAGCG	CTCGAATCTC	ATTGGACACAT	ACGCCCATGT	TGACCGTCC	180
50	ACCGCGCAGG	CTGTAACCTG	TGACACAGTG	CCAGCAGGAA	CCTATGTCTC	TGAGCATTTG	240
	AACCAACAA	CGCTGCGCGT	CTGACAGTAG	TGCGCTGTGG	GGACCTTTAC	CAGGCTAGAG	300
	ATTGGCATAT	AGAAATGCCA	TGACTGTAGT	CAGCCATGCC	CATGCGCCAA	GATTGAGAAA	360
	TTACCTTTGT	CTGCGCTTGA	TGACCGAGAA	TGCATCTGCC	CACCTGGCAT	GTTCACGTCT	420
	AACGCTTACT	TGTGCCCCCC	TACGGTGTGT	CTCTGTGGTT	GGGGTGTGCG	GAAAGAAGGG	480
55	ACAGAGACTC	AGGATGTGGG	GTGTAAAGCA	TGTGTCTGGG	GTACCTTCTC	AGATGTGCCT	540
	TCGTAGTGTG	TGAAATGCAA	AGCATACACA	GATGTGCTGA	GTGAGAACTC	GTTGGTGATC	600
	AAGCGCGGGA	CCAAAGGACG	AGACAACGTC	TGCCGTCTCT	TCCCGTCTCT	CTCCAGCTC	660
	ACCTCACCTT	CCCCTGGCAC	AGCCATCTTT	CCACGCGCTG	AGCAGCATGA	AACCCATGAA	720
	TGTCCTTCTCT	CCACITATGT	TCCCCAAGCG	ATGAACCTCA	AGCAATCCAA	CTCTTCTGCC	780
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	GGCGAGAAGT	CCAGCACGCC	CATCAAGGGC	CCCAAGAGGG	GACATCCTAG	ACAGAACTTA	1020
	CACAAGCAAT	TTGACATCAA	TGAGCATATT	CCCTTGATGA	TTGTGCTTTT	CTCTGCTGCT	1080
65	GTGCTTTGTG	TGATTTGTGT	TGTCAGTATG	CGGAAAGACT	CGAGGAAGCT	GAAAAAGGGG	1140
	CCCCGGCAGG	ATCCCAAGTG	CATTGTGGAA	AAGCAGGGCG	TGAAGAAATC	CATGACTCCA	1200
	ACCCAGACAG	GGGAGAAATG	GATCTACTAC	TGCAATGGCC	ATGGTATCGA	TATCTCTGA	1260
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70	CTCTCTCTGC	AGCACTGGAC	CCCTCGGGGC	CCGAGGCCCA	CGCTCGCCCA	CGTAATTAGC	1440
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	ACCAACCCAGC	TGGAACTTGA	CAAACTAGCT	CTCCGATATG	GCCCCAGCCC	GCTTGAACCG	1560
	AGCCCCATCC	ACGCGCCCCA	CGCGAGAACT	GAGAAATCCG	CTCTCTCTAG	GGTGGGCTCT	1620
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	AGCTTCACTA	CCAGCGGCTC	CTCGCGCTCG	AGCAGGAAGC	GTCTCTTTAT	TACCAAGAA	1740
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CAGACCCCTCC TGGACTCTGT TTATAGCCAT CTTCCTGACC TGCTGTAG

Seq ID NO: 76 Protein Sequence
 Protein Accession #: NP_055267.1

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VPSSTYVPKG	MNSTESNSA	SVRPKVLSSI	QEGTVPDNTS	SARGKEDVNK	TLPLNQLVNVH	300
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VLVVIVVCSI	RKSSRTLKKG	PRQDPSAIVE	KAGLKKSMTP	TQNREKWIYY	CNGHGIDILK	420
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Seq ID NO: 77 DNA sequence
 Nucleic Acid Accession #: NM_003105.3
 Coding sequence: 123..6767

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CAGACGCTTA	TGCCCTGCTG	CTCTGGATCA	CGTTTGACTT	CTGCAACACT	CTTCAAGGCT	720
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Seq ID NO: 79 DNA sequence
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Coding sequence: 120-755

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AGCTGGGGC CAGGGCCTTA CCGGGCTGGG TTCCTGTGTG GGGGTGGAG CTGGGGCTGA 2160
AGTGGAGGGG ACCGGCCTGC GGGCCCCAGC ACTGTGTTT CTCCAGGTGC ACCTTACCTT 2220
CCTCCTTACC TGCCCGAGCC TCAACTCAGG GTCAGCAGCC TCACCGAGC CAGCCCCACC 2280
TGCCCGAAAA CCACTGAAGC CACCCTCCGC CCGACGTCAA CCGGATCCA CTAGTTTAGA
GCGCGCCCC CGGTGTC

Seq ID NO: 80 Protein sequence:
Protein Accession #: Bos sequence

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1      11      21      31      41      51
|      |      |      |      |      |
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AHGSLNLLKA MVEAVTGRSA ILSFVGYGCV CGLGGRGQPK DEVDWCCAH DCCYQELFDQ 120
5 GCHPYVDHYD HTIENNTIIV CSDLNKTEDC KQTCMCDKNM VLCLMNQTYR EEYRGFLNVY 180
CQGPPTNCSI YEPPPEEVTC SHQSPAPPAP P

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Seq ID NO: 81 DNA sequence
Nucleic Acid Accession #: NM_018136.1
Coding sequence: 38..2218

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15 AAATGTATCA GAGGAAAAGA TGGCAGCCAT .TGTTAAACCA TCTGCCTCT GCTGTTACAG 120
AAGCAAACTC CAGTATGAAG CTGTTCAAAG TGAAGGTGTT ATGATTCAG AGTGGTATAA 180
AGCTTCTGGC CTGCTTGTT CACAGGAAGC AGAGTATCAT TCTCAAAGTA GGGCTGCAGT 240
AACAAITCAA AAAGCTTTTT GTAGAATGGT CACAAGAAAA CTGGAACAC AGAAATGTGC 300
TGCCCTACGG ATTCACTTCT TCCTTCAGAT GGCTGTGTAT CGGAGAAGAT TTGTTACGCA 360
20 GAAAAGAGCT GCTATCACTT TACAGCATTA TTTTAGGAGC TGGCAAACCA GAAAACAGTT 420
TTTACTATAT AGAAAAGCAG CAGTGGTTTT ACAAAATCAC TACAGAGCAT TTCTGTCTGC 480
AAAACATCAA AGACAAGTCT ATTTACAGAT CAGAAGCAGT GTTATCATT TCAAGCTAG 540
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TCAGGCTATG TGGAGGAGAT ATAGAGCCAA GAAATATTTA TGTAAGTGA AAGCTGCCTG 660
25 CAAGATTCAA GCCTGGTATA GATGTTGGAG AGCACACAAA GAATATCTAG CTGTATTAAA 720
AGCTGTTAAA ATTATTCAG GTTGCTTTCT TACCAAACTA GAGAGAACAC GGTTTTGTAA 780
TGTCAGAGCA TCAGCAATTA TCATTACAGG AAAATGGAGA GCTATACTTC CTGCAAGAT 840
AGCTCATGAA CACTTCTTAA TGATAAAAAG ACATCGAGCT GCTTGTTTGA TCCAAGCACA 900
30 TTATAGAGGA TATAAAGGAA GGCAGGTCTC TCTTCGGCAG AAATCTGCTG CTTTGATCAT 960
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TAAAAATCTC ACAGTTATCC TACAAGCACT GGTGCGTGGT TGGCTAGTAC GAAAAAGATT 1080
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35 GCAGGTTAAT TCAGTCACTC GTATTACAG ATGGTTTCGA GCAAGATTAC AAGAAAAGAG 1260
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40 TAATAGGAG ATTCGAGAAG AAAACAACT CTACAAAAGA ACTGCCTTG CACTTCATTA 1560
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TACTAGATTG TCTCCACTTT GTTGAGGAA CATGGCCAG AGTGAGGCAA TTTCTAAAAT 1680
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TGTGCAAGTC TTGCTTAATG TATCTAAGTA TGAGAAAAC ACTTCAGCAG TTTATGATGT 1800
45 AGAAAAATGT ATAGATATAC TATTGGAGCT TTTCAGATA TACCGAGAAA AGCCTGTAA 1860
TAAAGTTGCA GACAAAGCGG GAAGCATTTT TACAAAAACT TGTTGTTTGT TGGCTATTTT 1920
ACTGAAGACA ACAATAGAG CCTCTGATGT ACGAAGTAGG TCCAAAGTTG TTGACCGTAT 1980
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CAGAATAGTT TCAAGACTTA AGCCAGATTG GGTTTTGAGA AGAGATAACA TGGAAGAAAT 2160
50 CACAAATCCC CTCGAGCTTA TTCAATGGT GATGGATACG CTTGGCATTG CTTATTAGTA 2220
AATGTAAACA TTTTCAGTAT GTATAGTGT AAGAAATATT AAAGCCAATC ATGAGTACGT 2280
AAAGTGATT TTGCTCTCTG TGTACAAGTT TAAAATCTG ACTTTGTTTT AAAAAACAT 2340
AAACTGTTCA TTACATCTT CATTTTTATC ATTTATAGTT TTATGCATGT AATAAACTAA 2400
55 TATGTCATAA GATG

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Seq ID NO: 82 Protein Sequence
Protein Accession #: NP_060606.1

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1      11      21      31      41      51
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TWQTRKQPLL YRKAADVLLQ HYRAFLSAKH QROYVLQIRS SVIIIQARSK GFIIQKRFQE 180
65 IKNSTIKIQA MWRRYRAKRY LCKVKAACKI QAWRYCWRHA KEYLAVLKAV KIIQGCFFYTK 240
LERTRFLNVR ASAIIIQRKM RAILPAKIAH EHFLMIKRHR AACLIQAHYR GYKGRQVSLR 300
QKSAALLIQK YIRAREAGKH ERIKYEFPK STVILQALVR GWLVRKRFLE QRAKIRLLHP 360
TAAAYYHLNA VRIQRAYKLY LAVKNANKQV NSVICIQRFW RARLQEKRFI QKYHSIKKIE 420
HEGQECLSQR NRAASVIQKA VRHFLLRKKQ EKFTSGIIKI QALWRGYSWR KXNDCTKIKA 480
70 IRLSLQVVRN EIREENKLYK RTALALHYLL TYKHLAILE ALKHLEVVTR LSPLCENMA 540
QSGAISKIFV LIRSCNRSIP CMEVIRYAVQ VLLNVSKYEK TTSVAVDVEN CIDILLELLQ 600
IYREKPNKV ADKGGSIFTK TCCLLAILLK TTNRASDVRS RSKVVDRIYS LYKLTAHKHK 660
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TLGIPY

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Seq ID NO: 83 DNA sequence
Nucleic Acid Accession #: NM_000612.2
Coding sequence: 553..1095

1 11 21 31 41 51
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2 CTCCCCCCT CACGCCCGCC CTCTGGCCTT CGCCGAACCA AAGTGGATTA ATTACACGCT 120
3 TTCTGTTTCT CTCGGTGTCT TTCTCTCCCG CTGTGGCCTT GCCCGCCTCT CGCTGTCTCT 180
4 TCTCCCCCTC GCCCTCTCTT CGGCCCCCCC CTTTCAAGTT CACTCTGTCT CTCCTACTAT 240
5 CTCTGCCCCC CTCTATCTCT GATACACAG CTGACCTCAT TTCCCGATAC CTTTTCCTCC 300
6 CCGAAAGTA CAACATCTGG CCGCCCCCAG CCGGAAGACA GCCCGTCTCT CCTGGACAAT 360
7 CAGACGAATT CTCCCCCCC CCCCAGGATC AAAAGCCATC CCCCCGCTCT GCCCGTCTG 420
8 ACATTGGGCC CCGCGACTC GGCCAGAGCG GCGTGGCAG AGGAGTGTCC GGCAGGAGG 480
9 CCAACGCCCG CTGTTGGGTT TGGGACACGC AGCAGGAGG TGGGCGGCG CGTCCCGGC 540
10 TTCCAGACAC CAATGGGAAT CCCAATGGGG AAGTCGATGC TGGTGTCTCT CACCTTCTTG 600
11 GCCTTGGCCT CGTGTGCTAT TGCTGCTTAC CCGCCAGTG AGACCTCTGT CGGCGGGGAG 660
12 CTGTGGGACA CCCTCCAGTT CGTCTGTGGG GACCGCGGCT TCTACTTCAG CAGGCCCGCA 720
13 AGCGGTGTGA GCCGTGCGAG CGGTGGCATC GTTGAGGAGT GCTGTTTCCG CAGCTGTGAC 780
14 CTGGCCCTCC TGGAGACGTA CTGTGTACCC CCGCCCAAGT CCGAGAGGGA CGTGTGACC 840
15 CCTCCGACCG TGCTTCCGGA CAACTTCCCC AGATACCCCG TGGGCAAGTT CTTCCAATAT 900
16 GACACCTGGA AGCAGTCCAC CCAGCGCCTG CCGAGGGGCC TGCTGCTCTT CCTGCGTGCC 960
17 CGCGGGGTC ACCTGCTCGC CAAGGAGCTC GAGGCGTTCA GGGAGGCCAA ACCTCACCGT 1020
18 CCGCTGATTG CTCTACCCAC CCAAGACCCC GCCACCGGG GCGCCCCCCC AGAGATGGCC 1080
19 AGCAATCGGA AGTGAGCAAA ACTGCCGCAA GTCTGCAGCC CGGCGCCACC ATCTGCAGC 1140
20 CTCTCTCTGA CCAAGGACGT TTCCATCAGG TTCCATCCCG AAAATCTCTC GGTTCACGT 1200
21 CCGCTGGGG CTCTCTCTGA CCGAGTCCCC GTGCCCGGCC TCCCGGAAC AGGTACTCT 1260
22 CTGCGCCCC CTTCATGGG CTGAGGAAGC ACAGCAGCAT CTTCAAAATC GTACAAATC 1320
23 GATTGGCTTT AAACACCTTT CACATACCTT CCCCC

Seq ID NO: 84 Protein Sequence
Protein Accession #: NP_000603.1

30 1 11 21 31 41 51
1 MGIPMGKSM LLLTFLAFAS CCIAAYRPSE TLGGELVDT LQFVCGDRGF YFSRPASRVS 60
2 RRSRGIVEEC CFRSCDLALL ETYCATPAKS BRDVSTPPTV LPDNFPYRPV GKFFQYDTWK 120
3 QSTQRLRRGL PALLRARRGH VLAKELEAPR EAKRHRPLIA LPTQDPAHGG APPEMASNRK 180

Seq ID NO: 85 DNA sequence
Nucleic Acid Accession #: XM_092643.1
Coding sequence: 1-5352

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2 GACGACCTGG GGCCTCTTGA ATTACATGAC AGTGGTACCT TTCAACAAGT CGTGAACCTT 120
3 CTGGACATCA TTGACAGCGA GTACAGCAAG ACGGACACAA CAGGGGCAAG CCTTGACATG 180
4 CGGAAGACCC TGCCCTCGGT GATAATCATG GAGAAGGCCA CCACTGAGCC TTCTGTAGTG 240
5 ATAAACACTC TCATCCGCTG CCTGCAGGTG CCAGAGATTT CCACCCAGCG CAAGGTCAAC 300
6 ATTTACAACA TCCTCCAGGA CATCATCCAG CAGGAGGGGG AGCTGGAGGA GCAGTGCCTG 360
7 CAGAGGCTGG TGCCCATGTC CTCGAAGGAG ATGAGGGAGA TCCAGAGATG GAGGGCTAT 420
8 ATGAAGGCAG AGGTGGCCAG CGACACACTG GTGGCTCTGT CCGAAACCA CTTCAAGCTT 480
9 GTCATGTAGC AGCTGCAGCA CCACCTCAAG CCCCTCAACC TCACTGATGA ATTTGTCTATC 540
10 ATCACACTGG CCAAGCTGGC CAACGGCAAT GTGTTTGTAG TCATGCCATA CATGGGCATC 600
11 ACCCTGGCTA CCATATTAC CATGCTGAGA CTGCGCAATG AAGCCCAAGT ACGCCAGCG 660
12 ATCTGCAGTG CCATGGAGAC CTTCTGTGAG ACGGTGCAGT TTTATCTGAA GCACCTGGAG 720
13 GAGAGCGTGT ACCCGTGTAT GACTGAGGAG GAGTTTGGCC TGAAGGTGTT CCCCATGTAT 780
14 CGCTACTTCG TGACAGTGTG GCTGAGGCAC TACAACCCCG AGGTGAAGCT GGGGTGATC 840
15 AAGTCCCTGA AGCCCATGCT GGGCTCTCTT CTGCCCAAG ATGACCTGCG GGAGCAGGTC 900
16 TACGACTACA TCCCTCTGCT GCTGGCGGAG TACCAGGCA GTCTGGAGGT CTTGAGGCAG 960
17 ATCCTGGAAC TGTCACTCAC CACCAACACC CCTGTCCCC AAATGCAGCT ACACACCATT 1020
18 TTACAGAAC TGCACGTCCA GGTGTGCAAC AAGGCCCGG CCCAGCATCA GTACAGCAGC 1080
19 CAGAATCTGA TGGAGATGTT GCACCTGCTT GTAGCCCTTG CTGCTCTCTA CCCCAGGAG 1140
20 CTGATGAAGT TCTTCTCTAG CCAGATGGAG ACAACAAGG AGGCGTCCG CGTGGGGACT 1200
21 CTGAATCTGA TTAGGGCTAT AGTGAGCGCA GATGAGCCCA GGTAGATGAT CAGGGCCATC 1260
22 TACCTGGCTA TCCGGGTAGT CAAGAACACC ATCTCTGATA CCGGTCCAA GGTGAGGATG 1320
23 GCTATTCTCC ACATCATTTG GCAGTTGGCT CTCTGTGGCT ACCAGGAGAG AATCAAAGGC 1380
24 TGGGGCTTGA AGTACCTGTC TGTGCAGCTG ACCTTATCCA CCTACAACT GACAAATGCG 1440
25 CGGGAGAAGT TTTATCAGAG GGAATGGGAG GAGAGGATGG TCCACAAAGT CACCATGGAC 1500
26 ACTGTGAAGA TCATTACCTC TTCTGTCACT GGAATGACCA CCGAGTTTGT GGTGAGGCTG 1560
27 CTGTGCTACA TCATGGAGAC AGACTACGTG GAAGCTTTGA CTCTATCTG TATCAGCTC 1620
28 ACAAACTGCG CAGAACACCA GCTCCATGGC CAGGATGTGG ATGTGAGCGT GGCTGGCAAG 1680
29 AGCAGGCAAG TGGACCTGCC TGCACTCAG AAGCTGTGCG CCGCTCTCTT GGTGCTGATG 1740
30 TCATCACTT ACAAGGGGGA GGGTCTGGGG ATAGCCATGC TCAACCTCTT GAGGACCTG 1800
31 AGCCAGAGCA TGCACCTCTC CATGGCCGAC ATGTGGGAGC TGGAGATGTC GCTACTGTGTC 1860
32 CGGTACCTGG AAGAATATAC TGAGTTCACT TGGGATCAGA AAGCCTGGGA AGACAAGCTG 1920
33 ATTCAGTTTC TCGAAATCTC CCTCAAGAAG ACCCGGGGGT CTAGCTGGAG CTGCGCTTT 1980
34 AGTAAAGAGC TGAACAACCA GATTGCGAGC TTGACAGCC CCTCTCTGGA GAAGGGCTTT 2040
35 CTGTACCGGG CCTTGGGCTT CACCTTGGCC ACAGGCTGG AGGCCAGCAA GGTGGAGGTC 2100
36 CTGCTGTGAG AGCTGCTGTA CAAGACGAGC TACAGCAATG ACTTTGACAG CGAGGGTGTG 2160

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Seq ID NO: 86 Protein sequence:
 Protein Accession #: XP_092643.1

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 QRLVAIASKE MREIPEMBGY MKAEVASDTL VALSRNHPSL VMYELQHHLK PLNLTDEFVI 180
 ITLAKLANGN VFEPMPYMG I TLATIFTMLR LANEAKIRQA ICSAMETPCE TVQFYLKHL 240
 ESVPVMTTEE EFALKVPFMY RYFVTVWLRH YNPEVKLGVI KSLKPLMLGLL LPNDDLREQV 300
 YDYIPLLLAE YQGSLEVLQ ILELSVTINT FVPQMLQHTI FTELHVQVCN KAPAQHQYSS 360
 QNLMEMVHCF VALARSYPKE LMKFFFSQME TNKEAVRVGT LNLIRAI VSA DEPRMSIRAI 420
 YLAIRVVKNT ISDTRSKVRM AILHIIGQLA LCGYQERIKG WGLKYL SVQL TLSTYKLTNR 480
 REKFYQRDLE ERMVHKVTMD TVKIIITSSVS GMTTFEFWRL LCYIMETD YV EALTPICTSL 540
 TNLAEHLHG QDVDSVAGK SRQVDLPAPQ KLLARLLVLM SSPYKGBGRG IAMLNLLRTL 600
 SQSIAPSMAD MWLEBIALIV RYLEEHTEFT WDQKAWEDKL IQFLRNLSKK TRGSSWSRL 660
 SKELNNQIAS FDSPLSKGPF LYRALGFTLA TGLEASKVEV LLELLYKTD YSNDFDSEGV 720
 IMCFGLCARG QVKTVLNVLH DFEERIQESE QSWQISAWRK DHPWRRETVK SALVMVYSCV 780
 ASYCHPQLLL NLVDSPIITAK IHHYVSSCQ DICLKMAMFK SVVQVTKAIN NIKDLEDHPH 840
 AQKTTLSII VAVIKAEPTD NLVSPVRALA MEALSHLSKL KPFFYSTBENS ELMDISHSV 900
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 EKAVSLHLYL MWIYVHSTAV CIHLKLGQFG TMVGLIAPCT CDAHQRTMA SMNVLSLLD 1020
 LEASQTCSLW GPSKQKELEK CKGDLOSTDV EKIPASSRI ARVVMCFSC DEVVSLIQLK 1080

5 CENTGAMNLQ HDKASVTWIA FFLQMRKAKEL EDKVAEILSA ILVHLPVVDH PEVRRLLIDG 1140
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SATSKADIWR LAAVDPLMTL CTIHLIQLK DENDKLPDFL PDLIYTLILLQ LGSSHRPEAA 1260
PPVLKMKLV HTTPLEEMN LQRCRGRVT IKSMQLLFKR VKSQAHLAHL DEQAVWDLQ 1320
10 DGGTFLEGVS LLARLQMCHV EGHQRRLAEL VLRGMDSEVL SCRISSTAVC VEMRHRFMSG 1380
PVLVQEKLLK PAALLLEKGA DQSEDEALRV LSLRALGNMA LGAPKKVKQY RVLLEKCLG 1440
PLREPVNSV TABGMEALTK ILAELREGDV GSSFDAMSEQ CRIFPDNESE LLRLKAPILF 1500
GKLARVVMS KKHFFKGEVK KAWIPLMLHS QDPCSNAAQV RYILGFVSQS GARCSPRKQV 1560
LGSAGSACMA TMFQCVHFWG WKSLEHPSGP SDTATDDKMT VFQTTMCSIL TRKKPAVLVYR 1620
15 FLLETMAVVK NNLRSIRIAA CNLAGIIMQK MSHYLLKLD FPALRNSLQE LQLDPDPGPT 1680
GPKGRKLALC LHSEFIHTHA DSVPKARHCA KRAGKPLGN CSQSNQQRNS PSGVPSTGES 1740
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15 Seq ID NO: 87 DNA sequence
Nucleic Acid Accession #: CAT cluster

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25 CAGCCTGGGG TGGTGAGTCA TGCAAGACTC TTTCACTGCT GTTCCCTGAG GTCAAGAGCC 360
CTGCAGGTCA GCCCTGAGGA CTATCCGGCC TCCAGCCCTT GATGTTAACT TCACCTCATG 420
CCTTTCAAGG CAGGGGAAA AGTTAGCAAT CCTTGGAGAC TTAACAGGGT GCAGTGAAAC 480
CAGGCCCTTT GAAGAGCTTA CCAATCAGTC TGCCCTTGTG CATCCCGAG CAGATGTGTG 540
GTGGTATTGC TGGGGACTAC TGCTGGGTAC TCTGCCAAGT AATTAGAGCA GCACCTCATG 600
30 TCTAGTCCAA CTGGCCATCC CTTTCAACCT AGCATTCTGT CAATATGATA AAAAAAATG 660
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35 Seq ID NO: 88 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..759

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45 CACACATGTT TAGTTTAAAT TAATTACCAT ACAAAGGTCC GACCAGACCT AGGAGAAACT 360
CCCTTCAGGA CCGGACAAACA CTTTATAGAT GGTTCCTCCC AGGTGATAGA GGGAAAAAGA 420
TACAAATGGT ATTCAAGTAT TGATAGAGAA ACTCTGTGAG AAATAGAGTT AGGAAAAATTG 480
CCTAATAATT GGTCTGCTCA AACATGTGAG CTGTTTGAC TCAGCCAAGC CTTAAAGGAC 540
TTACAGAAAC AGGAAGGAAC CATCTATACA GATTCTAAGT ACGCCTTTGG AGTGGCTCAT 600
50 ACATTGTGAA AAATTTGAGC TGAACGAGGT CTTATTAATA GCAATGCGCA AGACTTGGTC 660
CATAAGGAAT TAATCACCCA AGTATTAAT AACCTTCAGC TGCCAAAGA AACAGCTATT 720
GACCATGTCC CCGGACACCA AAAAGGCTT TCTTTTAA

55 Seq ID NO: 89 Protein Sequence
Protein Accession #: FGENESH predicted

1 11 21 31 41 51
60 MQEETGWQLG ERILTYHGDQ VTLCTDPEES RKISFGNLI VNTPHQVRTI LSQKAERWLT 60
DSRILKYEAI LLEKDDLTLT TNSLNPAGF LTGDLVQKRE HTCLVLINXH TKVRPDLGET 120
PFRTGQHFID GSSQVIEGKR YNGYSVIDRE TLVEIELGKL PNMNSAQTC LFAISQALKD 180
LQNQEETIYT DSKYAFGVAR TFGKIWTERG LINSKQDLV HKELITQVLT NLQLPKETAI 240
DHPVGHQKSL SF

65 Seq ID NO: 90 DNA sequence
Nucleic Acid Accession #: NM_000756.1
Coding sequence: 186..776

1 11 21 31 41 51
70 AGAAACTCAG AGACCAAGTC CATTGAGAGA CTGAGGGGAA AGAGAGGAGA GAAAGAAAAA 60
GAGAGTGGGA ACAGTAAAGA GAAAGGAAGA CAACCTCCAG AGAAAGCCCC CGGAGACGTC 120
TCTCTGAGA GAGGCGGCG CACCCGCTC ACCTGCGAAG CGCCTGGGAA GCGAGTGCCC 180
CTAATATGCG GCTGCGGCTG CTTGTGTCCG CGGAGTCTCT GCTGGTGGCT CTCCTGCCCT 240
75 GCCCGCATG CAGGCGGCTC CTGAGCCGCG GGCCGGTCCC GGGAGCTCGG CAGGCGCGC 300
AGCACCTCA GCCCTTGGAT TTCTTCCAGC CGCCCGCGCA GTCCGAGCAG CCCAGCAGC 360
CGCAGGCTCG GCGCGTCTG CTCGCGATGG GAGAGGAGTA CTTCTCCGCG CTGGGGAAAC 420
TCAACAAGAG CCCGCGGCTC CCGCTTTCG CCGCTCTCCT GCTCTCGGCC GGAGGCAGCG 480
GCAGCGGCC TTCCCGCGAA CAGGCGACCG CCAACTTTTT CCGCTGTGTG CTGAGCAGC 540

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TGCTGCTGCC TCGCGCTCG CTGACAGCC CCGCGGCTCT CGCGGAGCGC GCGCTAGGA 600
ATGCCCTCGG CGGCCACCAG GAGGCACCGG AGAGAGAAAG GCGGTCCGAG GAGCCTCCCA 660
TCTCCTCGGA TCTCACCTTC CACCTCCTCC GGGAAAGTCTT GGAATGGCC AGGGCCGAGC 720
AGTTAGCACA GCAAGCTCAC AGCAACAGGA AACTCATGGA GATTATTGGG AAATAAAACG 780
GTGCGTTTGG CCAAAAAGAA TCTGCATTTA GCACAAAAAA AATTAAAAAA AATACAGTAT 840
TCTGTACCAT AGCGCTGCTC TTATGCCATT TGTTTATTTT TATATAGCTT GAAACATAGA 900
GGGAGAGAGG GAGAGAGCCT ATACCCCTTA CTTAGCATGC ACAAAGTGTA TTCACGTGCA 960
GCAGCAACAC AATGTTATTCT GTTTTGTCTA CGTTTAGTTT CCGTTTCCAG GTGTTTATAG 1020
TGGTGTTTTA AAGAGAATGT AGACCTGTGA GAAAAAGTTT TGTTTGAAAA AGCAGACAGA 1080
AGTCACTCAA TTGTTTGTGT TGTGGTCTGA GCCAAAGAGA ATGCCATTCT CTGGGTGGG 1140
TAAGACTAAA TCTGTAAGCT CTTTGAACA ACTTCTCTT GTAAACGTTT CAGTAATAAA 1200
ACATCTTTC AGTCCTTGGT CAGTTTGGTT GTGTAAGAGA ATGTTGAATA CTTATATTTT 1260
TAATAAAGT TGCAAGGT
```

Seq ID NO: 91 Protein Sequence
Protein Accession #: NP_000747.1

20
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35
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1 11 21 31 41 51
| | | | |
MRLPLLVSAG VLLVALLPCP PCRALLSRGP VPGARQAPQH PQPLDFFQPP PQSEQPQQPQ 60
ARPVLLRMGE EYFLRLGNLN KSPAAPLSPA SLLLAGSGSG RPSPEQATAN FFRVLLQQLL 120
LPRRSIDSPA ALAERGARNA LGGHQEPAPER ERRSEEPPI SLDLTFHLLRE VLEMARAEQL 180
AQAHSNRKL MEIIGK
```

Seq ID NO: 92 DNA sequence
Nucleic Acid Accession #: NM_004217.1
Coding sequence: 58..1092

30
35
40
45
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1 11 21 31 41 51
| | | | |
GGCCGGGAGA GTAGCAGTGC CTTGGACCCC AGCTCTCCTC CCCCTTCTC TCTAAGGATG 60
GCCCAGAAGG AGAAGCTCTTA CCCCTGGCCC TACGGCCGAC AGACGGCTCC ATCTGGCCTG 120
AGCACCTGCG CCCAGCGAGT CCTCCGGAAA GAGCCTGTCA CCCCATCTGC ACTTGTCTCT 180
ATGAGCCGCT CCAATGTCCA GCCCACAGCT GCCCCTGGCC AGAAGGTGAT GGAGAATAGC 240
AGTGGGACAC CCGACATCTT AACCGCGCAC TTCACAATTG ATGACTTTGA GATTGGGCGT 300
CCTCTGGGCA AAGGCAAGTT TGGAAAAGTG TACTTGGCTC GGGAGAAGAA AAGCCATTTC 360
ATCCTGGGCG TCAAGTCTCT CTTCAAGTCC CAGATAGAGA AGGAGGGCGT GGAGCATCAG 420
CTGGCGAGAG AGATCGAAAT CCAGGCCAC CAGCACCATC CCAACATCCT GGTCTCTAC 480
AACTATTTTT ATGACCGGAG GAGGATCTAC TTGATTCTAG AGTATGCCCC CGCGGGGAG 540
CTCTACAAGG AGCTGCAGAA GAGCTGCACA TTGACGAGC AGCGAACAGC CACGATCATG 600
GAGGAGTTGG CAGATGCTCT AATGTACTGC CATGGGAAGA AGGTGATCA CAGAGACATA 660
AAGCCAGAAA ATCTGCTCTT AGGGCTCAAG GGAGAGCTGA AGATTGCTGA CTTGGGCTGG 720
TCTGTGCATG CGCCTCCCT GAGGAGGAAG ACAATGTGTG GCACCTCGGA CTACCTGCCC 780
CCAGAGATGA TTGAGGGGCG CATGCACAA GAGAAGGTGG ATCTGTGGTG CATTGGAGTG 840
CTTTGCTATG AGCTGTGTTT GGGGAACCCA CCCTTTGAGA GTGCATCACA CAACGAGACC 900
TATCGCCGCA TCGTCAAGGT GGAACATAAG TTCCCGCTT CTGTGCCAC GGGAGCCAG 960
GACCTCATCT CCAAACTGCT CAGGCATAAC CCCTCGGAAC GGCTGCCCTT GGCCAGGTC 1020
TCAGCCACCC CTTGGGTCCG GGCCAACTCT CGGAGGGTGC TGCCTCCCTC TGCCCTTCAA 1080
TCTGTGCCT GATGTCCCT GTCAATCACT CGSGTGCGTG TGTTTGTATG TCTGTGTATG 1140
TATAGGGGAA AGAAGGGATC CTTAACTGTT CCCTTATCTG TTTTCTACCT CCTCCTTTGT 1200
TTAATAAAG CTGAAGCTTT TTGT
```

Seq ID NO: 93 Protein Sequence
Protein Accession #: NP_004208

55
60
65

```
1 11 21 31 41 51
| | | | |
MAQKENSYPW PYGRQTAPSG LSTLPQVRVR KEPVTPSALV LMSRSNVQPT AAPGQKVMEN 60
SSGTPDILTR HPTIDDPBIG RPLGKGFEN VYLAREKSH FIVALKVLFK SQIEKEGVEH 120
QLRREIEIQA HLHHPNLR LYNFYDRRI YLILEYAPRG ELYKELQKSC TFDEQRTATI 180
MEELADALMY CHGKVIHRD IKPENLLGL KGLKIAIDFG WSVHAPSLR KTMCGTLDYL 240
PPEMIEGRMH NEKVDLWICG VLYCYELLVGN PPFESASHNE TYRRIKVDL KPPASVPTGA 300
QDLISKLLRH NPSERLPLAQ VSAHPWVRAN SRRVLPPSAL QSVA
```

Seq ID NO: 94 DNA sequence
Nucleic Acid Accession #: NM_007019.1
Coding sequence: 41..580

70
75

```
1 11 21 31 41 51
| | | | |
GGCAGGAGCG AGTCTCTGTC TCTCTGCCAA CGCGGCCCGG ATGGCTTCCC AAAACCGCGA 60
CCCAGCCGCG ACTAGCGTGC CCGCGGCCCG TAAAGGAGCT GAGCGAGCG GGGGCGCGC 120
CCGGGTCCG GTGGGCAAAA GGCTACAGCA GGAGCTGATG ACCCTCATGA TGTCTGGCGA 180
TAAAGGATT TCTGCTCTCC CTGAATCAGA CAACCTTTT AAATGGGTAG GGACCATCCA 240
TGGAGCAGCT GGAACAGTAT ATGAAGACCT GAGGTATAAG CTCTCGCTAG AGTCCCCAG 300
TGGCTACCCT TACAATGCGC CCACAGTGAA GTTCTCTCAG CCCTGCTATC ACCCAACGT 360
GGACACCCAG GGTAAACATAT GCCTGGACAT CCTGAAGGAA AAGTGGTCTG CCCTGTATGA 420
TGTCAGGACC ATCTGCTCTT CCATCCAGAG CCTTCTAGGA GAACCAACA TTGATAGTCC 480
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5 CTTGAACACA CATGCTGCCG AGCTCTGGAA AAACCCACCA GCTTTTAAGA AGTACCTGCA 540
 AGAAACCTAC TCAAGCAGG TCACCAGCCA GGAGCCCTGA CCCAGGCTGC CCAGCCTGTC 600
 CTTGTGTCGT CTTTAAATTT TTCTCTAGA TGGTCTGTCC TTTTGTGAT TTCTGTATAG 660
 GACTCTTTAT CTTGAGCTGT GGTATTTTTC TTTTGTGTTT GTCTTTTAAA TTAAGCCTCG 720
 GTTGAGCCCT TGTATATTAA ATAAATGCAT TTTTGTCTTT TTTTAAAAAA AAAAAAAAAA 780
 AAA

Seq ID NO: 95 Protein Sequence
 Protein Accession #: NP_008950.1

10 1 11 21 31 41 51
 MASQNRDPAA TSVAARAKGA EPSGGAARGP VGKRLQOELM TLMMSGDKGI SAPPESDNLF 60
 15 KMWGTIHGAA GTVYEDLRYK LSLFPPSGYP YNAPTVMKFLT PCYHPNVDTQ GNICLDILKE 120
 KWSALYDVRT ILLSIQSLLG EPNIDSPLNT HAAELWKNPT AFKKYLQETV SKQVTSQEP 179

Seq ID NO: 96 DNA sequence
 Nucleic Acid Accession #: AK055663
 Coding sequence: 38..1423

20 1 11 21 31 41 51
 AGAACGGCTT CCGCGGGGAG CTGTGCAGCT CCTTATCATG GGGACAATTC ATCTCTTTTG 60
 25 AAAACACCAA AGATCCTTTT TTGGCAAGTT GTTACGGGAA TTTAGACTTG TAGCAGCTGA 120
 CCGAAGGTCC TGAAGATAC TGCTCTTTGG TGTAAATAAC TTGATATGTA CTGGCTTCCT 180
 GCTTATGTGG TGCAGTTCTA CTAATAGTAT AGCTTTAACT GCCTATACCT ACCTGACCAAT 240
 TTTTGATCTT TTTAGTTTAA TGACATGTTT AATAAGTTAC TGGGTAACAT TGAGGAAACC 300
 TAGCCCTGTC TATTCATTG GGTTTGAAAG ATTAGAAGTC CTGGCTGTAT TTGCCTCCAC 360
 30 AGCTCTGGCA CAGTTGGGAG CTCTCTTTAT ATTTAAAGAA AGTGCGAAGC GCTTTTGGGA 420
 ACAGCCCGAG ATACACACGG GAAGATTATT AGTTGGTACT TTTGTGGCTC TTTGTTTCAA 480
 CCTGTTACAG ATGCTTTCTA TTCGGAATAA ACCTTTTGCT TATGTCTCAG AAGCTGCTAG 540
 TACGAGCTGG CTTCAGAGC ATGTTGCAGA TCTTAGTCGA AGCTTGCTG AGAATTATTC 600
 GGGACTTAGC AGTATCTTCC TTCCCCGAAT GAATCCATTT GTTTTGATTG ATCTGTCTGG 660
 35 AGCATTTGCT CTTTGTATTA CATATATGCT CATTTGAAAT AATAATTATT TTGCCGTAGA 720
 CACTGCCTCT GCTATAGCTA TTGCCCTTGT GACATTTGGC ACTATGTATC CCATGAGTGT 780
 GTACAGTGGG AAAGTCTTAC TCCAGACAAC ACCACCCCAT GTTATGTGTC AGTTGGACAA 840
 ACTCATCAGA GAGGTATCTA CCTTAGATGG AGTTTATAGAA GTCCGAAATG AACATTTTGT 900
 GACCCTAGGT TTTGGCTCAT TGGCTGGATC AGTGCATGTA AGAATTCGAC GAGATGCCAA 960
 40 TGAACAAATG GTTCTTGCTC ATGTGACCAA CAGGCTGTAC ACTTAGTGT CTACTCTAAC 1020
 TGTTCAAATT TTCAGGATG ACTGGATTAG GCCTGCCTTA TTGTCTGGGC CTGTTGCAGC 1080
 CAATGTCTTA AACTTTTCAG ATCATCACGT AATCCCAATG CCTCTTTTAA AGGGTACTGA 1140
 TGATTTGAAC CCAGTTACAT CAACTCCAGC TAAACCTAGT AGTCCACCTC CAGAATTTTC 1200
 ATTTAAACACT CCTGGGAAAA ATGTGAACCC AGTTATTCTT CTAACACAC AAACAAGGCC 1260
 45 TTATGGTTT GGTCTCAATC ATGGACACAC ACCTTACAGC AGCATGCTTA ATCAAGGACT 1320
 TGGAGTTCCA GGAATTGGAG CAACTCAAGG ATTGAGGACT GGTTTTACAA ATATACCAAG 1380
 TAGATATGGA ACTAATAATA GAATTGGACA ACCAAGACCA TGATAGACTC TAACTTATTT 1440
 TTATAAGGAA TATTGACTCC TTGGCTTCCA ATTTATTTAG TAACTCAACT TTGCATTGAC 1500
 TGTTTAATCA TTTACTCTAA ATGTTAGATA ATAGTAGTCT TGTTCACATT TCATGAAACC 1560
 50 TATGAACTA TATTTTGTGA AAATGTATTT GTGACAGTGA AATCCCTCGTA AATGTTAAAG 1620
 GCTTTAAATA GGCTTCCTTT AGAAAATGTG TTTCTTTAAA TTTGGATTTT GGTATCTTTG 1680
 GTTTTGTAGT TGACTGCACT GTGATGTGAC CTTACCTTTA TAAGAGCCAC TTGATGGAGT 1740
 AGATCTGTCA CATTACTAAG ATACGATATT TCTTTTTTT TCCGAGACGG AGTCTTGCTC 1800
 TGCCACTGTG CCGGCCCAAT ACATTATTAT TAACTTAAGG CTGTACTTTA TTAAGGCTTC 1860
 55 CTTAGTTTTT GTTTTGTTTT GTTTTTTGAG ATGGAGTCTC ACTCTGTGCC CCAGGCTGGA 1920
 ATGCAAGTGGC ATGATCTCAG CTCACCTGCA CCTCTGCCTC CTGAGTTCAA ATGATTCTCC 1980
 TGCCCTCAGC TCCCGAGTAG CTGGGATTAC AGGCACCTGC CACCACGCCC AGCTAATTTT 2040
 TGTATTTTAA GTAAAGACGG GGGATTTCAC CATGTTGGCC AGGCTGGTCT TGAACCTCTG 2100
 ACCTCATGAT CCACCCACCT TAGCCTCCCA AAGTGTCTGG ATTAGGTGTG AGCCACCGCA 2160
 60 CCTGGCCGAT ATTTCTTTA ATGAAATTTA TAAATATGCT TCTTGARTAA TACACATTTT 2220
 GGGAAAGGGA AAAATGTCTG TTCAAAAAGT AAAGGTCTCT TTTATAGCTT TTCCAAACTT 2280
 AATTGCTAAA TTTTCTTTTG AGGTCTCTCT GAATTATGTC TTACAAACTA AAAGCAAAAA 2340
 TTTTGTAGCA AAATTTTGA ATACATTCTA TCTAGCACAA TTTGAATTTT TAATTATCAA 2400
 GATTTTGTGT AAAGTTTCTC TCCTTTAAAA ATTTTAGTAC ATTTGTAAAT

Seq ID NO: 97 Protein Sequence
 Protein Accession #: BAB70980.1

70 1 11 21 31 41 51
 MGTIHLFRKP QRSFFGKLLR EFRLVAADRR SWKILLFGVI NLICTGFLM WCSSTNSIAL 60
 TAYTYLTIFD LFLSLMCLIS YWVTLRKPSV VYSFGFERLE VLAVFASTVL AQLGALFILK 120
 ESAERFLEQP EIHTGRLLVG TFVALCFNLF TMLGIRNKPF AYVSEAASTS WLQEHVADLS 180
 RSLCGIIPGL SSIFLPRMNP FVLIDLAGAF ALCITYMLIE INNYFAVDTA SAIAIALMTF 240
 75 GTMYPMSVYS GKVLQQTTPP HVIGQLDKLI REVSTLDGVL EVRNEHFWTL GFGSLAGSVH 300
 VRIRRDANQ MVLAHVTNRL YTLVSLTLVQ IFKDDWIRPA LLSGFVAANV LNFSDHHVIP 360
 MPLLKGTDDL NPVTSTPAKP SSPPEFSFN TPGKNVNPVI LLNTQTRPYG FGLNHGHTPY 420
 SSMLNQGLGV PGIGATQGLR TGFTNIPSRY GYNNRIGQPR P

Seq ID NO: 98 DNA sequence
Nucleic Acid Accession #: CAT cluster

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5 1 11 21 31 41 51
| | | | |
ATGGACTTAA CCAATGCTTC ACAATACCA AGAAAAAAT ATTCAATGT GATAAATATA 60
GGAAAGTTTT TCATAAATTT TCAAATTCAA ACTGACATAA GAGAAGACAT ACGGGAAAAA 120
AGACCTTTCA AATGTATAGA ATGTGGCAA GCTTTTAACA AGTTTCAAC CCTTACTACA 180
CATAAGAAAA TTCATACTAG AGAGAAACCC TACAAATGTG AAGAATGTGG CAAAGCCTTC 240
10 AACTGGTCTC CATACCTTAC TATACATAAG AGAATTCATA CTGGAGAGAA ACTCTACAAA 300
TGTGAAGAAT GTGGCAAAGC CTTCACCTGG TCCTCATACC TTACTGCATA TAAGATAACT 360
CATACTAGAG AGAAACCCCTA CAAATGTGAA GAATGTGGCA AAGCCTTTAA GTACTCCTCG 420
AACCTCACTA CACATAAGAT AATTCATACT GGAGAGCATC TCTACAAGTG TGAAGAATGT 480
15 GGCAAAGCGT TTAACCATGC TGCATGCTTC TTTGTCATTT TGAAGATTG A
```

Seq ID NO: 99 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..531

```
20 1 11 21 31 41 51
| | | | |
ATGGACTTAA CCAATGCTTC ACAATACCA AGAAAAAAT ATTCAATGT GATAAATATA 60
GGAAAGTTTT TCATAAATTT TCAAATTCAA ACTGACATAA GAGAAGACAT ACGGGAAAAA 120
25 AGACCTTTCA AATGTATAGA ATGTGGCAA GCTTTTAACA AGTTTCAAC CCTTACTACA 180
CATAAGAAAA TTCATACTAG AGAGAAACCC TACAAATGTG AAGAATGTGG CAAAGCCTTC 240
AACTGGTCTC CATACCTTAC TATACATAAG AGAATTCATA CTGGAGAGAA ACTCTACAAA 300
TGTGAAGAAT GTGGCAAAGC CTTCACCTGG TCCTCATACC TTACTGCATA TAAGATAACT 360
CATACTAGAG AGAAACCCCTA CAAATGTGAA GAATGTGGCA AAGCCTTTAA GTACTCCTCG 420
30 AACCTCACTA CACATAAGAT AATTCATACT GGAGAGCATC TCTACAAGTG TGAAGAATGT 480
GGCAAAGCGT TTAACCATGC TGCATGCTTC TTTGTCATTT TGAAGATTG A
```

Seq ID NO: 100 Protein Sequence
Protein Accession #: FGENESH predicted

```
35 1 11 21 31 41 51
| | | | |
MDLTNASQIP RKYPNVINI GKFFINFQIQ TDIREIREK RPFKCIEGK AFNKFSTLTT 60
HKKIHTREKP YKCEECGKAP NWSSYLTIHK RIHTGEKLYK CEECGKAFNW SSYLTAHKIT 120
40 HTREKPKYKCB ECGKAPKYSS NLTHKIIHT GEHLYKCEEC GKAFNHAACF FVILKI
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Seq ID NO: 101 DNA sequence
Nucleic Acid Accession #: NM_032589.1
Coding sequence: 147-422

```
45 1 11 21 31 41 51
| | | | |
GGCAGAGGCT CTGTGTTATGC AAATAGGCTT CCCACTTGGC AGGGGCGGTC TTGTCCACTC 60
GTTTCTGTAA ACATGGGTGG CAAAAGAGA AGATGGAGCT GCCATTTAGA ACATGCCTAA 120
50 TCCAGCTTTC ATCTTGCTGA GCAAAATGA AGGAGCTGG ACCCAACTTT GTTACTGTGA 180
GAAAGGGTCT TCATTCACTC AAGATGGCAT TTGTTAAGCA CCTACTGCTG GAGTGCAGTG 240
GTTCAATCAC GGATCACTGC AGCCTCCACC TCCAGTTTCA AGAAATCTTC ATGTCTCAGC 300
CTCTGAGACA GCTAGGATTA CAGACAAACC TTGGAATCA AGAAAGTTCT GGAATGATGA 360
AGCTGTTTAT GCCAAGACCG AAGTGCTGG CCCAGTATGA GTCCATTGAG TTCTATGCCG 420
55 GACAATTTTC TTGGAAGTCC TTTTATTGT TAGTTCTCAC TTGTTTCCAT ATTTAGTGAA 480
TGTACATTTA ATTGCAAGC TGTCTAAT AAAAAATCTT ATAGTACCTC ACTGCAC
```

Seq ID NO: 102 Protein sequence:
Protein Accession #: NP_115978.1

```
60 1 11 21 31 41 51
| | | | |
MKEPGPNFVT VRKGLHSFKM AFVHLLLEC SGSITDHCSL HLPVQEILMS QPPEQLGLQT 60
65 NLGNQESSGM MKLFMPRPKV LAQYESIQFM P
```

Seq ID NO: 103 DNA sequence
Nucleic Acid Accession #: NM_014501.1
Coding sequence: 60..737

```
70 1 11 21 31 41 51
| | | | |
GGCGGACCGA AGAAGCGAGG AAGGGGGCCG GGGGGACCGC CCCCAGGCGC GCCGACGCA 60
TGAAGTCCAA CGTGGAGAAC CTACCCCGCG ACATCATCCG CTGGGTGTAC AAGGAGGTGA 120
CGACACTGAC CGCAGACCCA CCCGATGGCA TCAAGGTCTT TCCCAACGAG GAGGACCTCA 180
75 CGGACCTCCA GGTCAACATC AGGGGCCCTG AGGGGACCCC ATATGCTGGA GGTCTGTTCC 240
GCATGAAACT CCTGCTGGGG AAGGACTTCC CTGCCTCCCC ACCCAAGGGC TACTTCCTGA 300
CCAAGATCTT CCACCCGAAC GTGGGCGCCA ATGGCGAGAT CTGCGTCAAC GTGCTCAAGA 360
GGGACTGGAC GGCTAGAGCTG GGCATCCGAC ACGTACTGCT GACCATCAAG TGCTGCTGTA 420
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TCCACCTAA CCCCAGTCT GCACTCAACG AGGAGGCGGG CGCCTGCTC TTGAGAACT 480
 ACGAGGAGTA TCGCGCTCGG GCCCGTCTGC TCACAGAGAT CCACGGGGGC GCCGCGGGC 540
 CCAGCGGAG GCGCGAAGCC GGTGCGGCCC TGGCCAGTGG CACTGAAGCT TCCTCCACCG 600
 ACCCTGGGGC CCCAGGGGGC CCGGAGGGG CTGAGGGTCC CATGGCCAAG AAGCATGCTG 660
 GCGAGCGGA TAAGAAGCTG GCGGCAAGA AAAAGACGGA CAAGAAGCGG GCGCTGCGGG 720
 CGCTGCGGG GCTGTAGTGG GCTCTCTTCC TCCTTCACC GTGACCCCAA CCTCTCCTGT 780
 CCCTCCCTC CAACTCTGTC TCTAAGTTAT TTAATATATG GCTGGGGTCG GGGAGGGTAC 840
 AGGGGCACT GGGACCTGGA TTGTGTTTTC TAAATAAAGT TGGAAAAGCA

10 Seq ID NO: 104 Protein Sequence
 Protein Accession #: NP_055316.1

1 11 21 31 41 51
 15 MNSNVENLPP HIIRLVYKEV TTLTADPPDG IKVFPNEEDL TDLQVTIEGP EGTPTYAGGLF 60
 RMKLLLGKDF PASPPKGYFL TKIFHPNVGA NGEICVNVLK RDWTAELGIR HVLLTIKCLL 120
 IHPNPESALN EEAGRLLEN YEYAARARL LTEIHGGAGG PSGRABAGRA LASGTBASST 180
 DPGAPGGPG AEGPMAKKHA GERDKKLAAL KKTDKKRALR ALRRL

20 Seq ID NO: 105 DNA sequence
 Nucleic Acid Accession #: NM_005101
 Coding sequence: 76..573

25 1 11 21 31 41 51
 CGGCTGAGAG GCAGCGAACT CATCTTTGCC AGTACAGGAG CTTGTGCGGT GGCCACACGC 60
 CCACAGCCCA CAGCATGGG CTGGGACCTG ACGGTGAAGA TGCTGGCGGG CAACGAATTC 120
 CAGGTGTCCC TGAGCAGCTC CATGTCGGTG TCAGAGCTGA AGGCGCAGAT CACCAGAAG 180
 30 ATTGGCGTGC ACGCTTCCA GCAGCGTCTG GCTGTCCACC CGAGCGGTGT GGCGCTGCAG 240
 GACAGGGTCC CCCTTGCCAG CCAGGGCCTG GGCCCTGGCA GCACGGTCTT GCTGGTGGTG 300
 GACAAATGCG ACGAACCCTT GAGCATCCTG GTGAGGAATA ACAAGGGCCG CAGCAGCACC 360
 TACGAGGTCC GGCTGACGCA GACCGTGCC CACCTGAAGC AGCAAGTGAG CGGGCTGGAG 420
 35 GGTGTGCAGG ACGACCTGTT CTGGCTGACC TTCGAGGGGA AGCCCTGGA GGACCACTC 480
 CGCTGGGGG AGTACGGCTT CAAGCCCTG AGCACCGTGT TCATGAATCT GCGCTGCGG 540
 GGAGGCGCA CAGAGCTTGG CGGCGGAGC TAAGGGCCTC CACCAGCATC CGAGCAGGAT 600
 CAAGGGCCG AATAAAGGC TGTGTAAGA GAAT

40 Seq ID NO: 106 Protein Sequence
 Protein Accession #: NP_005092

1 11 21 31 41 51
 45 MGNDLTVKML AGNEFQVSL SSMVSSELKA QITQKIGVHA FQQLAVHPS GVALQDRVPL 60
 ASQGLPGST VLLVVDKDE PLSILVRNKK GRSSTYEVRL TQTVHLKQQ VSGLEGVQDD 120
 LFWLTFBKP LEDQLPLGEY GLKPLSTVPM NLRLRGGGTE PGGRS

50 Seq ID NO: 107 DNA sequence
 Nucleic Acid Accession #: NM_006018
 Coding sequence: 1..1161

1 11 21 31 41 51
 55 ATGAATCGGC ACCATCTGCA GGATCACTTT CTGGAATAG ACAAGAAGAA CTGCTGTGTG 60
 TTCCGAGATG ACTTCATTGC CAAGGTGTTG CCGCCGGTGT TGGGCTGGA GTTTATCTTT 120
 GGGCTTCTGG GCAATGGCCT TGCCCTGTGG ATTTTCTGTT TCCACCTCAA GTCCTGGAAA 180
 TCCAGCGGA TTTTCTGTT CAACCTGGCA GTAGCTGACT TTCTACTGAT CATCTGCCTG 240
 CGTTGCTGA TGACTACTA TGTGCGCGT TCAGACTGGA AGTTTGGGA CATCCCTTGC 300
 CGGCTGTGTC TCTCATGTT TGCCATGAAC CGCCAGGGCA GCATCATCTT CCTCAOGGTG 360
 60 GTGGCGGTAG ACAGGTATTT CCGGTGGTTC CATCCCCACC ACGCCCTGAA CAAGATCTCC 420
 AATTGGCAG CAGCCATCAT CTCTTGCTT CTGTGGGGCA TCACTGTTGG CCTAACAGTC 480
 CACTCCTGA AGAAGAAGTT GCTGATCCAG AATGGCCCTG CAAATGTGTG CATCAGCTTC 540
 AGCATCTGCC ATACCTTCCG GTGGCAGGAA GCTATGTTCC TCCTGGAGT CCTCCTGCC 600
 CTGGGCATCA TCCTGTTCTG CTCAGCCAGA ATTATCTGGA GCTTGGGCA GAGACAAATG 660
 65 GACCGCATG CCAAGATCAA GAGAGCCATC ACCITCATCA TGGTGGTGG CATCGTCTTT 720
 GTCATCTGCT TCCTTCCAG CGTGGTGTG CGGATCCGCA TCTTCTGGCT CCTGCACACT 780
 TGGGCAAGC AGAATTGTGA AGTGTACCGC TCGGTGGACC TGGGTTCTT TATCACTCTC 840
 AGCTTCACTC ACATGAACAG CATGCTGGAC CCGTGGTGT ACTACTTCTC CAGCCCATCC 900
 70 TTCCCAACT TCTTCTCCAC TTTGATCAAC CTACAGGGG ACCCAACAA AACAGAGGC 960
 CCAGATAATA ACCGACGAC GAGCGTCGAG CTCACAGGG ACCCAACAA AACAGAGGC 1020
 GCTCCAGAGG CGTTAATGGC CAACTCCGGT GAGCCATGGA GCCCTCTTA TCTGGGCCCC 1080
 ACCTCAAATA ACCATTCCAA GAAGGACAT TGTACCAAG AACACAGCAT TCTGGAGAAA 1140
 CAGTTGGGAT GTTCATCGA G

75 Seq ID NO: 108 Protein Sequence
 Protein Accession #: NP_006009.1

1 11 21 31 41 51

5 MNRHHLQDHF LEIDKKNCCV FRDDFIKVL PPVLGLEPIF GLLGNGLALW IFCFHLKSWK 60
 SSRIFLNL VADFLLIICL PFVMDYYVRR SDWKFGDIPC RLVLFMFAMN RQGSIIFLT 120
 VAVDRYFRV HPHHALNKIS NWTAAIISCL LMGITVGLTV HLLKKLLIQ NGPANVCISF 180
 SICHTRWHE AMFLLEFLLP LGIILFCSAR IISLRQRQM DRHAKIKRAI TFMVVAIVF 240
 VICFLPSVVV RIRIFWLLHT SGTQNCVYR SVDLAFFITL SPTYMNSMLD PVVYFSSPS 300
 FPNFFSTLIN RCLQRKMTGE PDNNRSTSV L TGDPNKTRG APEALMANS G EPWSPSYLGP 360
 TSNHSHKKGH CHQEPASLEK QLQCCIE

10 Seq ID NO: 109 DNA sequence
 Nucleic Acid Accession #: NM_005030.2
 Coding sequence: 63..1874

15 1 11 21 31 41 51
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 TCCCGGAGGT CCTAGTGGAC CCACGAGGCC GCGGGCGCTA TGTCCGGGCG CGCTTTTGG 240
 20 GCAAGGGGCG CTTTGCCAA GCTTCGAGA TCTCGGACGC GGACACCAAG GAGGTGTTCC 300
 CGGGCAAGAT TGTGCCTAAG TCTCTGCTGC TCAAGCCGCA CCAGAGGGAG AAGATGTCCA 360
 TGGAAATATC CATTACCCG AGCCTCGGCC ACCAGCACGT CGTAGGATTC CACGGCTTTT 420
 TCGAGGACAA CGACTTCGTG TCTCGTGTGT TGGAGCTCTG CCGCCGGAGG TCTCTCTCGG 480
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 25 TTGTGCTTGG CTGCCAGTAC CTGCAACGAA ACCGAGTTAT TCATCGAGAC CTCAAGCTGG 600
 GCAACCTTTT CCTGAATGAA GATCTGGAGG TGAATAAGG GGATTTTGG CTGGCAACCA 660
 AAGTCGAATA TGACGGGAG AGGAAGAAGA CCTGTGTGG GACTCCTAAT TACATAGCTC 720
 CCGAGGTGCT GAGCAAGAAA GGGCACAGTT TCGAGGTGGA TGTGTGGTCC ATTGGGTGTA 780
 TCATGTATAC CTGTGTAGTG GGCACACACC CTTTTGAGAC TCTTTGCGTA AAAGAGACCT 840
 30 ACCTCCGGAT CAAGAAGAA GAATACAGTA TTCCCAAGCA CATCAACCCC GTGGCCCGCT 900
 CCCTCATCCA GAAGATGCTT CAGACAGATC CCACTGCCCC CCCAACCAAT AACGAGCTGC 960
 TTAATGACGA GTTCTTTACT TCTGGCTATA TCCCTGCCCG TCTCCCATC ACCTGCCTGA 1020
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 35 AACCAGTGGT TCGAGAGACA GGTGAGGTGG TCGACTGCCA CCTCAGTGAC ATGCTGCAGC 1200
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 CACGCCCTCAT CCTCTACAAT GATGGTGACA GCCTGCAGTA CATAGAGCGT GACCGCACTG 1440
 40 AGTCCTACCT CACCGTAGT TCCCATCCCA ACTCCTTGAT GAAGAAGATC ACCCTCCTTA 1500
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 45 GCACATACCG CCTGAGTCTC CTGGAGGAGT ACGGCTGCTG CAAGGAGCTG GCCAGCCGGC 1800
 TCCGCTACGC CCGCACTATG GTGGACAGC TGCTGAGCTC ACGCTCGGCC AGCAACCGTC 1860
 TCAAGGCCCT CTAATAGCTG CCCTCCCTC CGGACTGGTG CCTCCTCAC TCCCACTGTC 1920
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 CGGTGGCTGG GCAGAGCTGC ATCATCCTTG CAGGTGGGGG TTGCTGTGTA AGTTATTTT 2040
 50 GTACATGTT CAGGTGTGGT TCTACAGCCT TGTCCCTC CCCTCAACC CCACCATATG 2100
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55 Seq ID NO: 110 Protein Sequence
 Protein Accession #: NP_005021.2

60 1 11 21 31 41 51
 MSAAVTAGKL ARAPADPGKA GVPVAAAPGA PAAAPPAKEI PEVLVDPRSR RRYVRGRFLG 60
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 EDNDFVFFVL ELCTRRSLLE LHKRRKALTE PEARYYLRLQI VLGCQYLHRN RVIHRDLKLG 180
 NLFLNEDLEV KIGDFGLATK VEYDGERKKT LCCTPNYIAP EVLSKKGHSF EVDVWSIGCI 240
 65 MYTLVVKFPF FETSCLKETY LRIKNEYSI PKHINPVAAS LIQKMLQTD TARPITINELL 300
 NDEFFTSGYI PARLPITCLT IPRFSAIAPS SLDPSNRKPL TVLNKGLNLP LPERPREKEE 360
 FVVRETGEVV DCHLSMLQO LHSVNASKPS ERGLVRQEEA EDPACIPIFW VSKWVDYSDK 420
 YGLGYQLCDN SVGLFPNDST RLILYNDGDS LQYIERDGE SYLTVSSHNP SLMKKITLLK 480
 YFRNYMSEHL LKAGANITPR EGDELARLPY LRTWFRTRSA IILHLSNGSV QINFFQDHTK 540
 70 LILCPLMAAV TYIDEKRDFR TYRLSLLEEY GCCKELASRL RYARTMVDKL LSSRSASNRL 600
 KAS

75 Seq ID NO: 111 DNA sequence
 Nucleic Acid Accession #: NM_005409.3
 Coding sequence: 94..378

1 11 21 31 41 51
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 TGTCTTTGCA TAGGCCCTGG GGTAAAAGCA GTGAAAGTGG CAGATATTGA GAAAGCCTCC 240
 10 ATAATGTACC CAAGTAACAA CTGTGACAAA ATAGAAGTGA TTATTACCCT GAAAGAAAT 300
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 GAAAGAAAGA ATTTTAAAA ATATCAAAAC ATATGAAGTC CTGAAAAAGG GCATCTGAAA 420
 AACCTAGAAC AAGTTTAACT GTGACTACTG AAATGACAAG AATTCTACAG TAGGAAACTG 480
 AGACTTTTCT ATGGTTTGTG GACTTTCAC TTTGTACAG TTATGTGAAG GATGAAAGGT 540
 GGGTGAAAGG ACCAAAAACA GAAATACAGT CTTCTGAAT GAATGACAAT CAGAATTCCA 600
 15 CTGCCCAAAG GAGTCCAGCA ATTAAATGGA TTTCTAGGAA AAGCTACCTT AAGAAAGGCT 660
 GGTACCATC GAGTTTACA AAGTGCTTTC ACGTCTTAC TTGTGTATT ATACATTCAT 720
 GCATTTCTAG GCTAGAGAAC CTTCTAGATT TGATGCTTAC AACTATTCTG TTGTACTAT 780
 GAGAACATTT CTGTCTCTAG AAGTTATCTG TCTGTATTGA TCTTATGCT ATATTACTAT 840
 CTGTGTTTAC AGTGGAGACA TTGACATTAT TACTGGAGTC AAGCCCTTAT AAGTCAAAAG 900
 CATCTATGTG TCGTAAAGCA TTCTCAAAC ATTTTTCAT GCAAAATACAC ACTTCTTCC 960
 CCAATATACA TTGAGCAGAT CAATATGTAG GGAACATTC TTATGCATCA TTTGGTTTGT 1020
 TTTATAACCA ATTCATTAAA TGTAAATCAT AAAATGTACT ATGAAAAAAA TTATACGCTA 1080
 TGGGATCTG GCAACAGTGC ACATATTTCA TAACCAAAT AGCAGCACC GTCTTAATTT 1140
 20 GATGTTTTTC AACTTTTATT CATGTAGATG TTTTGAAGCA ATTAGGATAT GTGTGTTTAC 1200
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 TACAAAATGT TTTTGTCTAC CAAGAAAAA TGTGAAAAA TAAGCAAAATG TATACCTAGC 1320
 AATCACTTTT CTATTGTTGA ATTCTGTCTC TTAGAAAAAT ACATAATCTA ATCAATTTCT 1380
 25 TGTTCATGC CATATACTG TAAATTTAG GTATACCTAA GACTAGTTTA AAGAAATCAA 1440
 GTCATTTTTT TCTCTAATAA ACTACCACAA CCTTCTTTTT TAAAAAAA AAA

Seq ID NO: 112 Protein Sequence
 Protein Accession #: NP_005400.1

30 1 11 21 31 41 51
 MSVKGMAL AVILCATVVQ GPFMPKRGRC LCIGPGVKAV KVADIEKASI MYPNNCDKI 60
 EVIITLKENK GQRCLNPKSK QARLIKKVE RKNF

35 Seq ID NO: 113 DNA sequence
 Nucleic Acid Accession #: NM_001110.1
 Coding sequence: 470..2716

40 1 11 21 31 41 51
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 GCGGCTCCGC GTGCCAGTTG GGTGCCCCGG CGTCACGTGG TGAGGAAGGA GCGGAGGTC 180
 45 TGAGTTTCGA GGGAGGGGGG GAGAGAAGAG GGAACGAGCA AGGGAAGGAA AGCGGGGAAA 240
 GGAGGAAGGA AACGAACGAG GGGGAGGGAG GTCCCTGTTT TGGAGGAGCT AGGAGCGTTG 300
 CCGGCCCTTG AAGTGGAGCG AGAGGGGAGT GCTTCGCGGT TTCTCTGCCC AGGGGAGGTC 360
 CCGGCTTCCC GTGGAGGCTC CGGACCAAGC CCCTTCAGCT TCTCCCTCCG GATCGATGTG 420
 CTGCTGTTAA CCGTGAGGGA GCGGCGGCGG GCGGCGAGCG CAGCGGAAGA TGTGTGTTCT 480
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 50 TTTAAATAAA TATATCAGAC ATTATGAAGG ATTATCTTAC AATGTGGATT CATTACACCA 600
 AAAACACGAG CGTGCCAAAA GAGCAGTCTC ACATGAAGAC CAATTTTAC GTCTAGATT 660
 CCATGCCCAT GGAAGACATT TCAACCTACG AATGAAGAGG GACACTTCCC TTTTCAGTGA 720
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 55 TGAAGGATTC ATCCAGACTC GTGGTGGCAC ATTTTATGTT GAGCCAGCAG AGAGATATAT 900
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 TGTGCCAGAA CTCTGAGGA AAAAAAGTAC AACTTCAGCT GAAAAAATA CTGTGAGCT 1140
 60 TTATATTCAG ACTGATCATT TGTTCCTTAA ATATTACGGA ACACGAGAAG CTGTGATTGC 1200
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 GGACCCTACA AATCCTTTCC GTTTCCTCAA TATTGTTGTG GAGAAGTTTC TGAATTGAA 1380
 65 TTCTGAGCAG AATCATGATG ACTACTGTTT GGCTATGTC TTCACAGACC GAGATTGTTGA 1440
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 TGAATAAAGT AACTCTATT CAGATGGTAA GAAGAAGTCC TTAACACTG GAATTATTAC 1560
 TGTTCAGAAC TATGGGTCTC ATGTACTCTC CAAAGTCTCT CACATTACTT TTGCTCACGA 1620
 AGTTGGACAT AACTTTGGAT CCCACATGA TTCTGGAACA GAGTGACAC CAGGAGAATC 1680
 70 TAAGAATTGG GGTCAAAAG AAAATGGCAA TTACATCATG TATGCAAGAG CAACATCTGG 1740
 GGACAAACTT AACACAATA AATTCTCACT CTGTAGTATT AGAAATATAA GCCAAGTTCT 1800
 TGAGAAGAAG AGAAACAAT GTTTTGTGTA ATCTGGCCAA CCTATTGTG GAAATGGAAT 1860
 GGTAGAACAA GGTGAAGAAT GTGATTGTGG CTATAGTGAC CAGTGTAAG ATGAATGCTG 1920
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 75 TCCAAGTCAA GGTCTTGTG GTACAGCACA GTGTGCACTT AAGTCAAAG CTGAGAAGTG 2040
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 TTCTGATGGC AAAGATGATA AAGAATTATG CCATGTATGC TGTATGAAGA AAATGGACCC 2280

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ATCAACTTGT GCCAGTACAG GGTCTGTGCA GTGGAGTAGG CACTTCAGTG GTCGAACCAT 2340
CACCTCGCAA CCTGGATCCC CTTGCAACGA TTTTAGAGGT TACTGTGATG TTTTCATGCG 2400
GTGCAGATTA GTAGATGCTG ATGGTCTCT AGCTAGGCTT AAAAAAGCAA TTTTAGTCC 2460
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GGGAATTGCT CTGATCATGC TAATGGCTGG ATTTATTAAG ATATGCACTG TTCATACTCC 2580
AAGTAGTAAT CCAAGTTGCG CTCTCTCTAA ACCACTTCCA GGCACCTTAA AGAGGAGGAG 2640
ACCTCCACAG CCCATTACAG AACCCGAGCG TCAGCGGCCC CGAGAGAGTT ATCAAAATGGG 2700
ACACATGAGA CGCTAACTGC AGCTTTTGCC TTGGTTCTTC CTAGTGCCTA CAATGGGAAA 2760
ACITTCACCTC AAGAGAAAC CTATTAAGTC ATCATCTCCA AACTAAACCC TCACAAGTAA 2820
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TAAAGCTGA AAATTTCAAT TTGGGGGTGG GAGGTGGAAA AGGAACCCAA TTTTCTTATG 2940
AACAGATATT TTTAACTTAA TGGCACAAAG TCCTAGAATA TTATTATGTG CCCCGTGTTC 3000
CCTGTCTTC GTTGCTGCAT TTTCTTCACT TGCAGGCAA CTGGCTCTC AATAAACTTT 3060
TACCACAAAT TGAATAAAT ATATTTTTC CAACTGCCAA TCAAGGCTAG GAGGCTGAC 3120
CACCTCAACA TTGGAGACAT CACTTGCCAA TGTACATACC TTGTTATATG CAGACATGTA 3180
TTCTTACGT ACACGTACT TCTGTGTGCA ATTGTAAACA GAAATTGCAA TATGGATGTT 3240
TCTTGTATT ATAAATTTT TCCGCTCTTA ATTAATAAAT ACTGTTTAAAT TGACATACTC 3300
AGGATAACAG AGAATGGTGG TATTCAGTGG TCCAGGATTC TGTAAATGCTT TACACAGGCA 3360
GTTTGAAAT GAAATCAAT TTACCCCATG GTACCCGAT CCTCGAATTC

Seq ID NO: 114 Protein Sequence
Protein Accession #: NP_001101.1

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1 11 21 31 41 51
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RLDFHAHGRH FNLRMKRDTS LFSDEFKVT SNKVLDDYDTS HIYTGHIYGE EGSFSGHSVI 120
DGRFEGFIQT RGGTFYVEPA ERYIKDRITLP FHSVIYHEDD INYPHKYGPQ GGCADHSVFE 180
RMRYQMTGV EEVQIPQEE HAANGPELLR KKRRTSAEKN TCQLYIQTDH LFFKYGTRE 240
AVIAQISSHV KAIDTIYQTT DFGGIRNISP MVKIRIRINT ADEKDPNPF RFPNIGVEKF 300
LELNSEQNHD DYCLAYVPTD RDPDDGVILG AWVGAPSGSS GGICEKSKLY SDGKKKSLWT 360
GIITVQNYGS HVPKVSHT FAHEVGHNFG SPHDSGTBCT PGESKMLGQK ENGNVIMYAR 420
ATSGDKLNNN KFSLCSIRNI SQVLEKKRNN CFVESGQPIC GNGMVEQGE ECDGYSQDCK 480
DECCFDANQP EGRCKLKLP KQCSFSPQGPC CTAQCAFKSK SEKCRDSDC AREGICNGFT 540
ALCPASDPKP NPTDCNRHTQ VCINGQCAGS ICEKYGLEEC TCASSDGKDD KELCHVCCMK 600
KMDPSTCAST GSVQSRHFS GRITITLQPGS PCNDFRGYCD VPMRCRLVDA DGFLARLKA 660
IFSPRLVENI AEWIVAHWA VLLMGIALIM LMAFGIKICS VHTPSSNPKL PPKPLPLPTL 720
KRRRPPQPIQ QPQRQRPRES YQMGHMRR

Seq ID NO: 115 DNA sequence
Nucleic Acid Accession #: NM_000577.2
Coding sequence: 41-520

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1 11 21 31 41 51
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GAAGACCTTC TATCTGAGGA ACAACCAACT AGTTGCGGGA TACTTGCAAG GACCAATAGT 180
CAATTTAGAA GAAAAGATAG ATGTGGTACC CATTGAGCCT CATGCTCTGT TCTTGGGAAT 240
CCATGGAGGG AAGATGTGCC TGTCTGTGT CAAGTCTGGT GATGAGACCA GACTCCAGCT 300
GGAGGCAGTT AACATCACTG ACCTGAGCGA GAACAGAAAG CAGGACAAGC GCTTCGCCTT 360
CATCCGCTCA GACAGTGGCC CCACCACCAG TTTTGAGTCT GCCGCTGCC CCGTTGGTT 420
CCTCTGCACA GCGATGGAAG CTGACCAGCC CGTCAGCCTC ACCAATATGC CTGACGAAGG 480
CGTCATGGTC ACCAAATFCT ACTTCCAGGA GGACGAGTAG TACTGCCCAG GCCTGCCTGT 540
TCCCATTTCT GCATGGCAAG GACTGCAGGG ACTGCCAGTC CCGCTGCCCC AGGGCTCCCG 600
GCTATGGGG CACTGAGGAC CAGCCATTGA GGGGTGGACC CTCAGAAGGC GTCAACAA 660
CCTGTGCACA GGACTCTGCC TCCTCTTCAA CTGACCAGCC TCCATGCTGC CTCAGAAATG 720
GTCTTTCTAA TGTGTGAATC AGAGCACAGC AGCCCTTGCA CAAAGCCCTT CCATGTGCC 780
TCTGCATTCA GGATCAAAAC CCGACCACTT GCCCAACCTG CTCTCTCTT GCCACTGCT 840
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GAGCAGGAAA CATGACTCGT ATATGTCTCA GGTCCCTGCA GGGCAAGCA CTAAGCTCG 1560
CTCTTGGCAG GACTCAGCG AATGAATGCT GTATATGTTG GGTGCAAGT TCCCTACTTC 1620
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AAAAA AAAAAA AAAAAA AAAAAA

Seq ID NO: 116 Protein Sequence
Protein Accession #: NP_000568.1

1 11 21 31 41 51
 MALETICRPS GRKSSKMQAF RIWDVNQKTF YLRNNQLVAG YLQGNVNLB EKIDVVPFEP 60
 HALFLGIHGG KMCLSCVKSG DETRLQLEAV NITDLSNRK QDKRFAPIRS DSGPTTSFES 120
 AACPGWFLCT AMEADQPVSL TNMPDEGVMV TKFYFQEDE

Seq ID NO: 117 DNA sequence
 Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
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 CATCAATGGT TCCTTTTCGT CGCTTGGCTT TATTTCATGAG GCTCAGGTGCG GGGAAAGACT 180
 GATGGTCCAC TGTGACAGCA AGACAGGTAA TGCAAAATACG GATTTCATCT GGGTGGGTCC 240
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 AAGTCTGTGT ATAGAAAGCC CTCGTTTGA GGATGCTGGA GTGTATTCTT GTATCGCAAT 360
 GAATAAGCAA CGCCTGTATA ATGAACTGT GGACGTCACA ATAAATGTGA GCAATTCAC 420
 TGTAAAGCAGA TCCCATGCTC ATGAGGCATT TAACACAGCT TTTACCACTC TRGTGCTGTG 480
 CGTGGCCAGT ATCGTTTGG TACTTTTGT CCTCTATCTG ACTCCATGCC CCTGCAAGTG 540
 TAAACCAAG AGACAGAAAA ATATGCTACA CCAAGCAAT GCCCATTCAT CGATTCTCAG 600
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 GGTGTTTTTG GAACCCCTGA AGGATACTGC AGCAGGGCAG AACGGGAAAG TCAGGCTCTT 720
 TCCAGCGGAG GCAGTGATAG CTGAGGGCAT CCTAAAGTCC ACGAGGGGGA AATCTGACTC 780
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Seq ID NO: 118 DNA sequence
 Nucleic Acid Accession #: AB032989.1
 Coding sequence: 1..1316

1 11 21 31 41 51
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 ACCACCTGAA CTTCATCTCC TCTGAGGCTT TTCCCGGCT ACCCAACCTG CGCTACCTGG 180
 ACCTCTCTCT CAACAGAGCT CGTACACTGG ATGAGTTCTT GTTCAGTGAC CTGCAAGTAC 240
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 ACATGGCCCA GCTGCAGAAA CTCTACTTGA GCCAGAACCA GATCTCTCGC TTCCCTCTGG 360
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 CCAAGAGAGT GCACATATGC TTCAACCTGA GTTTCCTCAA CTGTGGCGAG TACAAGGAGC 660
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 GTATATATCT CCTCTGTGTG GACAAAGGTT CTTGCTCCT CTCAGAGATA CCACCTCTGC 2520
 TGCAGAGTCA AAGCATGGGG TTTTGACAT AGAAGGGTTG GAATTGGGTG GTCTCTACCC 2580
 CAGAAATGCA ATTTGGAGTG CAGCTTCAAG TTTCTGCCCT TCCACAGATT CCAGGCAATC 2640
 CTGAAGCAGA GATAATCAGT AGTACTAAAC TTTTCAAGAG GGAGTTCTGC CACCCCATTC 2700

CTCACATCGAG AGGTCTTTGC AGTTGTGGTT GTGAGGCCAG AGSAACTTAA GAAGAATGAG 2760
 CTCACATTC CATTCCATCC AAGGTTGCAG AATACTTTGA GTATGGAGAT GACCGATCCC 2820
 TTAAACCTTT CCCTTTGACT ATACTGCATG CCCTGTGAGT GGCTGCTCTG AGCTTTGGCG 2880
 GGGGATGAGC AGGGTGAAGG TGAAAATGTT CTCTGATGTT GGTTTTCTT AGTGCTCTCT 2940
 5 CTCTCCACG TTTCTAGTCC ATTGAAGTT CTCCAGATCC TCTAGATTTC TGACCTCTTT 3000
 TTACATTCTA AGAGGTGTCA TTTACCTGTG GGTGAGGGGC TTGAGGGGCC TGACTATTAA 3060
 GCTTCTTATT ATGATTGGGG AAGGGGACTC AACATCTTCC CCTGTCTGG TCCTGGGAAC 3120
 TCAAGACTGC TGTCCATCCT TTATTAGTAA CCTAGTTTGG TTGAGAGAGA GGTGCAGCAT 3180
 10 TTCCCTCAAG TACCTGCATG CTCATAGGTA TGCATGCTTA TAGGTATGCA TGCACACCAG 3240
 CACCTTGAAT TCCACCAGGA CAGTGAATCT GTAGTCCCA TTAATGATAC TCTCAGAAATG 3300
 GTCTCCACCA ATGTGCACAA CTTCATGCAC ACAATTGTAT TCCTCTTTAG GAGAGACAGT 3360
 GACCATGCCA GGCTCTTCAA ATACACACTC CTGTATTTTC ATTTCTGAAC TCCTGGAAGC 3420
 TTACCCACCA TCTCCATGGC ACTGAATCAC TTTTCTGCCC AGGCTGGAGT TAGAAGAACC 3480
 15 ATGGGTGAA GGCTTTGGGA GAAGAGGTGG TAAGGAGCTA CCTGGTCTT TGGACTCCTC 3540
 AGAAACCTCC CGTGAAGACT ATATATATGA GCAATATATG AGCAATTAAG ATAGAAGTAG 3600
 GTCATTGAAG GACTCAGAAG GAAACTGGCA AGGGGCTAAG TAGCTGTGAG CTGCTCTTCC 3660
 TGTAACTGT CTTGAGGAGA GAAAAGTTGT CTTGATTAT TCCAGAGACT CTTGAGAAAT 3720
 TTGTTACTGG AGCTATAGGA ACTAGGACTC CCTCCTCAGA CTCATCAGGA AATCTGGGAA 3780
 20 AATCTCATCT CCATGCTGCA GTCTCCCGC TTGGCAACCA CTAGGGCTCT GAAGATCTTT 3840
 AAATGAGCGG TTAATGAAG CAGGCCCTCT GGGGCATCGT GATGGAGCTC CTGAGGACTG 3900
 GGAGGGCGGT TTTCTTCATA ATTCCTACCC AGTTTAGGGA ATGAGAAAAG GCCCTGTGGC 3960
 TCTTAAGTGT CTTGACTATA TCCACTAGTT TGGCCTTGAG TTTGAGACAC CTGGTAGATG 4020
 TACCTGGCTG CCTACCAAG AGATTGATT TGTTCCTTCC CGTGGTTTCA GGTGATAGAA 4080
 25 CCCAAGATA GCTTTTAAAT TGGAGAATTG AATAATCAGC ATATGTAAAG GCACTAGAAC 4140
 CCTGTGTTGA AACTGCCAG GTGTGGGTAT AAGAAAAGGC CGAGAGATCA CCACCTCCTC 4200
 TTACCTTACC CCACCCCAT AAACAGACA TGTCTCCAG GAAGCAGGTG TCCCTGGACA 4260
 CAGAGGATGA CAGGGCTCTA CAATCTGTGT AATTATTATT ATTATTATTA TTTTGTATT 4320
 ATGGGGCCCA AGAAGGGGCG CAGGAGAGGG TACACCCAG CTGGGAGAG CAAAGCAGAT 4380
 30 GGATCCAGTT TCTGTGTGT TCTTACCTCT GTACTTCCTC GTAGCTCTGC TGACAAAGCA 4440
 AGCAGGCCTC CCGTGTCCAA GACCCCATTC CTCCCACTG GTTACACCTA GGCTGGCAAA 4500
 TCTTGGAGCC TCTGGGCTCT GAAAACTAGA CAATGATCAT TAAACCTGGC TTGAGTCTCT 4560
 GTTCTGGC

Seq ID NO: 119 Protein Sequence
 Protein Accession #: BAA86477.1

1 11 21 31 41 51
 | | | | |
 40 HSLPSYALL DLSHNNLSRL RAEWTPTRLT QLHSLLSLHN HLNFISSSEAF SPVPNLRYLD 60
 LSSNQLRLTD EFLFSDLQVL EVLLLYNNHI MAVDRCAFDD MAQLQKLYLS QNQISRPFLE 120
 LVKEGAKLPK LTLDDLSSNK LKNLPLPDLL KLPWIKNGL YLHNNPLNCD CELYQLFSHW 180
 QYRQLSSVMD FQEDLYCMNS KKLHNVFNLS FLNCGEYKER AWEAHLGDTL IIKCDTKQQG 240
 MTKVWVTPSN ERVLDEVING TVSVSKDGLS LFPQQVQVEDG GVYTCYAMGE TFNETLSVEL 300
 45 KVINFTLHGH HDTLNTAYTT LVGCILSVVL VLIYLYLTPC RCNCRGVEKP SSHQGDLSLS 360
 SMLSTTPNHD PMAGGDKDDG FDRRVAFLEP AGPGQQQNGK LKPGNTLPVP EATGKGQRMM 420
 SDPESVSVF SDTPIVV

Seq ID NO: 120 DNA sequence
 Nucleic Acid Accession #: NM_005071
 Coding sequence: 9..1703

1 11 21 31 41 51
 | | | | |
 55 GATAGACCAT GAGCAGCCAT GGCAACAGCC TGTTCCTTCG GGAGAGCGCG CAGOGGCTGG 60
 GCCGGGTGGG CTGGCTGCAG CGGCTGCAGG AAAGCCTGCA GCAGAGAGCA CTGCGCACGC 120
 GCCTGCGCCT GCAGACCATG ACCCTCGAGC ACGTGTCTCG CTTCCTGCGC CGAAACGCCT 180
 TCATTCTGCT GACGGTCAGC GCCGTGGTCA TTGGGGTCAG CTGGGCTTT GCCCTGCGCC 240
 CATATCAGCT CACCTACCGC CAGATCAAGT ACTTCTCTTT TCCTGGAGAG CTTCGTATGA 300
 60 GGATGCTGCA GATGCTGGTG TTACCTCTCA TTGTCTCCAG CCTGGTCACA GGTATGGCAT 360
 CCTGGACAA CAAGGCCACG GGGCGGATGG GGATGCGGGC AGCTGTGTAC TACATGGTGA 420
 CCACCATCAT CGCGGTCTTC ATCGGCATCC TCATGGTCAC CATCATCCAT CCCGGGAAGG 480
 GCTCCAAGCA GGGGCTGCAC CGGGAGGGCC GGATCGAGAC CATCCCCACA GCTGATGCCT 540
 TCATGGACCT GATCAGAAAT ATGTTTCCAC CAAACCTTGT GGAGGCCCTG TTTCAAACAGT 600
 65 TCAAGACGCA GTACAGCAGC AGGGTGGTAA CCAGGACCAT GGTGAGGACA GAGAACGGGT 660
 CTGAGCCGGG TGCTTCCATG CCTCTCCAT TCTCAGTGA GAACGGAACC AGCTTCTCTG 720
 AAAATGTCAC TCGGGCTCTG GGTACCTTGC AGGAGATGCT GAGCTTTGAG GAGACTGTAC 780
 CGGTGCTGCG CTCGCGCAAT GGCATCAACG CCCTGGGCTT CGTGGTCTTC TCTGTGGCCT 840
 TTGGGCTGCT CATGTGTGCG ATGAAACACA AGGGCAGAGT CCTCAGGGAC TTCTTCGACA 900
 70 GCCTCAATGA GGCATTATAT AGGCTGGTGG GCATCATTAT CTGGTATGCA CCTGTGGGCA 960
 TCTGTTCCT GATTGTCTGG AAGATTCTGG AGATGGAAGA CATGGCCGTC CTGGGGGGTC 1020
 AGCTGGGCAT GTACACCTCG ACCGTATCTG TGGGCTGTCT CCTCATGCC GGCATTGTCC 1080
 TTCCCTCAT CTACTTCCTC GTCACTCACC GGAACCCCTT CCCCTTCATT GGGGGCATGC 1140
 TACAAGCCCT CATCACCGCT ATGGGCACGT CTTCCAGCTC GGCAACGCTG CCTCATCCTC 1200
 75 TCCGCTGCTG GGAGGAGGCG CTGGGTGTGG ACCGCCCAT CACCAGGTTT GTCCTGCCCG 1260
 TGGGCGCCAC GGTCAACATG GATGGCACTG CCCTCTACGA GGCCTGGCT GCCATCTTCA 1320
 TTGCTCAAGT TAACAACTAC GAGCTCAACC TGGGTGAGAT CACAACCATC AGCATCACCG 1380
 CCACGACAGC CAGTGTGGG GCTGCTGGCA TCCCCAGGC GGGTCTGGTC ACCATGGTCA 1440
 TTGTGCTTAC GTGCGTGGC TTGCCACCG AAGACATCAC GCTCATCATC GCCCTGGACT 1500

GGTTCCTTGA CCGGCTTCGC ACAATGACCA ACGTACTGGG GGAICTCAATT GGAGCGGGCG 1560
 TCATCGAGCA CTTGTCTCAG CGGGAGCTGG AGCTTCAGGA AGCTGAGCTT ACCCTCCCCA 1620
 GCCTGGGGAA ACCCTACAAG TCCCTCATGG CACAGGAGAA GGGGGCATCC CGGGGACGGG 1680
 GAGGCAACGA GAGTGTATG TGAGGGGCCT CCAGCTCTG

Seq ID NO: 121 Protein Sequence
 Protein Accession #: NP_005062

1 11 21 31 41 51
 | | | | |
 MSSHGNSLFL RESGQRLGRV GWLQRLQESL QQRALRTRLR LQTMTEHLVL RFLRRNAPIL 60
 LTVSAVVIGV SLAFALRPYQ LTYRQIKYFS FPGELLMRML QMLVLPPLVS SLVTGMASLD 120
 NKATGRMGMR AAVYVMVTI IAVFIGILMV TIHPGKGSK EGLHREGRIE TIPTADAFMD 180
 LIRNMFPNNL VEACFKQFKT QYSTRVVTRT MVRTENGSEP GASMPPPPSV ENGTSFLENV 240
 15 TRALGTLQEM LSFETVPVP GSANGINALG LVVFSVAFGL VIGGMKHKGR VLRDPFDSLNL 300
 EAIMRLVGII IWAYFVGILF LIAGKILEME DMAVLGGQLG MYTLTVIVGL FLHAGIVLPL 360
 IYFLVTHRNP PFFIGGMLQA LITAMGTSSS SATLPITPRC LEEGLGVDRR ITRFVLVPGA 420
 TVNMDGTALY EALAAIFIAQ VNNYELNLGQ ITTISITATA ASVGAAGIPQ AGLVTMWIVL 480
 TSVGLPTEDI TLIIAVDWFL DRLRTMTNVL GDSIGAAVIE HLSQRELEIQ EAEPLPLSLG 540
 20 KPYKSLMAQE KGASRGRGGN ESAM

Seq ID NO: 122 DNA sequence
 Nucleic Acid Accession #: NM_031966.1
 Coding sequence: 178..1479

1 11 21 31 41 51
 | | | | |
 ACGAACAGGC CAATAAGGAG GGAGCAGTGC GGGGTTTAAA TCTGAGGCTA GGCTGGCTCT 60
 TCTCGGGCTG CTGCGGGCGA ACGGCTGTTG GTTCTGCTG GTTGTAGGTC CTTGGCTGGT 120
 CGGGCCTCCG GTGTTCTGCT TCTCCCGCTG GAGCTGCTGC CTGGTGAAGA GGAAGCCATG 180
 GCGCTCCGAG TCACAGGAGAA CTCGAAAATT AATGCTGAAA ATAAGCGGAA GATCAACATG 240
 GCAGGCGCAA AGCGGCTTCC TACGGCCCTC GCTGCAACCT CCAAGCCCGG ACTGAGGCCA 300
 AGAACAGCTC TTGGGACAT TGATAACAAA GTCACTGAAC AACTGCAGGC CAAATATGCT 360
 ATGAAGAAAG AAGCAAAACC TTCAGTACTT GGAAGAGTCA TTGATAAAAA ACTACCAAAA 420
 35 CCTCTTGAAA AGGTACCTAT GCTGGTGCCA GTGCCAGTGT CTGAGCCAGT GCCAGAGCCA 480
 GAACCTGAGC CAGAACCTGA GCGCTGTAAA GAAGAAAAAC TTTCGCTGTA GCCTATTTTG 540
 GTTGATATCT CCTCTCCAAG CCCAATGGAA ACATCTGGAT GTGCCCTGTC AGAAGAAGAC 600
 CTGTGTACAG CTTTCTCTGA TGTAATTCTT GCAGTAAATG ATGTGGATGC AGAAGATGGA 660
 GCTGATCCAA ACCTTTGTAG TGAATATGTG AAAGATATTT ATGCTTATCT GAGACAACCT 720
 40 GAGGAAGAGC AAGCAGTCAG ACCAAAATAC CTACTGGGTC GGAAGTCAC TGGAAACATG 780
 AGAGCCATCC TAATTGACTG GCTAGTACAG GTTCAAATGA AATTCAGGTT GTTGCCAGGAG 840
 ACCATGTACA TGACTGTGTC CATTATTGAT CGTTTCATGC AGAATAATTG TGTGCCCAAG 900
 AAGATGCTGC AGCTGGTTGG TGTCACTGCC ATGTTTATTT CAAGCAAATA TGAAGAAATG 960
 TACCCCTCAG AAATTGGTGA CTTTGCTTTT GTGACTGACA ACACCTTATC TAAGCACCAA 1020
 45 ATCAGACAGA TGGAAATGAA GATTCTAAGA GCTTTAAACT TTGGTCTGGG TCGGCCTCTA 1080
 CCTTTGCACT TCCTTCGGAG AGCATCTAAG ATTGGAGAGG TTGATGTGCA GCAACATACT 1140
 TTGGCCAAAT ACCTCATGGA ACTAATATG TTGGACTATG ACATGGTGCA CTTTCTCTCT 1200
 TCTCAAATTG CAGCAGGAGC TTTTTCCTTA GCACTGAAAA TTCTGGATAA TGGTGAATGG 1260
 ACACCAACTC TACAACATTA CCGTCTCATAT ACTGAAGAAT CTCTTCTTCC AGTTATGCCAG 1320
 50 CACCTGGTGA AGAATGTAGT CATGGTAAAT CAAGGACTTA CAAAGCACAT GACTGTCAAG 1380
 AACAAATATG CCACATCGAA GCATGCTAAG ATCAGCACTC TACCACAGCT GAATTCTGCA 1440
 CTAGTTCAAG ATTTAGCCAA GGCTGTGCA AAGGTGTAAC TTGTAAACTT GAGTTGGAGT 1500
 ACTATATTTA CAAATAAAAT TGGCACCATG TGCCATCTGT AAAAAAAAAA AAAAAAAAAA 1560
 AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 123 Protein Sequence
 Protein Accession #: NP_114172.1

1 11 21 31 41 51
 | | | | |
 MALRVTRNSK INAENKAKIN MAGAKRVPTA PAATSKPGLR PRTALGDIGN KVSEQLQAKM 60
 PMKKEAKPSA TGKVIDKKLP KPLEKVPMLV PVPVSEPVPE PEPEPEPEPV KEEKLSPEPI 120
 LVDITASPSM ETSGCAPAE DLQAFSDVI LAVNDVDAED GADPNLCSEY VKDIYAYLRQ 180
 65 LEESEQVRPK YLLGREVTGN MRALIDWLW QVQMKFRLQ ETMYMTVSII DRFMQNNCVP 240
 KKMILQLVGT AMPIASKYEE MYPPEIGDFA FVTDNTYTKH QIRQMEMKIL RALNFGLRP 300
 LPLHFLRRAS KIGESVDVEQH TLAKYLMELT MLDYDMVHFP PSQIAAGAF C LALKILDNGE 360
 WPTTLQHYLS YTESLPLVM QHLAKNVVMV NQGLTKHMTV KNKYATSKHA KISTLPQLNS 420
 70 ALVQDLAKAV AKV

Seq ID NO: 124 DNA sequence
 Nucleic Acid Accession #: Bos sequence
 Coding sequence: 13-1424

1 11 21 31 41 51
 | | | | |
 TAGAAGTTTA CAATGAAGTT TCTTCTAATA CTGCTCCTGC AGGCCACTGC TTCTGGAGCT 60
 CTTCCCTGTA ACAGCTCTAC AAGCCTGGAA AAAAATAATG TGCTATTG TGAAAGATAC 120

5 TTAGAAAAAT TTTATGGCCT TGAGATAAAC AAACCTCCAG TGACAAAAAT GAAATATAGT 180
 GGAAACTTAA TGAAGGAAAA AATCCAAGAA ATGCAGCACT TCTTGGGTCT GAAAGTGACC 240
 GGGCAACTGG ACACATCTAC CCTGGAGATG ATGCACGCAC CTCGATGTGG AGTCCCGGAT 300
 GTCCATCATT TCAGGGAAAT GCCAGGGGGG CCGSTATGGA GGAAACATTA TATCACCTAC 360
 AGAATCAATA ATTACACACC TGACATGAAC CGTGAGGATG TTGACTACGC AATCCGGAAA 420
 GCTTTCCAAG TATGAGTAA TGTTACCCCT TTGAAATTCA GCAAGATTAA CACAGGCATG 480
 GCTGACATTT TGGTGGTTTT TGCCCGTGGG GCTCATGGAG ACTTCCATGC TTTTGATGGC 540
 AAAGGTGAA TCCTAGCCCA TGCTTTTGGG CTGGATCTG GCATTGGAGG GGATGCACAT 600
 10 TTCCATGAGG ACGAATTCCT GACTACACAT TCAGGAGGCA CAACTTGTGT CCTCACTGCT 660
 GTTCACGAGA TTGGCCATTG CTTAGTCTTT GGCCATTCTA GTGATCCAAA GGCCGTAAATG 720
 TTCCCCCCTT ACAAATATGT TGACATCAAC ACATTTCCGC TCTCTGCTGA TGACATACGT 780
 GGCAATCAGT CCTGTATGG AGACCCAAA GAGAACCAAC GCTTGCCAAA TCCTGACAA 840
 TCAGAACCAG CTCTCTGTGA CCCCATTGTG AGTTTGTATG CTGTCACTAC CGTGGGAAAT 900
 AAGATCTTTT TCTTCAAAGA CAGGTTCTTC TGGCTGAAGG TTTCTGAGAG ACCAAAGACC 960
 15 AGTGTAAATT TAATTTCTTC CTTATGGCCA ACCTTGCCAT CTGGCATTGA AGCTGCTTAT 1020
 GAAATTGAAG CCAGAAATCA AGTTTTCTT TTTAAAGATG ACAAATACTG GTTAATTAGC 1080
 AATTTAAGAC CAGAGCCAAA TTATCCCAAG AGCATACATT CTTTGGTTT TCCTAACTTT 1140
 GTGAAAAAAA TTGATGCAGC TGTTTTAAAC CCACGTTTTT ATAGGACCTA CTCTTTGTGA 1200
 GATAACCACT ATTGGAGGTA TGATGAAAGG AGACAGATGA TGGACCTCGG TTATCCCAAA 1260
 20 CTGATTACCA AGAATCTCCA AGGAATCGGG CCTAAAATTG ATGCAGTCTT CTACTCTAAA 1320
 AACAAATACT ACTATTCTT CCAAGGATCT AACCAATTG AATATGACTT CCTACTCCAA 1380
 CGTATCACA AACCAATAGC AAGCAATAGC TGGTTTGGTT GTTGAAAAATG GTGTAATTAA 1440
 TGGTTTTTGT TACTTCATT CAGCTTAATA AGTATTATT GCATATTGCG TATGTCTCA 1500
 GTGTACCACT ACTTAGAGAT ATGTATCATA AAAATAAAAT CTGTAAACCA TAGGTAATGA 1560
 25 TTATATAAAA TACATAAAT TTTTCAATT TGAAACTCT AATTGTCCAT TCTTGCTTGA 1620
 CTCTACTATT AAGTTTGAAG ATAGTTACCT TCAAAGCAAG ATAATTCTAT TTGAAGCATG 1680
 CTCTGAAGT TGCTTCTTAA CATCCTTGGG CTGAGAAAT ATACTTACTT CTGGCATAAC 1740
 TAAATAAAG TATATATATT TTGGCTCAAA TAAATTG

Seq ID NO: 125 Protein sequence:
 Protein Accession #: Eos sequence

35 1 11 21 31 41 51
 MKFLILLQLQ ATASGALPLN SSTSLKXNNV LFGERYLEKF YGLEINKLPV TKMKYSGNLM 60
 KEKIQEMQHF LGLKVTGQLD TSTLEMMHAP RGVDPDVHVF REMPGGPVNR KHYITYRINN 120
 YTFDMNRDGV DYAIRKAPQV WSNVTLKFS KINTGMADIL VVFARGAHGD PHAFDGGKGI 180
 LAHAFPGPGSG IGGDAHFDEED EFWTTHSGGT NLFLTAVHEI GHSLLGLGHSS DPKAVMPEPTY 240
 KYVDINTFRL SADDIRGIQS LYGDPKENQR LPNPDNSEFA LCDPNLSPDA VTTVGNKIFF 300
 40 FKDRFFWLKV SERPKTSVNL ISSLWPTLPS GIEAAYEIEA RNQVFLPKDD KYWLISNLRP 360
 EPNYPKSIHS FGFPNFVKKI DAAVFNPRFY RTYFFVDNQY WRVDERRQMM DPGYPKLITK 420
 NFOGIGPKID AVFYSKXKY YFPQGSNQFE YDFLLQRITK TLKSNWFGC

Seq ID NO: 126 DNA sequence
 Nucleic Acid Accession #: NM_000077.2
 Coding sequence: 272..742

50 1 11 21 31 41 51
 CCCAACCTGG GGGCACTTCA GGTGTGCCAC ATTCTGCTAAG TGCTCGGAGT TAATAGCACC 60
 TCCTCCGAGC ACTCGCTCAC GGCCTCCCTT TGCCTGGAAA GATACCGCGG TCCCTCCAGA 120
 GGATTTGAGG GACAGGTCAG GAGGGGCTC TTCGCCAGC ACCGGAGGAA GAAAGAGGAG 180
 GGGCTGGCTG GTCAACAGAG GGTGGGCGG ACCCGGTGCG CTCGGCGGCT GCGGAGAGGG 240
 55 GGAGAGCAGG CAGCGGGCGG CGGGGAGCAG CATGGAGCCG GCGCGGGGGA GCAGCATGGA 300
 GCCTTCGGCT GACTGGCTGG CCAAGGCCGC GCGCGGGGT GGGGTAGAGG AGGTGCGGGC 360
 GCTGTGGAG GCGGGGCGC TGCCCAACGC ACCGAATAGT TACGGTCGGA GCGCGATCCA 420
 GGTCTGATG ATGGGCAAGC CCGAGTGGC GGAGCTGCTG CTGCTCCACG GCGCGGAGCC 480
 CAACCTGCGCC GACCCCGCCA CTCTCACCCG ACCCGTGCAC GACGCTGCCG GGGAGGGCTT 540
 60 CCTGGACAG CTGTGTGTGC TGCACCGGGC CGGGGCGCGG CTGGACGTGC GCGATGCGCT 600
 GGGCGGTCTG CCCGTGGACC TGGCTGAGGA GCTGGGCCAT CGCGATGTGC CACGGTACCT 660
 GCGCGCGGCT GCGGGGGGCA CCAGAGGCAG TAACCATGCC CGCATAGATG CCGCGGAAGG 720
 TCCTCAGAT ATCCCGGATT GAAAGAACCA GAGAGGCTCT GAGAAACCTC GGGAAACTTA 780
 GATCATCAGT CACGGAAGGT CCTACAGGCG CACAACCTGC CCGCCACAA CCCACCCGCG 840
 65 TTTCTAGTAT TTTATTAGA AAATAGAGCT TTTAAAAATG TCCTGCCTTT TAACGTAGAT 900
 ATATGCCTTC CCCCACTACC GTAAATGTCC ATTTATATCA TTTTATATAT ATTCTTATAA 960
 AAATGTAAAA AAGAAAAACA CCGCTTCTGC CTTTCACTG TGTGGAGTT TTCTGGAGTG 1020
 AGCACTCAGC CCTTAAGCGC ACATTCTATG GGGCATTCTT TGCAGCCTC GCAGCCTCCG 1080
 GAAGCTGTGC ACTTCATGAC AAGCATTTTG TGAAGTAGGG AAGCTCAGGG GGGTTACTGG 1140
 70 CTCTCTTGA GTCACACTGC TAGCAATGG CAGAACCAAA GCTCAATAA AAATAAAATA 1200
 ATTTTCACTC ATTCATC

Seq ID NO: 127 Protein Sequence
 Protein Accession #: NP_000068.1

75 1 11 21 31 41 51
 MEPAAGSSME PSADWLATAA ARGRIEEVRA LLEAGALPNA PNSYGRRPQI VMMMGSAARVA 60
 ELLLLHGAEP NCADPATLTR PVHDAAREGF LDTLVVLHRA GARLDVRDAN GRLPVDLAEE 120

LGHRDVARYL RAAAGGTRGS NHARIDAAEG PSDIPD

Seq ID NO: 128 DNA sequence

Nucleic Acid Accession #: NM_058196.1

Coding sequence: 104..421

5

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1      11      21      31      41      51
|      |      |      |      |      |
10  TGTGTGGGG TCTGCTTGGC GGTGAGGGGG CTCTACACAA GCTTCCTTTC CGTCATGCCG 60
    GCGCCACCCC TGGCTCTGAC CATTCTGTTC TCTCTGGCAG GTCATGATGA TGGGCAGCGC 120
    CCGAGTGGCG GAGCTGTGTC TGCTCCACGG CGCGGAGCCC AACTGCGCCG ACCCCGCCAC 180
    TCTCACCCGA CCCGTGCACG ACGCTGCCCG GGAGGGCTTC CTGGACACGC TGGTGGTGCT 240
    GCACCGGGCC GGGCGCGCGC TGGACGTGCG CGATGCCTGG GGCGTCTGCG CCGTGGACCT 300
    GGCTGAGGAG CTGGGCCATC GCGATGTGCG ACGGTACCTG CGCGCGGCTG CGGGGGGCAC 360
    CAGAGGCGCT AACCATGTCC GCATAGATGC CGCGGAAGGT CCCTCAGACA TCCCCGATTG 420
    AAGAAACAGG AGAGGCTCTG AGAAACCTCG GGAAACTTAG ATCATCAGTC ACCGAAGGTC 480
    CTACAGGGCC ACAACTGCCG CGGCCACAAC CCACCCGCGT TTGCTAGTTT TCATTAGAA 540
    AATAGAGCTT TAAAAATGT CCTGCCTTTT AACGTAGATA TAAGCCTTCC CCCACTACCG 600
    TAAATGTCCA TTTATATCAT TTTTATATA TTCTTATAAA AATGTAAAAA AGAAAAACAC 660
    CGCTTCTGCC TTTTCACTGT GTTGGAGTTT TCTGGAGTGA GCACTCACGC CCTAAGCGCA 720
    CATTCAATGT GGCATTTCCT GCGAGCCTCG CAGCCTCCGG AAGCTGTGCA CTTTCATGACA 780
    AGCATTTTGT GAACTAGGGA AGCTCAGGGG GGTTACTTGG TTCTCTTGAG TCACACTGCT 840
    AGCAATGGC AGAACCAAG CTCAAATAAA AATAAAATAA TTTTCATTCA TTCCTC
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25

Seq ID NO: 129 Protein Sequence

Protein Accession #: NP_478103.1

30

```
1      11      21      31      41      51
|      |      |      |      |      |
30  MMGSGARVAE LLLLHGAEPN CADPATL/TRP VHDAAREGFL DTLVVLHRAG ARLDVRDAWG 60
    RLPVDLAEL GHHRDVARYLR AAGGTRGSN HARIDAAEGP SDIPD
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35

Seq ID NO: 130 DNA sequence

Nucleic Acid Accession #: NM_058197.1

Coding sequence: 272..646

40

45

50

55

60

65

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1      11      21      31      41      51
|      |      |      |      |      |
40  CCCAACCTGG GCGACTTCA GGTGTGCCAC ATTGCTAAG TGCTCGGAGT TAATAGCACC 60
    TCCTCGAGAC ACTCGCTCAC GCGTCCCCT TGCTGGAAA GATACCGCGG TCCCTCCAGA 120
    GATTTGAGG GACAGGGTGG GAGGGGGCTC TTCGCCACG ACCGAGGAA GAAAGAGGAG 180
    GGGCTGGCTG GTCACAGAG GGTGGGGCGG ACCGCTGCG CTGCGCGGCT GCGGAGAGGG 240
    GGAGAGCAGG CAGCGGGCGG CGGGGAGCAG CATGGAGCCG GCGGCGGGGA GCAGCATGGA 300
    GCGGCGGGCG GGGAGCAGCA TGGAGCCTTC GGCTGACTGG CTGGCCACGG CCGCGGCGCG 360
    GGGTCGGGTA GAGGAGGTGC GGGCGCTGCT GGAGGCGGGG GCGCTGCCCA ACGCACCGAA 420
    TAGTTACGCT CGGAGGCCGA TCCAGGTGGG TAGAAGGCTC GCAGCGGGAG CAGGGGATGG 480
    CGGGCAGCTC TGGAGGACGA AGTTTGCAGG GGAATTGGA TCAGGTAGCG CTTGATTCT 540
    CCGAAAAAGG GGGAGGCTTC CTGGGAGTTC TTCAGAAAGG GTTTGTAATC ACAGACCTCC 600
    TCCTGGCGAC GCCTCGGGGG CTTGGGAAAC CAAGGAAGAG GAATGAGGAG CCACGCGCGT 660
    ACAGATCTCT CGAATGCTGA GAAGATCTGA AGGGGGGAAC ATATTGTAT TAGATGGAAG 720
    TCATGATGAT GGGCAGCGCC CGAGTGGCGG AGCTGTCTGT GCTCCACGGC GCGGAGGCCA 780
    ACTGCGCCGA CCCCGCACT CTCACCCGAC CCGTGCAAGA CGCTGCCCGG GAGGGCTTCC 840
    TGGACACGCT GGTGGTGTCT CACCGGGCCG GGGCGCGGCT GGAAGTGGCG GATGCTTGGG 900
    GCGGTCTGCC CGTGACCTG GCTGAGGAGC TGGGCCATCG CGATGTGCGA CGGTACCTGC 960
    GCGCGGCTGC GGGGGGCACC AGAGGCAGTA ACCATGCCCG CATAGATGCC GCGGAAGGTC 1020
    CCTCAGACAT CCCCAGTTGA AAGAACCAGA GAGGCTCTGA GAAACCTCGG GAACTTAGAT 1080
    CATCAGTCAC CGAAGGTCTT ACAGGCCAC AACTGCCCCC GCCACAACCC ACCCGCTTT 1140
    CGTAGTTTTC ATTTAGAAAA TAGAGCTTTT AAAAAATGCC TGCCTTTAA CGTAGATATA 1200
    TGCCTTCCCC CACTACCGTA AATGTCCATT TATATCATTT TTTATATATT CTTATAAAAA 1260
    TGTAAAAAAG AAAAACACCG CTTCTGCCCT TCACTGTGT TGGAGTTTTC TGGAGTGAGC 1320
    ACTCAGCCCC TAAGCGCACA TTCATGTGGG CATTTCCTGC GAGCCTCGCA GCCTCCGGAA 1380
    GCTGTGCACT TCATGACAAG CATTTTGTGA ACTAGGGAAG CTCAGGGGGG TTAAGTGGCT 1440
    CTCTTGAGTC AACTGCTAG CAAATGGCAG AACCAGAGCT CAAATAAAAA TAAAAATATT 1500
    TTCATTCACT CACTC
```

65

Seq ID NO: 131 Protein Sequence

Protein Accession #: NP_478104.1

70

```
1      11      21      31      41      51
|      |      |      |      |      |
70  MEPAAGSSME PAAGSSMEPS ADWLATAAAR GRVEEVALL EAGALPNAPN SYGRRPIQVG 60
    RRSAGAGDGD GRWRTKFGA ELESASIL RKGRLPGEF SEGVNHRPP PGDALGAWET 120
    KEEE
```

75

Seq ID NO: 132 DNA sequence

Nucleic Acid Accession #: NM_058195.1

Coding sequence: 163..684

1 11 21 31 41 51
| | | | |
CCTCCCTACG GGCCTCTCCG GCAGCCCTTC CCGCGTGGCG AGGGCTCAGA GCCGTTCCGA 60
GATCTTGGAG GTCCTGGTGG GAGTGGGGGT GGGGTGGGGG TGGGGGTGAA GGTGGGGGGC 120
5 GGGCGCGCTC AGGGAAGGCG GGTGCGCGCC TCGCGGGCGG AGATGGGCAG GGGCGCGTGC 180
GTGGGTCCCA GTCTGCAGTT AAGGGGGCAG GAGTGGCGCT GCTCACCTCT GGTGCCAAAG 240
GGCGGCGCAG CGGCTGCGCA GCTCGGCCCT GGAGGCGCGC AGAACATGGT GCGCAGGTTT 300
TTGGTGACCC TCCGGATTGG GCGCGCGTGC GGCCCGCGCG GAGTGAGGGT TTTGTTGGTT 360
10 CACATCCCCG GGCCTACGGG GAGTGGGCA GCGCCAGGGG CGCCGCGCGC TGTGGCCCTC 420
GTGCTGATGC TACTGAGGAG CCAGCGTCTA GGGCAGCAGC CGCTTCCTAG AAGACCAGGT 480
CATGATGATG GGCAGGCGCC GAGTGGCGGA GCTGCTGCTG CTCCACGGCG CGGAGCCCAA 540
CTGCGCGCAG CCCGCCACTC TCACCCGACC CGTGCAAGAC GCTGCCCGGG AGGGCTTCCT 600
GGACACGCTG GTGGTGTCTG ACCGGGCGCG GGCGCGGCTG GACGTGCGCG ATGCTTGGGG 660
15 CCGTCTGCCG GTGGACCTGG CTGAGGAGCT GGGCCATCGC GATGTCGCAC GGTACCTGCC 720
CGCGGCTGGG GGGGGCACCA GAGGCAGTAA CCATGCCCGC ATAGATGCCG CGGAAGGTCC 780
CTCAGACATC CCGGATTGAA AGAACCCAGG AGGCTCTGAG AAACCTCGGG AAACCTTAGAT 840
CATCAGTCAC CGAAGGTCTC ACAGGGCCAC AACTGCCCCC GCCACAACCC ACCCGCTTT 900
CGTAGTTTTT ATTTAGAAAA TAGAGCTTTT AAAAAATGCC TGCCCTTTTAA CGTAGATATA 960
20 TGCCCTTCCCC CACTACCGTA AATGTCCATT TATATCATT TTTATATATT CTTATAAAAA 1020
TGTAATAAAG AAAAACACCG CTTCCTGCCCTT TTCACTGTGT TGGAGTTTTT TGGAGTGAGC 1080
ACTCAGCGCC TAAGCCGACA TTCATGTGGG CATTTCTTGC GAGCCTCGCA GCCTCCGGAA 1140
GCTGTGCGAC TCATGTCAAG CATTTTGTGA ACTAGGGAAG CTCAGGGGGG TTAAGTGCTT 1200
CTCTTGAGTC ACATGTCTAG CAAATGGCAG AACCAGAGCT CAAATAAAAA TAAATAAATT 1260
TTCATTCATT CACTC

Seq ID NO: 133 Protein Sequence
Protein Accession #: NP_478102.1

30 1 11 21 31 41 51
| | | | |
MGRGRCVGPS LQLRGQEWRC SPLVPKGGAA AELGPGGGE NMVRRFLVTL RIRACGPPR 60
VRVFPVHPR LTGEWAAPGA PAAVALVLM LRSQRLGQOP LPRRPGHDDG QRPSSGAAAG 120
PRRGAQLRRP RHSHPTRRAR CPGLPGHAG GAAPGRGAAG RARCLGPSAR GPG

35 Seq ID NO: 134 DNA sequence
Nucleic Acid Accession #: NM_023915
Coding sequence: 1..1077

40 1 11 21 31 41 51
| | | | |
ATGGGGTTCA ACTTGACGCT TGCAAAATTA CCAATAAAG AGCTGCACGG CCAAGAGAGT 60
CACAAATTCAG GCAACAGGAG CGACGGGCCA GGAAAGAACA CCACCTTCA CAATGAATTT 120
GACACAATTG TCTTGCCGGT GCTTTATCTC ATTATATTTG TGGCAAGCAT CTGTCTGAAT 180
45 GGTTTAGCAG TGTGGATCTT CTTCACATTT AGGAATAAAA CCAGCTTCAT ATTCTATCTC 240
AAAAACATAG TGGTTCGAGA CCTCATAATG ACGCTGACAT TTCCATTTCC AATAGTCCAT 300
GATGCAGGAT TTGGACCTTG GTACTTCAAG TTTATTCTCT GCAGATACAC TTCAGTTTGT 360
TTTTATGCAA ACATGTATAC TTCCATCGTG TTCCTTGGGC TGATAAGCAT TGATCGCTAT 420
CTGAAGGTGG TCAAGCCATT TGGGACTCT CGGATGTACA GCATAACCTT CACGAAGGTT 480
50 TTATCTGTTT GTGTTGGGT GATCATGGCT GTTTTGTCTT TGCCAAACAT CATCCTAACA 540
AATGGTCAGC CAACAGAGGA CAATATCCAT GACTGCTCAA AACTTAAAG TCCTTTGGGG 600
GTCAAATGGC ATACGGCAGT CACCTATGTG AACAGCTGCT TGTTTGTGGC CGTGTCTGGT 660
ATTCTGATCG GATGTTACAT AGCCATATCC AGGTACATCC ACAAATCCAG CAGGCAATTC 720
ATAAGTCAGT CAAGCCGAAA GCGAAAACAT AACCAAGACA TCAGGTTGT TGTGGCTGTG 780
55 TTTTTTACCT GCTTTCTACC ATATCACTTG TGCAGAATTC CTTTACTTTT TAGTCACTTA 840
GACAGGCTTT TAGATGAATC TGCAAAAAA ATCCTATATT ACTGCAAGA AATTACACTT 900
TTCTGTCTCG CGTGAATGT TTGCTGGAT CCAATAAATT ACTTTTTCAT GTGTAGGTCA 960
TTTTCAAGAA GGCTGTTCAA AAAATCAAAT ATCAGAACCA GGAGTGAAAG CATCAGATCA 1020
CTGCAAGTG TGAGAAGATC GGAAGTTCGC ATATATTATG ATTACACTGA TGTGTAA

60 Seq ID NO: 135 Protein Sequence
Protein Accession #: NP_076404

65 1 11 21 31 41 51
| | | | |
MGFNLTLAKL PNNELHQES HNSGNRSDGP GKNTTLHNEF DTIVLPVLYL IIFVASILLN 60
GLAVWIFFHI RNKTSFIFYL KNIVVADLIM TLTFPPRIVH DAGFGPWYFK FILCRYTSVL 120
FYANMYTSIV FLGLISIDRY LKVVKPFGDS RMYSTPTKV LSVCVWVIMA VLSLPIIILT 180
NGOPTEDNIH DCSKLKSPLG VKWHTAVTVV NSCLFVAVLV ILIGCYIAIS RYIHKSSRQP 240
70 ISQSSRRKRH NQSRVWVAV FFTCFLPYHL CRIPFTFSLH DRLDDESAQK ILIYCKEITL 300
FLSACNVCLD PIIFYFMCRS PSRRLPKKSN ITRSESIRS LQSVRRSEVR IYDYDITV

Seq ID NO: 136 DNA sequence
Nucleic Acid Accession #: NM_005329.1
Coding sequence: 1..1662

75 1 11 21 31 41 51
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ATGCCGCTGC AGCTGACGAC AGCCCTGCGT GTGGTGGGCA CCAGCCTGTT TGCCCTGGCA 60
GTGCTGGGTG GCATCCTGGC AGCCTATGTG ACGGGCTACC AGTTCATCCA CACGGAAAAG 120
CACTACCTGT CCTTCGGCCT GTACGGCGCC ATCCTGGGCC TGCACTGCTT CATTGAGAGC 180
CTTTTTCGCT TCCTGGAGCA CCGGCGCATG CGACGTGCCG GCCAGGCCCT GAAGCTGCCC 240
TCCCCGCGGC GGGGCTCGGT GGCATGTGTC ATTGCCGCGT ACCAGGAGGA CCCTGACTAC 300
TTGCGCAAGT GCCTGCGCTC GGCCAGCGC ATCTCCTTCC CTGACCTCAA GGTGGTCATG 360
GTGGTGGGAT GCAACCGCCA GGAGGACGCC TACATGCTGG ACATCTTCCA CGAGGTGCTG 420
GGCGGCGACG AGCAGGCGCG CTCTTTGTG TGGCGCAGCA ACTTCATGTA GGCAGGCGAG 480
GGTGAGACCG AGGCGAGCCT GCAGGAGGGC ATGGACCGTG TGCGGGATGT GGTGCGGGCC 540
AGCACCTTCT CGTGATCAT GCAGAAATGG GGAGGCAAGC GCGAGGTGAT GTACACGGCC 600
TTCAAGGCCC TCGGCGATTC GGTGGACTAC ATCCAGGTGT GCGACTCTGA CACTGTGCTG 660
GATCCAGCAT GCACCATCGA GATGCTTGA GTCCCTGGAG AGGATCCCCA AGTAGGGGGA 720
GTGCGGGGAG ATGTCCAGAT CCTCAACAAG TACGACTCAT GGATTTCCTT CCTGAGCAGC 780
GTGCGGTACT GGTGGCCTT CAACGTGGAG CGGGCCTGCC AGTCTACTT TGGCTGTGTG 840
CAGTGTATTA GTGGGCCCTT GGGCATGTAC CGCAACAGCC TCCTCCAGCA GTTCTGGAG 900
GACTGGTACC ATCAGAAGTT CCTAGGCAGC AAGTGCAGCT TCGGGGATGA CCGGCACCTC 960
ACCAACCGAG TCCTGAGCCT TGGCTACCGA ACTAAGTATA CCGCGCGCTC CAAGTGCCTC 1020
ACAGAGACCC CCACTAAGTA CCTCGGTGG CTCAACAGC AAACCCGCTG GAGCAAGTCT 1080
TACTTCGGG AGTGGCTCTA CAACTCTCTG TGGTTCCATA AGCACCACCT CTGGATGACC 1140
TACGAGTCAG TGGTCAACGG TTTCTTCCCC TTCTTCCTCA TTGCCACGGT TATACAGCTT 1200
TTCTACCGGG GCGCGCATCT GAACATTCTC CTCTTCCTGC TGACGGTGCA GCTGGTGGGC 1260
ATTATCAAGG CCACCTACGC CTGCTTCCTT CGGGGCAATG CAGAGATGAT CTTTCATGTC 1320
CTCTACTCCC TCCTCTATAT GTCCAGCCTT CTGCGGGCCA AGATCTTTCG CATTGCTACC 1380
ATCAACAAT CTGGCTGGGG CACCTCTGGC CGAAAAACCA TTGTGGTGAA CTTTCATTGGC 1440
CTCATTCTG TGTCCATCTG GGTGGCAGTT CTCCTGGGAG GGCTGGCCTA CACAGCTTAT 1500
TGCCAGGACC TGTTCACTGA GACAGAGCTA GCCTTCCTTG TCTCTGGGGC TATACTGTAT 1560
GGCTGCTACT GGGTGGCCCT CCTCATGCTA TATCTGGCCA TCATCGCCCG GCGATGTGGG 1620
AAGAACCGG AGCAGTACAG CTTGGCTTTT GCTGAGGTGT GA
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Seq ID NO: 137 Protein Sequence
Protein Accession #: NP_005320.1

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1 11 21 31 41 51
| | | | |
MPVQLTTALR VVGTSFLPAL VLGGLAAYV TGYQPIHTEK HYLSFGLYGA ILGLHLLIQS 60
LFAFLHRRM RRAGQALKLP SPRRGSVALC IAAQIEDPDY LRKCLRSAQR ISFPDLKVVM 120
VVDGNRQEDA YMLDIFHEVL GGTEQAGFFV WRSNPFHEAGE GETEASLQEG MDRVRDVVRA 180
STFSCIMQKW GKGREVMYTA FKALGDSVDY IQVCDSDTVL DPACTIEMLR VLEEDPQVGG 240
VGGDVQILNK YDSWISPLSS VRYWMAFNVE RACQSYFGCV QCISGPLGMV RNSLLQFLE 300
DWYHQKPLGS KCSFGDDRHL TNRVLSLGYR TKYTARSKCL TETPTKYLWR LNQQRWSKS 360
YPREWLYNSL WFKHKLHWMY YESVVTGFFP FFLIATVIQL FYRGRINNIL LFLLTVQLVG 420
IIKATYACFL RGNAMIFMS LYSLLYMSSL LPAKIFAIAI INKSGWGTSG RKTIVVNFPG 480
LIPVSIWVAV LLGGLAYTAY CQDLFSETEL AFLVSGAILY GCVWVALLML YLAIIARRCG 540
KKPEQYSLAF AEV
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Seq ID NO: 138 DNA Sequence
Nucleic Acid Accession #: NM_001327.1
Coding sequence: 89..631

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1 11 21 31 41 51
| | | | |
AGCAGGGGGC GCTGTGTGTA CCGAGAATAC GAGAATACCT CGTGGGCCCT GACCTTCTCT 60
CTGAGAGCCG GGCAGAGGCT CCGAGGCCAT GCAGGCCGAA GGCCGGGGCA CAGGGGGTTC 120
GACGGGCGAT GCTGATGGCC CAGGAGGCCC TGGCATTCTT GATGGCCAG GGGGCAATGC 180
TGGCGGCCCA GGAGAGGCGG GTGCCACGGG CGGCAGAGGT CCGCGGGCGC CAGGGGCAGC 240
AAGGGCCTCG GGGCGGGGAG GAGGCGCCCC GCGGGGTCCG CATGGCGCGC CGGCTTCAGG 300
GCTGAATGGA TGCTGCAGAT GCGGGGCCAG GGGGCCGGAG AGCCGCCTGC TTGAGTTCTA 360
CCTCGCCATG CCTTTCGCGA CACCCATGGA AGCAGAGCTG GCCCGCAGGA GCCTGGCCCA 420
GGATGCCCCA CCGCTTCCCC TGCCAGGGGT GCTTCTGAAG GAGTTCACCTG TGTCCGGCAA 480
CATACTGACT ATCCGACTGA CTGCTGCAGA CCACCGCCAA CTGCAGCTCT CCATCAGCTC 540
CTGTCTCCAG CAGCTTCCC TGTGTATGTG GATCACGCAG TGCTTCTGTC CCGTGTTTT 600
GGCTCAGCTC CCTCAGGGC AGAGGCGCTA AGCCAGCCTT GCGCGCCCTT CCTAGGTGAT 660
GCCTCTCTCC CTAGGGAATG GTCCAGCAC GAGTGGCCAG TTCATTGTGG GGGCCTGATT 720
GTTTGTGCTG GGAGGAGGAC GGCTTACATG TTTGTTTCTG TAGAAAAATA AACTGAGCTA 780
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Seq ID NO: 139 Protein Sequence
Protein Accession #: NP_001318.1

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1 11 21 31 41 51
| | | | |
MQAEGRGTTG STGDADGPGG PGIPDGPGGN AGGPGEAGAT GGRGPRGAGA ARASGPGGGA 60
PRGPHGGAAS GLNGCCRCGA RGPESRLLEF YLAMPFATPM EAEIARRSLA QDAPPLPVFG 120
VLLKEFTVSG NILTIRLTAA DHRQLQLSIS SCLQLSLLM WITQCFLPVF LAQPPSGQRR 180
```

Seq ID NO: 140 DNA Sequence
Nucleic Acid Accession #: Bos sequence

Coding sequence: 53..459

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1      11      21      31      41      51
5      |      |      |      |      |
   CCTCGTGGGC CCTGACCTTC TCTCTGAGAG CCGGGCAGAG GCTCCGAGC CATGCAGGCC 60
   GAAGGCCAGG GCACAGGGGG TTCGACGGGC GATGCTGATG GCCCAGGAGG CCCTGGCATT 120
   CCTGATGGCC CAGGGGGCAA TGCTGGCGGC CCAGGAGAGG CGGGTGCCAC GGGCGGCAGA 180
   GGTCCCGGGG GCGCAGGGGC AGCAAGGGCC TCGGGGCCGA GAGGAGGCGC CCGCGGGGT 240
   CCGCATGGCG GTGCCGCTTC TGCGCAGGAT GGAAGGTGCC CCTGCGGGGC CAGGAGGCCG 300
10      GACAGCCGCC TGCTTCAGTT CCGACTGACT GCTGCAGACC ACCGCCAACT GCAGCTCTCC 360
   ATCAGCTCCT GTCTCCAGCA GCTTTCCTTG TTGATGTGGA TCACGCAAGT CTTTCTGCC 420
   GTGTTTGTGG CTCAGGCTCC CTCAGGGCAG AGGCGCTAAG CCCAGCCTGG CGCCCTTCC 480
   TAGGTATGTC CTCCTCCCTC AGGGAATGGT CCCAGCAGA GTGGCCAGTT CATTGTGGGG 540
15      GCTGTATTGT TTGTCGTGG AGGAGGACGG CTTACATGTT TGTTCGTGTA GAAAATAAAG 600
   CTGAGCTA
```

Seq ID NO: 141 Protein Sequence
Protein Accession #: Eos sequence

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20      1      11      21      31      41      51
   MQAEGQGTGG STGDADGPGG PGIPDGPGGN AGGPGEAGAT GGRGPRGAGA ARASGPRGGA 60
   PRGPHGGAAS AQDGRCPGGA RRPDSRLQLF RLTAADHRQL QLSISSCLQQ LSLLMWITQC 120
25      FLPVFLAQAP SQGRR
```

Seq ID NO: 142 DNA Sequence
Nucleic Acid Accession #: NM_130467.2
Coding sequence: 246..638

```
30      1      11      21      31      41      51
   AGGCAGAGCT CTGCAAGGAG AGGTGTGTGC TTCGTTCITT CCGCCATCTT CGTCTTTCC 60
   AACATCTTCG TTTCTTCTCA CTGACCGAGA CTCAGCCGGT AGGTCTGCAG AGTGGTCTTC 120
35      CTGGTAATTT AGTTGTGAGT GAATGTGTGG AGGAGCCAGC GGGCTTAGGA CAGGTCTCTGT 180
   GGCACAGTCC GTGGCTTTGA GGGAAAAGGG CCTCGCGGTG GTCTCCGCC TTCCCCCAGG 240
   TCGTATGCA GCGGCCATGG GCCGGTAATC GTGGCTGGGC TGGAACGAGG GAGGAAGTGA 300
   GAGATATGAG TGAGCATGTA ACAAGATCCC AATCCTCAGA AAGAGGAAAT GACCAAGAGT 360
40      CTTCCCAGCC AGTTGGACCT GTGATTGTCC AGCAGCCCAC TGAGGAAAAA CGTCAAGAAG 420
   AGGAACCAAC AACTGATAAT CAGGGTATTG CACCTAGTGG GGAGATCAAA AATGAAGGAG 480
   CACCTGTCTG TCAAGGGACT GATGTGGAAG CTTTCAACA GGAAGTGGCT CTGCTTAAGA 540
   TAGAGGATGC ACCTGGAGAT GGTCTGATG TCAGGGAGGG GACTCTGCC ACTTTTGATC 600
   CCCTAAAGT GCTGGAAGCA GGTGAAGGGC AACTATAGGT TTAACCAAG ACAATGAAG 660
45      ACTGAAACCA AGAATAITGT TCTATGCTG GAAATTGAC TGCTAACATT CTCTTAATAA 720
   AGTTTTACAG TTTTC
```

Seq ID NO: 143 Protein Sequence
Protein Accession #: NP_569734

```
50      1      11      21      31      41      51
   MSEHVTRSQS SERGNDQESS QPVGPIVQQ PTEEKQEEE PPTDNQGIAP SGEIKNEGAP 60
   AVQGTDEAF QQELALLKIE DAPGDGPDVR EGTLPFDFT KVLEAGEGQL
```

Seq ID NO: 144 DNA Sequence
Nucleic Acid Accession #: NM_001476.1
Coding sequence: 82..435

```
60      1      11      21      31      41      51
   GCACGGGAGC TGTGAGGCAG TGCTGTGTGG TTCCTGCCGT CCGGACTCTT TTTCTCTAC 60
   TGAGATTTCAT CTGTGTGAAA TATGAGTTGG CGAGGAAGAT CGACCTATTA TTGGCTAGA 120
   CCAAGGCGCT ATGTACAGCC TCCTGAAATG ATTGGGCCTA TGCGGCCGA GCAGTTCAGT 180
   GATGAAGTGG AACCAGCAAC ACCTGAAGAA GGGGAACCAG CAACTCAACG TCAGGATCCT 240
65      GCAGCTGCTC AGGAGGGAGA GGATGAGGGA GCATCTGCAG GTCAAGGGCC GAAGCCTGAA 300
   GCTGATAGCC AGGAACAGGG TCACCCACAG ACTGGGTGTG AGTGTGAAGA TGGTCTGTAT 360
   GGGCAGGAGG TGGACCCGCC AAATCCAGAG GAGGTGAAAA CGCCTGAAGA AGGTGAAAG 420
   CAATCAGT GTTAAAGAA GACACGTTGA AATGATGCAG GCTGCTCTTA TGTGGAAT 480
70      TTGTCATTA AAATCTCCC AATAAGCTT TACAGCCTTC TGCAAAA
```

Seq ID NO: 145 Protein Sequence
Protein Accession #: NP_001467.1

```
75      1      11      21      31      41      51
   MSWRGRSTYY WPRPRRYVQP PEVIGPMRPE QFSDEVEPAT PEEGEPATQR QDPAAQEGE 60
   DBGASAGQP KPEADSQEQG HPQTGCCECD GPDQEVDPF NPEEVKTPEE GEKQSQC
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Seq ID NO: 146 DNA Sequence
Nucleic Acid Accession #: NM_005562
Coding sequence: 90..3671

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1	11	21	31	41	51	
ACAGCGGAGC	GCAGAGTGAG	AACCAACCAAC	CGAGGCGCGC	GGCAGCGACC	CCTGCAGCGG	60
AGACAGAGAC	TGAGCGGCCC	GGCACCGCCA	TGCCTGCGCT	CTGGCTGGGC	TGCTGCCTCT	120
GCTTCTCGCT	CCTCCTGCC	GCAGCCCGGG	CCACCTCCAG	GAGGGAAGTC	TGTGATTGCA	180
ATGGGAAGTC	CAGGCAGTGT	ATCTTTGATC	GGGAACCTCA	CAGACAAACT	GGTAATGGAT	240
TCCGCTGCCT	CAACTGCAAT	GACAACTCTG	ATGGCATTTCA	CTGCGAGAAG	TGCAAGAATG	300
GCTTTTACCG	GCACAGAGAA	AGGGACCGCT	GTTTGCCCTG	CAATTGTAACT	TCCAAGGTT	360
CTCTTAGTGC	TCGATGTGAC	AACCTGAGAC	GGTGCAGCTG	TAAACCAAGT	GTGACAGGAG	420
CCAGATGCGA	CCGATGTCTG	CCAGGCTTCC	ACATGTCTAC	GGATGCGGGG	TGCACCCCAAG	480
ACCAGAGACT	GCTAGACTCC	AAGTGTGACT	GTGACCCAGC	TGGCATCGCA	GGGCCCTGTG	540
ACGCGGGCCG	CTGTGTCTGC	AAGCCAGCTG	TTACTGGAGA	ACGCTGTGAT	AGGTGTGATG	600
CAGGTTACTA	TAATCTGGAT	GGGGGAAC	CTGAGGCTG	TACCCAGTGT	TTCTGTCTATG	660
GGCATTGAGC	CAGCTGCCGC	AGCTCTGCAG	AATACAGTGT	CCATAAGATC	ACCTCTACCT	720
TTCATCAAGA	TGTTGATGCG	TGGAAGGCTG	TCCAACGAAA	TGGGTCTCCT	GCAAAGCTCC	780
AATGGTCAAG	GCGCCATCAA	GATGTGTTTA	GCTCAGCCCA	ACGACTAGAC	CCTGTCTATT	840
TTGTGGCTCC	TGCCAAATTT	CTTGGGAATC	AACAGGTGAG	CTATGGGCAA	AGGCTGTCTCT	900
TTGACTAGCC	TGATGACAGA	GGAGGCAGAC	ACCCATCTGC	CCATGATGTG	ATTCTGGAAG	960
GTGCTGGTCT	ACGGATCACA	GCTCCCTTGA	TGCCACTTGG	CAAGACACTG	CCTTGTGGGC	1020
TCACCAAGAC	TTACACATTC	AGGTTAAATG	AGCATCCAAG	CAATAATTGG	AGCCCCCAGC	1080
TGAGTTACTT	TGAGTATCGA	AGGTTACTGC	GGAATCTCAC	AGCCCTCCGC	ATCCGAGCTA	1140
CATATGGAGA	ATACAGTACT	GGGTACATTG	ACAATGTGAC	CCTGATTTC	GCCCCCCTGT	1200
TCTCTGGAGC	CCAGCACCC	TGGGTTGAAC	AGTGTATATG	TCTGTGTGGG	TACAAGGGGC	1260
AATCTGCCA	GGATTGTGCT	TCTGGCTACA	AGAGAGATTC	AGCGAGACTG	GGGCTTTTG	1320
GCACCTGTAT	TCCTTGTAACT	TGTCAAGGGG	GAGGGGCTGT	TGATCCAGAC	ACAGGAGATT	1380
GTTATTTCAG	GGATGAGAAT	CCTGACATTG	AGTGTGCTGA	CTGCCCAATT	GSTTTCTACA	1440
ACGATCCGCA	GCACCCCGCG	AGCTGCAAGC	CATGTCCCTG	TCATAACGGG	TTGAGCTGCT	1500
CAGTGTAGCC	GGAGACGGAG	GAGTGGTGT	GCAATAACTG	CCCTCCCGGG	GTACCGGGT	1560
CCCGCTGTGA	GCTCTGTGCT	GATGGCTACT	TTGGGGAACC	CTTTGGTGAA	CATGGCCAG	1620
TGAGGCTTGT	TCAGCCCTGT	CAATGCAACA	ACAATGTGGA	CCCCAGTGCC	TCTGGGAATT	1680
GTGACCGGCT	GACAGGCAGG	TGTTTGAAGT	GTATCCACAA	CACAGCCGGC	ATCTACTCGG	1740
ACCAGTGCAA	AGCAGGCTAC	TTGGGGGACC	CATTGGCTCC	CAACCCAGCA	GACAAAGTGT	1800
GAGCTTGCAA	CTGTAAACCC	ATGGGCTCAG	AGCCTGTAGG	ATGTCGAAGT	GATGGCACT	1860
GTGTTTGCAA	GCCAGGATTT	GGTGGCCCA	ACTGTGAGCA	TGGAGCATT	AGCTGTCCAG	1920
CTTGCTATAA	TCAAGTGAAG	ATTGAGATGG	ATCAGTTTAT	GCAGCAGCTT	CAGAGAAATG	1980
AGGCCCTGAT	TTCAAAGGCT	CAGGGTGGTG	ATGGAGTAGT	ACCTGATACA	GAGCTGGAAG	2040
GCAGGATGCA	GCAGGCTGAG	CAGGCCCTTC	AGGACATTCT	GAGAGATGCC	CAGATTTGAG	2100
AAGGTGCTAG	CAGTCCCTT	GGTCTCCAGT	TGGCCAAAGT	GAGGAGCCAA	GAGAACAGCT	2160
ACCAGAGCCG	CCTGGATGAC	CTCAAGATGA	CTGTGGAAAG	AGTTCGGGCT	CTGGGAAAGT	2220
AGTACCAGAA	CCGAGTTCCG	GATACTCACA	GGCTCATCAC	TCAGATGCAG	CTGAGCCTGG	2280
CAGAAAGTGA	AGCTTCTCTG	GGAAACACTA	ACATTCCTGC	CTCAGACACC	TACGTGGGGC	2340
CAAAATGGCT	TAAAGTCTG	GCTCAGGAGG	CCACAAGATT	AGCAGAAAGC	CACGTTGAGT	2400
CAGCCAGTAA	CAGTAGCACA	CTGACAGGG	AAACTGAGGA	CTATTCCAAA	CAAGCCCTCT	2460
CACTGGTGCG	CAAGGCCCTG	CATGAAGGAG	TCGGAAGCGG	AAGCGTAGC	CCGACGGGTG	2520
CTGTGGTGCA	AGGGCTTGTG	GAAAAATTGG	AGAAAAACCA	GTCCCTGGCC	CAGCAGTTGA	2580
CAAGGGAGGC	CACCTAAGCG	GAAATTGAAG	CAGATAGGTC	TTATCAGCAC	AGTCTCCGCC	2640
TCCTGGATTG	AGTGTCTCGG	CTTCAGGGAG	TGAGTATGCA	GTCCCTTCAG	GTGGGAAGAG	2700
CAAAAGAGAT	CAAAACAAA	CGGATTCAC	TCTCAACGCT	GGTAACCAAG	CATATGGATG	2760
AGTTCAAGCG	TACACAAAAG	AATCTGGGAA	ACTGGAAGA	AGAAGCACAG	CAGCTCTTAC	2820
AGAAATGAGAA	AAGTGGGAGA	GAGAAATCAG	ATCAGCTGCT	TTCCCGTGCC	AATCTTGCTA	2880
AAAGCAGAGC	ACAAGAAGCA	CTGAGTATGG	GCAATGCCAC	TTTTTATGAA	GTTGAGAGCA	2940
TCCTTAAAAA	CCTCAGAGAG	TTTGACCTGC	AGGTGGACAA	CAGAAAAGCA	GAAAGCTGAG	3000
AAGCCATGAA	GAGACTCTCC	TACATCAGCC	AGAAGGTTTC	AGATGCCAGT	GACAAGACCC	3060
AGCAAGCAGA	AAGAGCCCTG	GGGAGCGCTG	CTGCTGATGC	ACAGAGGGCA	AAGAAATGGG	3120
CCGGGGAGGC	CCTGAAATTC	TCCAGTGAGA	TTGAAACAGGA	GATTGGGAGT	CTGAACTTGG	3180
AAGCCAAATG	GACAGCAGAT	GGAGCCTTGG	CCATGGAAAA	GGGACTGGCC	TCTCTGAAGA	3240
GTGAGATGAG	GGAGGTGAA	GGAGAGCTGG	AAAGGAAGGA	GCTGGAGTTT	GACACGAATA	3300
TGGATGCGAT	ACAGATGGTG	ATTACAGAAG	CCAGAAAGGT	TGATACCAGA	GCCAAAGACG	3360
CTGGGGTTAC	AATCCAAGAC	ACACTCAACA	CATTAGACGG	CCTCTGTCAT	CTGATGGACC	3420
AGCCTCTCAG	TGTAGATGAA	GAGGGGCTGG	TCTTACTGGA	GCAGAAAGCT	TCCCGAGCCA	3480
AGACCCAGAT	CAACAGCCAA	CTGCGGCCCA	TGATGTGAGA	GCTGGAAGAG	AGGGCAGGTC	3540
AGCAGAGGGG	CCACCTCCAT	TTGCTGGAGA	CAAGCATAGA	TGGGATTCTG	GCTGATGTGA	3600
AGAACTTGGG	GAACTATTAG	GACAACTGCT	CCCCAGGCTG	CTACAATACC	CAGGCTCTTG	3660
AGCAACAGTG	AAGCTGCCAT	AAATATTTCT	CAACTGAGGT	TCTTGGGATA	CAGATCTCAG	3720
GGCTCGGGAG	CCATGTGATG	TGAGTGGGTG	GGATGGGGAC	ATTGGAACAT	GTTTAATGGG	3780
TATGCTCAGG	TCAACTGAGC	TGACCCCAT	CCTGATCCCA	TGGCCAGGTG	GTTGCTTTAT	3840
TGCACCATAC	TCTTGTGCTC	CTGATGTGCG	GCAATGAGGC	AGATAGCACT	GGGTGTGAGA	3900
ATGATCAAGG	ATCTGGACCC	CAAAGAATAG	ACTGGATGGA	AAGACAACT	GCAAGGCAG	3960
ATGTTTGCTC	CATAATAGTC	GTAAGTGGAG	TCTTGGAAAT	TGGACAAGTG	CTGTTGGGAT	4020
ATAGTCAACT	TATTTCTTGA	GTAATGTGAC	TAAAGGAAAA	AACCTTGACT	TTGCCCAGGC	4080
ATGAAATCTT	TCTTAATGTC	AGAAACAGAT	GCAACCCAGT	CACACTGTGG	CCAGTAAAT	4140
ACTATTGCTC	CATATTGTCC	TCTGCAAGCT	TCTTGTCTGAT	CAGAGTTCCT	CCTACTTACA	4200

5 ACCCAGGGTG TGAACATGTT CTCCATTTTC AAGCTGGAAG AAGTGAGCAG TGTGGAGTGT 4260
 AGGACCTGTA AGGCAGGCC ATTACAGAGCT ATGGTGCTTG CTGGTGCCCTG CCACCTTCAA 4320
 GTTCTGGACC TGGGCATGAC ATCCTTTCTT TTAATGATGC CATGGCAACT TAGAGATTGC 4380
 ATTTTATTA AAGCATTTC TACCAGCAAA GCAAATGTTG GAAAGATATT TACTTTTTCG 4440
 GTTCAAGT GATAGAAAAG TGTGGCTTGG GCATTGAAAG AGTAAATTT CTCTAGATTT 4500
 ATTAGTCCTA ATTCATCTCT ACTTTTCGAA CACCAAAAT GATGCGCATC AATGTATTTT 4560
 ATCTTATTTT CTCAATCTCC TCTCTCTTC CTCCACCCAT AATAAGAGAA TGTCTCTACT 4620
 CACACTTCAG CTGGGTCACA TCCATCCCTC CATTTCATCT TCCATCCATC TTTCCATCCA 4680
 10 TTACCTCCAT CCATCCTTCC AACATATATT TATTGAGTAC CTACTGTGTG CCAGGGGCTG 4740
 GTGGGACAGT GGTGACATAG TCTCTGCCCT CATAGAGTTG ATGTCTAGT GAGGAAGACA 4800
 AGCATTTTTA AAAATAAAAT TTAACCTTAC AAACCTTGTT TGTCACAAGT GGTGTTTATT 4860
 GCAATAACCG CTGTGTTTGC AACCTCTTTC CTCAACAGAA CATATGTTGC AAGACCTCC 4920
 CATGGGGGCA CTTGAGTTTT GGCAAGGCTG ACAGAGCTCT GGGTGTGCA CATTCTTTTG 4980
 15 CATTCAGCT GTCACCTGT GCCTTTCTAC AACTGATTGC AACAGACTGT TGAGTTATGA 5040
 TAACACAGT GGAATTTGCT GGAGGAACCA GAGGCACCTC CACCTTGGCT GGAAGACTA 5100
 TGGTGCTGCC TTGCTTCTGT ATTTCTTGG ATTTCTCTGA AAGTGTTTTT AAATAAGAA 5160
 CAATTGTTAG ATGCC

20 Seq ID NO: 147 Protein Sequence
 Protein Accession #: NP_005553

1 11 21 31 41 51
 25 MPALWLGCCL CFSILLPAAR ATSRREVDCD NGKSRQCIFD RELHROTNGN FRCLNCNDNT 60
 DGIHCCKKN GFYRHRERDR CLPNCNSKG SLSARCDNSG RCSCPKPGVTG ARCDRLPGPF 120
 HMLTDAGCTQ DQRLDLSKCD CDPAGIAGPC DAGRCVCKPA VTGERCDRCR SGYYNLDGKN 180
 PEGCTCFYCY GHSASCRSSA EYSVHKITST FHQDVGDKWA QVRNGSPAKL QWSQRHQDVF 240
 SQAQLRDPVY FVAPAKFLGN QVSYGQSLG FDIYRVDGRGR HPSAHDVILE GAGLRITAPL 300
 30 MPLGKTLPCG LTKTYTFRIN EHPNNWSPQ LSYFEYRRLN RNLTLALIRA TYGEYSTGYI 360
 DNVTLISARP VSGAPAPWVE QCICPVGYKG QFCQDCASGY KRDSARLGPF GTCIPCNCQG 420
 GGACDPDGD CYSNDENPDI ECADCPIGFY NPDHDPSCSK PCPCNNGFSC SVMPETEEVV 480
 CNNPCPGVTG ARCELADGTY FGDPFGEHGP VRPCQPCQCN NNVDPSASGN CDRLTGRCLK 540
 CIHNTAGIYC DQCKAGYFGD PLAPNPADKC RACNCPNMG S EPGCRSDGT CVCKPGFPGP 600
 35 NCEHGAFSCP ACYNQVKIOM DQFMQQLQRM EALISKAQGG DGVVPDTELE GRMQQAEQAL 660
 QDILRDAQIS BGASRSLGLQ LAKVRSQENS YQSRLLDLKM TVERVRALGS QYQNRVREDTH 720
 RLITQMLSL AESEASLGNT NIPASDHYVG PNGFKSLAQE ATRLAESHVE SASNMEQLTR 780
 ETEDYSKQAL SLVRKALHEG VSGSGSPDG AVVQGLVEKL EKTSLAQQL TREATQAEIE 840
 ADRSYQHSRL LLDVSRLQGV VSDQSFQVEE AKRIKQKADS LSTLVTRHMD EPKRTQKNLG 900
 40 NWKEEAQQLL QNGKSGREKS DQLLSRANLA KSRAQBALSM GNATFYEVES ILKNLREBFL 960
 QVDNRKAEE EAMKRLSYIS QKVSASDKT QQAERALGSA AADAQRAKNG AGEALBISSE 1020
 IEQEIGSLNL EANTVADGAL AMEKGLASLK SEMREVEGEL ERKELEFDTN MDVAQMVITE 1080
 AQKVDTRAKN AGVTIQDTLN TLDGLLHLMQ QPLSVDEEGL VLLBQLKSLA KTQINSQRLP 1140
 MMSELEERAR QQRGHLHLLE TSIDGILADV KNLENIRDNL PPGCYNTQAL BQQ

45 Seq ID NO: 148 DNA Sequence
 Nucleic Acid Accession #: NM_021048.2
 Coding sequence: 327..1436

1 11 21 31 41 51
 50 GGCAACGAGG AGAAGCGAGG TTCTCGTTCT GAGGGACAGG CTGAGATCG GCTGAAGAGA 60
 GCGGGCCAG GCTCTGTGAG GAGGCAAGGG AGGTGAGAAC CTGCTCTCA GAGGGTGACT 120
 CAAGTCAACA CAGGGAACCC CTCTTTTCTA CAGACACAGT GGGTCGACAG ATCTGACAAG 180
 55 AGTCCAGGTT CTCAGGGGAC AGGGAGAGCA AGAGGTCAAG AGCTGTGGGA CACCACAGAG 240
 CAGCACTGAA GGAGAAGACC TGCCTGTGGG TCCCATCTCG CCAAGTCTCT CCCCACTCC 300
 CACCTGCTAC CCTGATCAGA GTCATCATGC CTCGAGCTCC AAAGCGTCAG CGCTGCATGC 360
 CTGAAGAAGA TCTTCAATCC CAAAGTGAGA CACAGGGCCT CGAGGGTGCA CAGGCTCCCC 420
 TGGCTGTGGA GGAGGATGCT TCATCATCCA CTTCACCCAG CTCTCTTTT CCATCTCTT 480
 60 TTCCCTCCTC CTCTCTTTCC TCCTCTCTCT CCTGTATCC TCTAATACCA AGCACCCAG 540
 AGGAGGTTTC TGCTGATGAT GAGACACCAA ATCCTCCCCA GAGTGCTCAG ATAGCCTGCT 600
 CCTCCCCCTC GGTGTTGCT TCCCTTCCAT TAGATCAATC TGATGAGGGC TCCAGCAGCC 660
 AAAAGGAGGA GAGTCCAAGC ACCCTACAGG TCCTGCCAGA CAGTGAGTCT TTACCCAGAA 720
 GTGAGATAGA TGAAGAGGTG ACTGATTGGT TGCAGTTTCT GCTCTTCAAG TATCAATGA 780
 65 AGGAGCCGAT CACAAAGGCA GAAATACTGG AGAGTGTCAT AAAAAATTAT GAAGACCACT 840
 TCCCTTTGTT GTTTAGTGAA GCCTCCGAGT GCATGCTGCT GGTCTTTGGC ATTGATGTAA 900
 AGGAAGTGGA TCCCACTGCG CACTCTTTTG TCCTTGTCAC CTCCCTGGGC CTCACCTATG 960
 ATGGGATGCT GAGTGATGTC CAGAGCATGC CCAAGACTGG CATTCTCATA CTTATCCTAA 1020
 GCATAATCTT CATAGAGGGC TACTGCACCC CTGAGGAGGT CATCTGGGAA GCATGAATA 1080
 70 TGATGGGGCT GTATGATGGG ATGGAGCACC TCATTATGG GGAGCCACAG AAGCTGCTCA 1140
 CCCAAGATTG GGTGCAGGAA AACTACCTGG AGTACCGGCA GGTGCTTGGC AGTGATCTCT 1200
 CACGGTATGA GTTCTGTGG GGTCCAAGGG CTCTAGCTGA AATTAGGAAG ATGAGTCTCC 1260
 TGAAATTTTT GGCCAAGGTA AATGGGAGTG ATCCAAGATC CTTCCCACTG TGGTATGAGG 1320
 AGGCTTTGAA AGATGAGGAA GAGAGAGCCC AGGACAGAAT TGCCACCACA GATGATACTA 1380
 75 CTGCCATGCG CAGTGCAAGT TCTAGCGCTA CAGGTAGCTT CTCTACCTCT GAATAAGATA 1440
 AGACAGATTG TTCACGTGTG TTTAAAAGGC AAGTCAAATA CCACATGATT TTACTCATAT 1500
 GTGGAATCTA AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 149 Protein Sequence
Protein Accession #: NP_066386.1

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5      1      11      21      31      41      51
      |      |      |      |      |      |
      MPRAPKRQRC MPEEDLQSQS ETQGLEGAQA PLAVEEDASS STSTSSSFPS SFPSSSSSSS 60
      SSCYPLIPST PEEVSADDET PNPPQSAQIA CSSPSVVASL PLDQSDGESS SQKEESPSTL 120
      QVLPDESLEP RSEIDEKVTD LVQPLLFKYQ MKEPITKAEI LESVIKNYED HFPLLFSEAS 180
      BCMLLVFGID VKEVDPTGHS FVLVTSGLT YDGLMSDVQS MPKTGILILI LSIIFIEGYC 240
10     TPBEVIWEAL NMMGLYDGM EHLIYGEPRKL LTQDHWQENY LEYRQVPGSD PARYEFLNGP 300
      RAHAEIRKMS LLKFLAKVNG SDPRSFLWY EALKDEBER AQDRIATTDD TTAMASASSS 360
      ATGSFSYPE

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Seq ID NO: 150 DNA Sequence
Nucleic Acid Accession #: NM_003695
Coding sequence: 12..398

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20     1      11      21      31      41      51
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      CAGCCCTTAC CCTGCGCTGC CACGTGTGCA CCAGCTCCAG CAACATGCAAG CATTCTGTGG 120
      TCTGCCCGGC CAGCTCTCGC TTCTGCAAGA CCACGAACAC AGTGGAGCCT CTGAGGGGGA 180
      ATCTGGTGAA GAAGGACTGT GCGGAGTCGT GCACACCCAG CTACACCCCTG CAAGGCCAGG 240
      TCAGCAGCGG CACCAGCTCC ACCCAGTGTG GCCAGGAGGA CCTGTGCAAT GAGAAGCTGC 300
25     ACAACGCTGC ACCCACCCTG ACCGCCCTCG CCCACAGTGC CCTCAGCCTG GGGCTGGCCC 360
      TGAGCCTCTT GGGCGTCATC TTAGCCCCCA GCCTGTGACC TTCCCCCAG GGAAGGCCCC 420
      TCAATGCTTT CTCTCCCTTT CTCTGGGGAT TCCACACCTC TCTTCCCCAG CCGGCAACGG 480
      GGGTGCCAGG AGCCCCAGGC TGAGGGGCTC CCCGAAAGTC TGGGACCAGG TCCAGGTGGG 540
      CATGGAATGC TGATGACTTG GAGCAGGCC CACAGACCCC ACAGAGGATG AAGCCACCCC 600
30     ACAGAGGATG CAGCCCCAG CTGCATGGAA GGTGGAGGAC AGAAGCCCTG TGGATCCCCG 660
      GATTTCACAC TCCTTCTGTT TTGTGCGGT TTATTTTGTA CTCAAATCTC TACATGGAGA 720
      TAAATGATT AAACC

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Seq ID NO: 151 Protein Sequence
Protein Accession #: NP_003686

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35     1      11      21      31      41      51
      |      |      |      |      |      |
      MRTALLLLAA LAVATGPALT LRCHVCTSSS NCKHSVVCPA SSRFCKTNT VEPLRGNLVK 60
40     KDCAESCTPS YTLQGQVSSG TSSTQCCQED LCNEKLHNAA PTRTALAHS LSLGLALSLL 120
      AVILAPSL

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Seq ID NO: 152 DNA Sequence
Nucleic Acid Accession #: NM_006398.1
Coding sequence: 19..516

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45     1      11      21      31      41      51
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      GGGCCCTTGT CTGCAGAGAT GGCTCCCAAT GCTTCTCTGCC TCTGTGTGCA TGTCCGTTCC 60
50     GAGGAATGGG ATTTAATGAC CTTTGATGCC AACCCATATG ACAGCGTGAA AAAAATCAAA 120
      GAACATGTCC GGTCTAAGAC CAAGGTTCTT GTGCAGGACC AGGTTCTTTT GCTGGGCTCC 180
      AAGATCTTAA AGCCACGGAG AAGCCTCTCA TCTTATGGCA TTGACAAAGA GAAGACCATC 240
      CACCTTACCC TGAAGTGGT GAAGCCAGT GATGAGGAGC TGCCCTTGT TCTTGTGGAG 300
      TCAGGTGATG AGGCAAGAG GCACCTCCTC CAGGTGCGAA GGTCCAGCTC AGTGGCACA 360
55     GTGAAAGCAA TGATCGAGAC TAAGACGGGT ATAATCCCTG AGACCCAGAT TGTGACTTGC 420
      AATGGAAGA GACTGGAAGA TGGGAAGATG ATGGCAGATT ACGGCATCAG AAAGGGCAAC 480
      TTAATCTTCC TGGCATCTTA TTGTATTGGA GGGTGACCAC CCTGGGGATG GGGTGTGGC 540
      AGGGGTCAA AAGCTTATTT CTTTAACTCT CTTACTCAAC GAACACATCT TCTGATGATT 600
60     TCCCAAAATT AATGAGAATG AGATCAGTAG AGTAAGATT GGGTGGGATG GGTAGGATGA 660
      AGTATATTGC CCAACTCTAT GTTCTTTGA TTCTAACACA ATTAATTAAG TGACATGATT 720
      TTTACTAATG TATTACTGAG ACTAGTAAAT AAATTTTAA GGCAAAATAG AGCATTC

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Seq ID NO: 153 Protein Sequence
Protein Accession #: NP_006389.1

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65     1      11      21      31      41      51
      |      |      |      |      |      |
      MAPNASCLCV HVRSEEDLM TFDANPYDSV KKIKEHVRSK TKVPVQDQVL LLGSKILKPR 60
70     RSLSSYGIDK EKTITLTKV VKPSDEELPL FLVESGDEAK RHLLQVRRSS SVAQVKAMIE 120
      TKTGIIPETQ IVTNCKRLE DGKMMADYGI RKGNNLFLAS YCIGG

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Seq ID NO: 154 DNA Sequence
Nucleic Acid Accession #: BC017490.1
Coding sequence: 74..2788

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75     1      11      21      31      41      51
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      GTGGGTCACG TGAACCACTT TTCGCGCGAA ACCTGGTGTG TGCTGTAGTG GCGGAGAGGA 60

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TCGTGGTACT GCTATGGCGG AATCATCGGA ATCCTTCACC ATGGCATCCA GCCCGGCCCA 120
 GCGTGGGOGA GGCAATGATC CTCTCACTC CAGCCCTGGC CGAAGCTCCC GGCGTACTGA 180
 TGCCCTCACC TCAGAGCCTG GCCGTGACCT TCCACCATTT GAGGATGAGT CCGAGGGGCT 240
 CCTAGGCACA GAGGGGCCCC TGGAGGAAGA AGAGGATGGA GAGGAGCTCA TTGGAGATGG 300
 CATGGAAGG GACTACCGCG CCATCCCAGA GCTGGACGCC TATGAGGCCG AGGGACTGGC 360
 TCTGGATGAT GAGGACGTAG AGGAGCTGAC GGCCAGTCAG AGGGAGGCAG CAGAGCGGGC 420
 CATGCGGCAG CGTGACCGGG AGGCTGGCGG GGGCTTGGGC CGCATGCGCC GTGGGCTCCT 480
 GTATGACAGC GATGAGGAGG ACGAGGAGCG CCCTGCCCGC AAGCGCCGCC AGGTGGAGCG 540
 GGCCACGGAG GACGGCGAGG AGGACGAGGA GATGATCGAG AGCATCGAGA ACCTGGAGGA 600
 TCTCAAAGG CACTCTGTGC GCGAGTGGGT GAGCATGGCG GGCCCCCGGC TGGAGATCCA 660
 CCACCGCTTC AAGAATCTCC TGCGCACTCA CGTCGACAGC CACGGCCACA ACCTCTTCAA 720
 GGAGCGCATC AGCAACATGT GCAAAGAGAA CCGTGAGAGC CTGGTGGTGA ACTATGAGGA 780
 CTTGGCAGCC AGGGAGCAGC TGCTGGCCTA CTTCTGCCT GAGGCACCGG CGGAGCTGCT 840
 GCAGATCTTT GATGAGGCTG CCCTGGAGGT GGTACTGGCT ATGTACCCCA AGTACGACCG 900
 CATCACCAAC CATCTCCATC TCCGCATCTC CCACCTGCCT CTGGTGGAGG AGCTGCGCTC 960
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 TGGGCTCCTG CCCCACTGCA GCATGGTCAA GTACAACTGC AACAGTGCA ATTTCTGCTC 1080
 GGGTCTTTTC TGCCAGTCCC AGAACCAGGA GGTGAAACCA GGCTCCTGTC CTGAGTGCCA 1140
 GTGCGCCGCG CCCTTTGAGG TCAACATGGA GGAGACCATC TATCAGAACT ACCAGCGTAT 1200
 CCGAATCCAG GAGAGTCCAG GCAAAGTGGC GGCTGGCGCG CTGCCCCGCT CCAAGGACGC 1260
 CATTTCTCCT GCGAGTCTGG TGGACAGCTG CAAGCCAGGA GACGAGATAG AGCTGACTGG 1320
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 CACTGTATC CTAGCCAACC ACGTGGCCAA GAAGGACAA CAGGTGCTG TAGGGGAACT 1440
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 GATCTTTGGC AGCATTTGCT CTTCCATCTA TGGTCATGAA GACATCAAGA GAGGCTGGC 1560
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 TGAGAAAGTG TCCAGCCGAG CCACTCTTAC CACTGGCCAG GGGCGGTCCG CTGTGGGCTC 1740
 CACGGCGTAT GTCCAGCGCG ACCCTGTCTG CAGGGAGTGG ACCTTGGAGG CTGGGGCCCT 1800
 GGTCTTGGCT GACCGAGGAG TGTGTCTCAT TGATGAATTT GACAAGATGA ATGACCGAGA 1860
 CAGAACCCAG ATCCATGAGG CCACTGGAGCA ACAGAGCATC TCCATCTCGA AGGCTGGCAT 1920
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 CCGCTTGTGG GTTGGGCGCG ACCTCAGACA CCACCCAGC AACAGGAGG AGGAGGGGCT 2160
 GGCCAAATGG AGCGCTGCTG AGCCCGCCAT GCCCAACAG TATGGCGTGG AGCCCTTGCC 2220
 CCAGGAGGTC CTGAGAAGT ACATCATCTA CGCCAAGGAG AGGGTCCACC CGAAGCTCAA 2280
 CCAGATGGAC CAGGACAAAG TGGCCAAGAT GTACAGTGAC CTGAGGAAAG AATCTATGGC 2340
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 CCACGCGCGC ATCCGATCTG GGGACTATGT GATCGAAGAC GACGTCAACA TGGCCATCCG 2460
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 CACTATTGAG GTCCCTGAGA AGGACTTGGT GGATAAGGCT CGTCAGATCA ACATCCACAA 2700
 CCTCTCTGCA TTTTATGACA GTGAGCTCTT CAGGATGAAC AAGTTTCAGC ACGACCTGAA 2760
 AAGGAAAATG ATCTGTCAGC AGTTCTGAGG CCCTATGCCA TCCATAAGGA TTCTTGGGA 2820
 TTCTGTGTTG GGGTGGTTCAG TGCCCTCTGT GCTTTATGGA CACAAAACCA GAGCACTTGA 2880
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 GTCGCGGGGG TGGGATGTGA GTCATGCGGA TTATCCACTC GCCACAGTTA TCAGCTGCCA 3360
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Seq ID NO: 155 Protein Sequence
 Protein Accession #: AAH17490.1

1 11 21 31 41 51
 MAESSESFTM ASSPAQRRR NDPLTSSPGR SSRRTDALTS SPGRDLPPFE DESEGLLGTE 60
 GPLEEEEDGE ELIGDGMERD YRAIPELDAY EAEGALADDE DVEELTASQR EAAERAMRQR 120
 DREAGRLGR MRRGLLYDS EDEEREPARK RRQVERATED GEEDEEMIES IENLEDLKGH 180
 SVREWVSMAG PRLEIHRFPK NPLRTHVDH GHNVFKERIS DMCKENRESL VVNVEDLAAR 240
 EHVLAFLPE APAELLQIFD EAALEVVLAM YPKYDRITNH IHVRISHLPL VEELRSLRQL 300
 HLNQLRTSG VVTSTGVLF QLSMVKYNCN KCNVLGPFC QSQNQEVKPG SCPEQCSAGP 360
 FEVNMETIY QNYQIRIQE SPGKVAAGRL PRSKDAILLA DLVDSCKPGD EIELTGIYHN 420
 NYDGLMTAN GFPPFATVIL ANHVAKKDNK VAVGELTDED VKMITSLSKD QOIGEIFAS 480
 IAPSIYGHED IKRKLALALP GGEPEKNPGK HKVRGDINVL LGDPGTAKS QFLKYIEKVS 540
 SRAIFTTGGQ ASAVGLTAYV QRHPVSREW LEAGALVLAD RGVCLIDEFD KMNDQRTSI 600
 HEAMEQQSIS ISKAGIVTSL QARCTVIAAA NPIGGRYDPS LTFSENVDLT EPIISRFDIL 660
 CVVRDVTDPV QDEMLARFVV GSHVRHHPN KEEEGLANGS AAEPAMPNTY GVEPLPQEV 720
 KKYIYAKER VHPKLNQMDQ DKVAKMYS DL RKESMATGSI PITVRHIESM IRMAEBAHARI 780
 HLRDYVIEDD VNMAIRVMLE SFIDTQKFSV MRSRKTFAR YLSFRDNDNE LLLFILKQLV 840
 ABQVTVQRNR FGAQQDTIEV PEKDLVDKAR QINIHNLASF YDSELFMRNK FSHDLKRM 900

LQQF

Seq ID NO: 156 DNA Sequence
Nucleic Acid Accession #: NM_002497.1
Coding sequence: 135..1472

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GCGACTGGCC	GGCCATGCCT	TCCCGGGCTG	AGGACTATGA	AGTGTGTAC	ACCATTTGGCA	180
CAGGCTCCTA	CGGCCGCTGC	CAGAAGATCC	GGAGGAAGAG	TGATGGCAAG	ATATTAGTTT	240
GGAAAGAACT	TGACTATGGC	TCCATGACAG	AAGCTGAGAA	ACAGATGCTT	GTTTCTGAAG	300
TGAATTTGCT	TOGTGAACCTG	AAACATCCAA	ACATCGTTCTG	TTACTATGAT	CGGATTATTG	360
ACCGGACCAA	TACAACACTG	TACATTGTAA	TGGAATATTG	TGAAGGAGGG	GATCTGGCTA	420
GTGTAATTAC	AAAGGGAACC	AAGGAAAGGC	AATACTTAGA	TGAAGAGTTT	GTTCTTCTGAG	480
TGATGACTCA	GTTGACTCTG	GCCCTGAAGG	AATGCCACAG	ACGAAGTGAT	GGTGGTCATA	540
CCGTATTGCA	TCGGGATCTT	AAACCAGCCA	ATGTTTTCTT	GGATGGCAAG	CAAAACGTCA	600
AGCTTGGAGA	CTTTGGGCTA	GCTAGAATAT	TAAACCATGA	CACGAGTTTT	GCAAAAACAT	660
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AATCAGATAT	CTGTGATTG	GGCTGCTTGC	TGTATGAGTT	ATGTGATTA	ATGCCTCCAT	780
TTAGAGCTTT	TAGCCAGAAA	GAACTCGCTG	GGAAAATCAG	AGAAGGCCAA	TTGAGGCGAA	840
TTCCATACCG	TTACTCTGAT	GAATTGAATG	AAATTATTAC	GAGGATGTTA	AACTTAAAGG	900
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CAGACGAGCA	AAGAAGAAAT	CTTGAGAGAA	GAGGGCGACA	ATTAGGAGAG	CCAGAAAAAT	1020
CGCAGGATTC	CAGCCCTGTA	TTGAGTGAGC	TGAAACTGAA	GGAAATTCAG	TTACAGGAGC	1080
GAGAGCGAGC	TCTCAAGACA	AGAGAAGAAA	GATTGGAGCA	GAAAGAACAG	GAGCTTTGTG	1140
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GCTTGTCTAA	GGAACCGAAG	TTCTGTCTC	TGGCAAGTAA	TCCAGAACTT	CTTAATCTTC	1260
CATCCTCAGT	AATTAAAGAA	AAAGTTTCAAT	TCAGTGGGGA	AAGTAAAGAG	AACATCATGA	1320
GGAGTGAGAA	TTCTGAGAGT	CAGCTCACAT	CTAAGTCCAA	GTGCAAGGAC	CTGAGAAAAA	1380
GGCTTCAAGC	TGCCAGCTG	CGGGCTCAAG	CCCTGTGAGA	TATTGAGAAA	AATTACCAAC	1440
TGAAAAGCAG	ACAGATCCTG	GGCATGCGCT	AGCCAGGTAG	AGAGACACAG	AGCTGTGTAC	1500
AGGATGTAAT	ATTACCAACC	TTTAAAGACT	GATATTCAAA	TGCTGTAGTG	TTGAATACTT	1560
GGCCCATGTA	GCCATGCCTT	TCTGTATAGT	ACACATGATA	TTTCGGAATT	GGTTTACTG	1620
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TATGCAGGAA	GAGTAGCACT	CACTGAATAG	TTTTAAATGA	CTGAGTGGTA	TGCTTACAAT	1860
TGTCATGTCT	AGATTTAAAT	TTTAAGTCTG	AGATTTTAAA	TGTTTTTGAG	CTTAGAAAAA	1920
CCAGTTAGAT	GCAATTTGGT	CATTAAATACC	ATGACATCTT	GCTTATAAAT	ATTCCATTGC	1980
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Seq ID NO: 157 Protein Sequence
Protein Accession #: NP_002488.1

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55
60

1	11	21	31	41	51	
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YYMSPEQMN	MSYNEKSDIW	SLGCLLYELC	ALMPPPTAFS	QKELAGKIRE	GKFRIPYRY	240
SDELNEIIR	MLNLKDYHRP	SVEEILENPL	IADLVADQR	RNLERRGRQL	GEPEKSDSS	300
PVLSELKLKE	TQLQERERAL	KAREERLEQK	EQELCVRERL	AKDLARAEN	LLKNYSLLKE	360
RKFLSLASNP	ELLNLPSVVI	KKKVHFSGES	KENIMRSSENS	ESQLTSKSKC	KDLKRLHAA	420
QLRAQALSDI	EKNYQLKSRQ	ILGMR				

Seq ID NO: 158 DNA Sequence
Protein Accession #: Eos sequence

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70
75

1	11	21	31	41	51	
TGAGTTTGCC	CCCTTACCCC	CATCCAGTG	AATATTGCA	ATTCTAAAG	ACGTGTTTTG	60
ATTGTCACAC	CTGGGTGGGG	AACATGCTAC	TGGCATCTAA	TGCATAGAGG	GCAGTAATGC	120
TGCTAAACAT	CTTTCAACGC	ACAGGACAGA	GCCCCACAAA	AGAGAATTAT	CTAGCCCCAA	180
ATGTCCATAA	CACCTGCTGT	GAGAAAACCT	ACCGCAGGAT	CTTACTGGSC	TTCATAGGTA	240
AGCTTGCTCT	TGTTCTGGCT	TCTGTAGATA	TATAAAATAA	AGACACTGCC	CAGTCCCTCC	300
CTCAACGTC	CGAGCCAGGG	CTCAAGGCAA	TTCCAAATAA	AGTAGAATGA	ACACTAAATA	360
TTGATTTCAA	AATCTCAGCA	ACTAGAAGAA	TGACCAACCA	TCCTGGTTGG	CCTGGGACTG	420
TCCTAGTTT	AGCATTGAAA	GTTTCAGGTT	CCAGGAAAGC	CCTCAGGCCT	GGGCTGCTGG	480
TCACCCTAGC	AGCTGAGGGA	CTCTTCAATA	CAGAATTAGT	CTTTGTGCAC	TGGAGATGAA	540
TATACTTTAA	TTTGTAACAT	GTGAAAACAT	CTATAAACAT	CTACTGAAGC	CTGTTCTGTC	600
TGCACCGACA	TTTTCAATTGA	GTACGGATTC	TTCTTACCAG	ATACAGCTGC	TCTACAACTT	660
TCGAGGGCTG	GTATAAAACT	AGCTTTTACC	TATTTTAA	AATTACATGA	ATAGTAAAAA	720
CTGGATTA	CCGATATTTC	GGGTATTTC	AATTTCTTGG	GGAGCTTAGA	GGAACGACAA	780
ATAAAAAGAT	TATTTCAACA	TCAAATATAY	GCTATTGTGT	ACATATGAAG	ATAACCACAT	840

ATATGTATAA ATTCCACGTT ACTTTTTCAG AATACTATAA AATCCAACAG AAAAAAATAG 900
CAITTTACTAT

5 Seq ID NO: 159 DNA Sequence
Nucleic Acid Accession #: E08 sequence
Coding sequence: 264..782

	1	11	21	31	41	51	
10	CCCTGCTCCA	GTCACACCCG	GAAGCTGACT	GGTCCACGCA	CAGCTGAAGC	ATGAGGAAAC	60
	TCATCGCGGG	ACTAATTTTC	CTTAAATTTT	AGACTTGAC	AGTAAGGACT	TCAACTGACC	120
	TTCTCTCAGAC	TGAGAACTGT	TTCCAGTATA	TACATCAAGT	CACTGAGATC	TCCAGCACCC	180
	TGCGCGTGGC	ACTACTGAGA	GACGAGGTGC	CAGGGTGGTT	CCTGAAAGTG	CCTGAGCCCC	240
	AACCTATCAG	CAAGGAGCTC	ATCATGCTGA	CAGAAGTCAT	GGAGGTCTGG	CATGGCTTAG	300
15	TGATCGGGGT	GGTGTCCCTC	TTCTGTCAGG	CCTGCTTCCT	CACCGCCATC	AACTACCTGC	360
	TCAGCAGGCA	CATGGCCAC	AAGAGTGAAC	AGATACTGAA	AGCGGCCAGT	CTCCAGGTTC	420
	CCAGGCCACG	CCCTGGCCAC	CATCATCCAC	CTGCTGTCAA	AGAGATGAAG	GAGACTCAGA	480
	CAGAGAGAGA	CATCCCAATG	TCTGATTCCC	TTTACAGGCA	TGACAGGAC	ACACCTCAG	540
	ATAGCTTGGA	TAGCTCTGCG	AGTTCCGCTC	CTGCCTGCCA	GGCCACAGAG	GATGTGGATT	600
20	ACACACAAGT	GGTCTTTTCT	GACCTGGAG	AACTAAAAAA	TGACTCCCCG	CTGGACTATG	660
	AGAACATAAA	GGAAATCACA	GATTATGTCA	ATGTCAATCC	AGAAAGACAC	AAGCCAGTT	720
	TCTGGTATTT	TGTCACCCCT	GCTCTGTCTG	AGCCAGCGGA	ATATGATCAA	GTGGCCATGT	780
	GAATTCACAA	TATTTTTAAT	GGGTCCAGT	TCTCTATGGA	TTCTTACATT	TAATTTGTAG	840
	GGAAATGCCA	TTTTTCCCCC	TTAAACAAGG	CATGGGGCTC	ACAAGTCTAT	GGAGACAGGC	900
25	CAAAAAGAA	GTGGAGAAGA	AAACTGATAA	ATACACAGAG	GTCCCTCAAGA	CCCATGGACT	960
	CCTGGTCTGT	ACCCAAAAAA	GCTGTTCTGT	CCTCAAAAC	AAAAACAAGG	CTTGGCTGGG	1020
	AAAACAGGCC	AATGCCCCCG	CAAGAAAGGT	TGAGATCAGA	TGTTAGGAAG	AACTTTCAGG	1080
	TAAAGTATGA	GAACATATGA	GTCCATCAGC	AGAGATAGTA	GTGAAGTCTC	TCCCCAGGGA	1140
30	AAATTTTAAA	AAGGTTGAAT	CAGCTGTTGT	AGAGTTCAT	TTGGCAATCT	CATGGTTAAA	1200
	TGACTTCCCT	TTGAGCTCTT	TAATTATTGG	CAATAAACAA	CTTCTTTAAA	AGTTTTAAAT	1260
	AAAATAGCAA	CCACCACCA					

35 Seq ID NO: 160 Protein Sequence
Protein Accession #: E08 sequence

	1	11	21	31	41	51	
40	MLTEVMEVWH	GLVIAVVSFL	LQACPLTAIN	YLLSRHMAHK	SEQILKAASL	QVPRPSPGHH	60
	HPPAVKEMKE	TQTERDIPMS	DSLYRHDSDT	PSDSLDSGCS	SPPACQATED	VDYTVVVFSD	120
	PGLKNDSDPL	DYENIKEITD	VYVNVNPERHK	PSFWYFVNPA	LSEPAEYDQV	AM	

45 Seq ID NO: 161 DNA Sequence
Nucleic Acid Accession #: NM_012152
Coding sequence: 43..1104

	1	11	21	31	41	51	
50	CTTCTTTAAA	TTTCTTTCTA	GGATGTTTAC	TTCTTCTCCA	CAATGAATGA	GTGTCACTAT	60
	GACAAGCACA	TGGACTTTTT	TTATAATAGG	AGCAACACTG	ATACTGTCGA	TGACTGGACA	120
	GGAAACAAGC	TTGTGATTGT	TTTGTGTGTT	GGGACGTTTT	TCTGCGTGT	TATTTTTTTT	180
	TCTAATATCT	TGGTCATCGC	GCCAGTGATC	AAAAACAGAA	AATTTTCATT	CCCCCTCTAC	240
	TACCTGTTGG	CTAATTTAGC	TGCTGCCGAT	TTCTTCGCTG	GAATTCGCTA	TGTATTCCTG	300
	ATGTTTAAAC	CAGGCCCACT	TTCAAAACT	TTGACTGTCA	ACCGCTGGTT	TCTCGCTCAG	360
55	GGGCTTCTGG	ACAGTAGCTT	GACTGCTTCC	CTCACCAACT	TGCTGGTTAT	CGCCGTGGAG	420
	AGGCACATGT	CAATCATGAG	GATGCGGGTC	CATAGCAACC	TGACCAAAAA	GAGGGTGACA	480
	CTGCTCATTT	TGCTTGTCTG	GGCCATCGCC	ATTTTATG	GGGCGGTCCC	CACACTGGGC	540
	TGGAATTGCC	TCTGCAACAT	CTCTGCCCTG	TCTTCCCTGG	CCCCCATTTA	CAGCAGGAGT	600
	TACCTTGT	TCTGGACAGT	GTCCAACCTC	ATGGCCTTCC	TCATCATGGT	TGTGGTGTAC	660
60	CTGCGGATCT	CGGTGTACGT	CAAGAGGAAA	ACCAACGTCT	TGCTTCGSCA	TACAAGTGGG	720
	TCCATCAGCC	CGCGGAGGAC	ACCCATGAAG	CTAATGAAGA	CGGTGATGAC	TGTCTTAGGG	780
	GCGTTTGTGG	TATGCTGGAC	CCCGGGCCTG	GTGGTTCTGC	TCCTGACGG	CCTGAACTGC	840
	AGGCAGTGTG	GCGTGCAGCA	TGTGAAAAGG	TGGTTCTCTG	TGCTGGCGCT	GCTCAACTCC	900
	GTCGTGAACC	CCATCATCTA	CTCTACAAG	GACGAGGACA	TGTATGGCAC	CATGAAGAAG	960
65	ATGATCTGCT	GCTTCTCTCA	GGAGAACCCA	GAGAGGCGTC	CCTCTCGCAT	CCCCTCCACA	1020
	GTCCTCAGCA	GGAGTGACAC	AGGCAGCCAG	TACATAGAGG	ATAGTATTAG	CCAAGGTGCA	1080
	GTCGTGCAATA	AAAGCACTTC	CTAAACTCTG	GATGCCTCTC	GGCCCAACCA	GTTGATGACT	1140
	GTCTTAGG						

70 Seq ID NO: 162 Protein Sequence
Protein Accession #: NP_036284

	1	11	21	31	41	51	
75	MNECHYDKHM	DFPYNRSNTD	TVDDWTGKTL	VIVLCVGTFF	CLFIFFSNSL	VIAAVIKNRK	60
	PHFPFYLLA	NLAADFFAG	IAYVFLMNT	GPVSKTLTVN	RWFLRQGLLD	SSLTASLTNL	120
	LVIAVERHMS	INRMVRHSNL	TKKRVTLIL	LVWAIAIFMG	AVPTLGWNL	CNISACSSLA	180
	PIYSRSLVLF	WTVSNLMAFL	IMVVVYLRIY	VYVKKRTNVL	SPHTSGSISR	RRTPMKLMKT	240

VMTVLGAFVV CWTPLGLVLL LDGLNCRQCG VQHVKNRFL LALLNSVNP IISYKDEDM 300
YGTMKMKICC FSQENPERRP SRIPSTVLSR SDTGSQYIED SISQGAVCNK STS

5

Seq ID NO: 163 DNA Sequence
Nucleic Acid Accession #: NM_020242
Coding sequence: 72..4240

10	1	11	21	31	41	51	
	CAGTGC	CGGTGC	GGGAGG	GGCACCGG	GCATTG	CGGGAT	CGAG
	GGGTGAGG	GCTATGGC	CCGGCTGC	AACTGAGT	CGCAGCGT	CAAAATGG	TCA
	GTCTAACCA	CCAAGTAAT	AAGGTGAT	CATCAAA	TTTGTGCG	TTCGTCTC	CTC
	TGCAGAAAG	TCTGGGT	CTGATGG	GCAGAACT	TGCTTATC	TGCTGTCT	CTC
15	CACGAGTCT	CGGCTGCA	CCAACCTG	GCCCAAG	TTCAAGTT	ATCATGTT	CTG
	AGATGTGG	ACCACTCAG	AATCTGT	TGCAACTG	GCTAAAAG	TTGTGGAG	CTC
	TTGCATGAG	GGTTATAAT	GTACCATCT	TGCATATG	CAGACTGG	CAGGGAAG	AC
	ATTTACTAT	ATGGGACCA	CTGAATCT	TAATTTTCT	CATAACCT	GAGGAGTA	AT
	CCCAGAGAT	TTTGAATAT	TGTTTTCCT	AATTGATCG	GAAAAGAAA	AGGCTGG	AGC
20	TGGAAGAG	TTCTTTTGA	AGTGTTCCT	TATTGAAAT	TACAACGAG	AGATATAT	G
	TCTACTGG	TCTGCATCG	CTGACTGT	CTTAAGGG	CATATCAAG	AGGAGTCT	T
	TGTTGTGG	CGGCTGAG	AGGTGGTA	CTCAGCTG	GAAGCCTAT	AGGTGCTG	T
	TGGAGGAT	AGGAATAG	GTGTGGCAT	AACATCAAT	AACAGAGA	CGTCTAGG	T
	TCATGCGCT	TTTACAATA	CAATAGAG	AATGGAGAA	AGTAATGAG	TTGTGAAT	T
25	ACGGACCT	CTGCTTCA	TGGTGGATT	AGCAGGAT	GAAAGGCC	AAGATACCA	C
	TGCAGAGGG	ATGAGATT	AGGAAGCAG	TAACATAAA	CGATCATT	GCTGCCTGG	G
	CCAAGTGAT	CCAGCAGTT	TGACGTGG	TAATGGAAA	CAGAGACAT	TTTGCTAC	A
	AGACTCCAA	CTTACCTTC	TACTACGG	TTCCCTTGG	GGTAATGCC	AAACAGCC	A
	AATTGCAAA	GTTTCATCT	GATCCAGTG	TTTGGGGAA	ACCCTATCA	CACCTAACT	T
30	TGCTCAAGA	GCCAAGCT	TTAAAAACA	GGCAGTAG	AATGAAGAC	CCCAAGGAA	A
	TGTGAGCC	CTCCAAGCT	AAGTGAAG	GCTCAAGAA	CACTGGCGG	AGCTTGCT	T
	AGGACAGAC	CCACAGAAA	GCTTCTGAC	CAGAGACAA	AAGAAGACT	ACTATATG	A
	GTATTTCC	GAAGCAAT	TATTTCTTA	GAAATCTGA	CAGGAAAAG	AGTCTCTG	A
	AGAAAAAG	ATCCAAAT	AGACCTCAC	CCTCAAAA	GAAAATTTA	TTCAATCT	A
35	TAAATATTC	GTGAATAT	GAGAGGAT	AATAATAC	TTGGAAGAG	TCCACAAG	A
	ATCCCGGG	GGTTTTCT	CTGAGGAG	GGATCGTT	CTCTCAGAA	TAAGGAAT	G
	GATTCAAA	CTGCCAGAA	AAATAGAG	CCACCCAGA	GTTGCAAA	ATGCTATG	A
	AAATCATTC	CTCAGGGAG	AGAAATAG	ACTGAGAT	TTAGAGCCT	TGAAAAGAG	C
	TCAAGAAAT	GATGCCAGA	CCATTGCAA	ACTAGAAAA	GCTTTCTCT	AAATAAGTG	G
40	CATGGAGAA	AGTGAACAA	ATCAGCAAG	ATTTTCAC	AAAGCTCAG	AAGAGCCAT	G
	TTTGTTCGA	AACACTGAG	AGTTAAAG	ACAACCTCG	CAAAATCAG	CAGAGCTGA	A
	TAATTCAAA	CAAGAAAT	AGAAATTC	AGAATTTCT	AGGAAAAGG	AGCTAGAA	T
	GGAAATCAG	CTTCAGTCT	TGCAAAAAG	GAACCTTAA	CTTGAAAAC	TTTTGGAAG	C
	AACAAAAG	TGCAAGCGC	AAGAAGTT	TCAGCTGAA	AAAAATCAT	CTGAAACAC	T
45	TAAGATTAT	GTCACACCA	CCAAGGCCT	CCAACCTCA	TCCCGACCA	TACCAAAAT	T
	AAGCCCTGA	ATGGGAAG	TTGGCTCT	ATCACTCAG	AATTCAGCA	TATTAGATA	A
	TGATATAT	AATGAGCC	TTCTCCTGA	GATGAATGA	CAAGCTTTG	AGGCCATTT	C
	TGAAGAGCT	AGAACAGTG	AGGAACAA	GAGTGCTCT	CAAGCCAA	TGGATGAAG	A
	AGAGCATAA	AACCTAAAG	TTCAGCAG	TGTTGACAA	CTGGAACAT	ATTCTACCA	C
50	AATGCAGAG	ATTTTCTCA	CAGAAAGAA	TGATTGGAC	AAACAGCAG	AAGAGCTTC	T
	CTCAGAGTG	AATGTCTTG	AAAAGCAG	TCAAGAGAC	CAAACTAAA	ATGACTTTT	T
	GAAAAGTG	GTACATGAC	TGCGAGTAG	CCTTCATT	GCTGCAAG	AGCTTTTTC	T
	AGTGAAAT	GAAATATAG	CATTCAAA	GAAATCAG	AAAGAATT	ACAACTTTC	T
	TGAAGACAC	ATGCATGAT	AGCTTCAAT	AGATAATCT	AGGTTAGAA	ACGAAAAG	C
55	GCTTGAGAG	AAAGCCTGC	TACAGGAT	CTATGACAA	TTACAAGAA	TAATGAAAT	T
	TGAGATTG	CAACTTTC	GAAACCTCC	AAACTTCAA	AAAGAAAAT	AAACTCTGA	A
	ATCTGATCT	AATAATTGA	TGGAGCTTC	TGAGGCAG	AAAGAACGC	ATAACAAAT	T
	ATCATTAC	TTTGAAGAG	ATAAAGAAA	CAGTTCTAA	GAAATCTTA	AGTTCTTGA	A
	GGCTGTAC	CAGGAGAAC	AGAAAGAG	GGCCAAAG	GAGCAGCAG	TGGCAAAAG	T
60	ACAGAAACT	GAAGAGAG	TGCTTGCT	TGAAAAGTG	ATCAGTTCC	TGAAAAGTG	C
	TAGAGATT	GATAAGAA	TTGTAGCT	CCTCATGAA	CAGATCCAG	AGCTAAGAA	C
	ATCGGTCT	GAGAAAAC	AACTATAG	CACCCTGAA	CAAGAACT	AGGCATAAA	A
	TTGCAAAAT	AACTCTGCT	TGGTTGAC	AGAAGAGAG	AGAGTGTGA	TCAAGAAG	C
	GGAGTGGAT	ATTCTGGAT	TGAAAGAA	CCTTAGGCT	AGAATACT	CTGAGGAC	T
65	AGAGAGGG	ATGCTCTGT	AGGACCTGG	TCATGCCAC	GAGCAGCT	ACATGCTCA	C
	AGAGGCTCA	AAAAACACT	CGGGCTGCT	GCACTCTGC	CAGGAAGAA	TGACCAAG	A
	GGAGGCTGT	ATTCAGGAA	TTCAAGCAA	GCTAAACCA	AAGAAAGAG	AAGTAGAA	C
	GAAGAAGAT	GAAATATA	TCAAAATG	GCAACTAG	CATGTGAT	ATTCTGCT	G
	TGAGGATCCC	CAGAGTCT	AGACACCAC	TCACTTCAA	ACACATTTG	CAAACTCT	C
70	GAAGAACAA	GAAACAAGA	TAGAAGAT	AAGAGCCT	AAGACTTCT	TGGAAACCT	T
	TGTAAACAA	CTAAATGAA	ACAGAGAAG	CAAAATGCT	GAAATCTCA	GAAATGAAG	A
	GCAGTTGCT	GAAATGAAA	ACCTACGCT	GGAAAGTC	CAGTTAAT	AGAAAACT	G
	GCTCTGCAA	GGTCAGCT	ATGATATT	AAGACAAA	GAAAACAG	ATCAGAAT	C
	TCCAGATA	CAACAGCT	AGAATGAAC	AGAAGAAAG	ATCAAGAAA	GACTTGCAA	A
75	AAGTAAATA	GTTGAAGAA	TGCTGAAA	GAAAGCAG	CTAGAAGAG	TCCAAGTG	C
	CCTTTACAC	AAAGAGAT	AATGCCTTA	AATGACTGA	GAGTCAAG	GAAACCAAC	A
	TTTGGAGTC	AAAGCATTC	AGGAAAAGA	ACAACTGAG	TCAAAGCT	AAGAAATGA	A
	TGAAGAAAG	GAGAGAAC	CCCAGGAG	GGAAATGTT	AGGAAGCAG	TGGAGTGT	T

5 TGCTGAGGAA AATGGAAAGT TGGTAGGTCA CCAAAATTG CATCAGAAGA TTCAGTACGT 4140
 AGTGCAGCTA AAGAAAGGAAA ATGTCAGGCT TGCTGAGGAG ACAGAAAAGT TGGTGCCGA 4200
 AAATGTATTT TTAAGAGAAA AGAAAAGAG TGAATCTTGA GGATTCGGGT CAGCTACCTA 4260
 GGCATCACCT TGTTTGAAGA TGTTCTTCT CTTTACAAG TAAGACCTAC TCCTGGCCAC 4320
 TTAGGAGAGC TGAATTTATG GACCTTAATT ATTAATAGTT TATAAGGTGG TGGTAACCAC 4380
 CTCAGTTTTC TGATGAACAT TCTGCATCCA TATACACCTC GTGACAGTCA GCAGTCTGCT 4440
 ATTAAGTGGC CTACTTCAAG GCTTTGAATC AACTTAAGGG AAAACCTTTT GTCTTTGTAA 4500
 AAATAAAGC CTGTAGCTAA GGTTTACAGT GGACATTAGC CAGATCATTT TCTTCTTAGA 4560
 10 TTATGCCATA ATCTCTTTG ATTCTTATGG AAGTTCTAAC AATATATGGT GGTTCACACA 4620
 CCTGCAGTGA GTTTAATGAC TGACTTAGTA GCAGGTACAA GAAGCAAAC TGTTAATATA 4680
 GATTATTTTT GTATTCTTAC TTTAGGTATT TTACTTGAGC ATTTTCCATG ACTGTAATAA 4740
 AAGCCATTTT TTAAGATAAA AAAAAAAAAA AAAAA

15 Seq ID NO: 164 Protein Sequence
 Protein Accession #: NP_064627

1 11 21 31 41 51
 20 MAPGCKTELK SVTNQSQNP SNEGDAIKVF VRIRPPAERS GSADGEQNL LSVLSSTSLR 60
 LHSNPEPKTF TFDHVADVD TQESVFATVA KSIVESCMG YNGTIFAYGQ TGSKTFPTMM 120
 GPSESDNFH NLRGVPRSF EYLFSLIDRE KEKAGAGKSF LCKCSFIEIY NEQIYDLDS 180
 ASAGLYLREH IKKGVPVVG VEQVVTSAE AYQVLSGGWR NRRVASTSMN RESSRSHAVF 240
 TTTIESMEKS NELVNIRTS LNLVDLAGSE RQDTHAEGM RLKEAGNINR SLSCLGQVIT 300
 25 ALVDVGNGKQ RHVCYRDSKL TFLRLDSLGG NAKTAIANV HPGSRFCGET LSTLNPAQRA 360
 KLIKNAVVN EDTQGNVSQL QAEVKRLKEQ LAELASGQTP PSSFLTRDKK KTNMYEYFQE 420
 AMLFFKSEQ EKKSLEIKVT QLEDLTKEK KFIQSNKMIV KFPREDQIIRL EKLHKESESG 480
 FLPEEQDRLL SELRNEIQTL REQIEHPRV AKYAMENHSL REENRRLRL EPVKRAQEMD 540
 AQTIKLEKA FSEISGMEKS DKNQGGFSK AQKEPCLFAN TEKLKAQLLQ IQTELNNKQ 600
 30 EYEEPKELTR KRQLESESL QSLQKANLNL ENLEATKAC KRQEVSQLNK IHAETLKIIT 660
 TPTKAYQLHS RVPVKLSPEM GSPGSLYTQN SSILDNDILN EPVPEPMNEQ AFEAISEELR 720
 TVQEQMSALQ AKLDEEHNH LKLQHVHDKL EHRSTQMDEL FSSERIDWTK QQEELLSQLN 780
 VLEKQLQETQ LKNDPLKSEV HDLRVVLHSA DKELSSVKLE YSSFKNQNEK EFNKLSERHM 840
 HVQLQDNLRL LENEKLLSEK ACLQDSYDNL QEIMKFEIDQ LSRNLQNFKK ENETLKSIDL 900
 35 NLMELLEAEK ERNKNLSLQF EEDKENSKE ILKVLEAVRQ EKQKETAKCE QOMAKVQKLE 960
 ESLLATEKVI SSLKSRSDS KKVVDLMNQ IQELRTSVCE KTETIDTLKQ ELKDINCKYN 1020
 SALVDREESR VLIKQEVDI LDLKETLRL ILSEDIERDM LCEDLAHATE QLNMLTEASK 1080
 KHSGLLQSAQ BELTKKEALI QELQHLNKK KEEVEQKKNE YNFKMRQLEH VMSAAEDPQ 1140
 SPKTPPHFQT HLAKLETOE QEIEDGRASK TSLEHLVTKL NEDREVKNAE ILRMKEQLRE 1200
 40 MENLRLESQ LIEKNWLLQ QLDLIRKQKE NSDQNHDPNQ QLKNEQEBSI KERLAISKIV 1260
 EEMLKMKADL EEVQSALYNK EMECLRMTE VERTQTLESK AFQSEQLRS KLEMYEERE 1320
 RTSQEMEMLR KQVECLAEN GKLVGHQNLH QKIQYVVRK KENVRLAET EKLRAENVFL 1380
 KEKKRSES

45 Seq ID NO: 165 DNA Sequence
 Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
 50 TTTTTTTTT TTTTTCACA TGCTGATGTT GCTGCCGATG ATTTCAACGC CTGGCTTTGA 60
 GATTCCGTGA GTAGTCTTGA ATAATTAAA ATTCGAAAT CAAATTCTAC TTAATTTCTC 120
 TTAATGCTAT TGTATTTCTT AATCTCAGC TTTAATCATG AAGAAAGTAC TTTGCTAGG 180
 GGTCTTAATT GAATGGTGGG GTCGAGATGA CTGCGTCAGA ATTAATCTC TGGAAAGCCT 240
 CTGAGCTCCT TTTAAATCA TCAACAAGCG AAAATCCCTA TCAATAGCGA TGTGGGAATG 300
 55 CATTAGGTAC AGTATTTTAA ACATACAAAA CCTAGGCATA TTAAGAAACA CTCCTCTGGT 360
 AATTTAATAA GGAATAATGA TGTCTTAAAG TTTATTTTAA TCAGCAAGTA TGACTCAATT 420
 TGAATATATG AGAACAATA GATTAAATA GGAACACCCA GTAAACTATG GTATGCAAT 480
 AAACCTCAGAG GTAAACTTGT GAATACATA ATCTAAATAA GTCAGTTACC ATCAAAATAT 540
 TACGTGATCC TATATTTTTC TGTCACGTC TTAAGATAT TTTTACCTT GGGGCTTTAT 600
 60 TTTCTTTCCC TCTTCCCAAG ATTATCCAAG GCAGTTCCAA TACCGGTTT CAATAATGGT 660
 AATTAAACTT TTGGAGGGTA ATGCCAGCT GTTCCAGAA AAATACTTTT AATAGGTGGT 720
 AGTCCTCCCT GTAACCTGGT TTTCCCGGGA ATCCGGGGGG GGCATGTTGT TTTTATGTG 780
 GCCATTTTGT TTTGTCCTTT TTTGTTTGT TGGTGGTCAG GTTTCTTTT CATAGCGGGG 840
 GAGAAGATTT TGGTCGACT AGCGCCATCC AGCGGGTTTA GAGAAGGAGC ACACCTTTTC 900
 65 CCGAATAGTG GCTTTTGGAT GAACAATGAA

70 Seq ID NO: 166 DNA Sequence
 Nucleic Acid Accession #: NM_006953.1
 Coding sequence: 33..896

1 11 21 31 41 51
 75 CGGTTCGCGC CTCTGGCGGC TCCTCCCGGG CGATGCCTCC GCTCTGGGCC CTGCTGGCCC 60
 TCGGCTGCTT GCGGTTTCGC TCGGCTGTGA ACCTGCAGCC CCAACTGGCC AGTGTGACTT 120
 TCGCCACCAA CAACCCACCA CTTACCACCT TGGCCTTGGA AAAGCCTCTC TGCATGTTTG 180
 ACAGCAAAGA GGCCCTCACT GGCACCCACG AGGTCTACCT GTATGTCCTG GTCGACTCAG 240
 CCATTTCAG GAATGCTCA GTGCAAGACA GCACCAACAC CCCACTGGGC TCAACGTTCC 300
 TACAACAGA GGGTGGGAGG ACAGGTCCCT ACAAAGCTGT GSCCTTTGAC CTGATCCCTC 360
 GCAGTGACCT GCCCAGCCTG GATGCCATTG GGGATGTGTC CAAGGCCTCA CAGATCTCTG 420

5 ATGCTACCT GGTGAGGTG GGTGCCAAG GGACCTGCCT GTGGGATCCC AACTTCCAGG 480
 GCCTCTGTAA CGCACCCCTG TCGGCAGCCA CGAGTACAG GTTCAAGTAT GTCTGGTCA 540
 ATATGTCCAC GGGCTTGGA GAGGACCAGA CCCTGTGGTC GGACCCATC CGCACCAACC 600
 AGCTCACCCC ATACTCGACG ATCGACACGT GGCCAGGCCG GCGGAGCGGA GGCATGATCG 660
 TCATCACTTC CATCTGGGC TCCCTGCCCT TCTTCTACT TGTGGGTTT GCTGGCGCCA 720
 TTGCCCTCAG CCTCGTGGAC ATGGGGAGTT CTGATGGGGA AACGACTCAC GACTCCCAA 780
 TCACTCAGGA GGCTGTTCCC AAGTCGCTGG GGGCCTCGGA GTCTTCTAC ACGTCCGTGA 840
 ACCGGGGGCC GCCACTGGAC AGGCTGAGG TGTATTCCAG CAAGCTCCAA GACTGAGCCC 900
 10 AGCACCACCC CTGGGACGCA GCATCCTCCT CTCTGGCCTT GCCCCAGGCC CTGCAGCGGT 960
 GGTGTGCACA CCCTGACTTC AGGGAAGGTG AAACAGGGCT TGTCCCTCCA ACTGCAGGAA 1020
 AACCTTAAT AAAATCTTCT GATGAGTTCT AAAAAAAA

Seq ID NO: 167 Protein Sequence
Protein Accession #: NP_008884.1

15 1 11 21 31 41 51
 | | | | |
 MPPLWALLAL GCLRFGSAVN LQPQLASVTF ATNNPTLITV ALEKPLCMFD SKEALTGTHE 60
 20 VYLVLVDSA ISRNASVQDS TNTPLGSTFL QTGGRTGPY KAVAFDLIPC SDSLPSLDAIG 120
 DVSKASQILN AYLVRVGANG TCLWDPNFGQ LCNAPLSAAT EYRPKYVLVN MSTGLVEDQT 180
 LWSDFIRTNQ LTPYSTIDTW PGRRSGGMIV ITSILGSLPF FLLVGFAGAI ALSLVDMGSS 240
 DGETTHDSQI TQEAVPKSLG ASESSTSVN RGPPLDRAEV YSSKLQD

Seq ID NO: 168 DNA Sequence
Nucleic Acid Accession #: NM_005672.1
Coding sequence: 18..389

30 1 11 21 31 41 51
 | | | | |
 AGGAGAGGC AGTGACCATG AAGGCTGTGC TGCTTGCCCT GTTGATGGCA GGCTTGGCCC 60
 TGCAGCCAGG CACTGCCCCTG CTGTGCTACT CTGCAAGC CCAGGTGAGC AACGAGGACT 120
 GCCTGCAGGT GGAGAACTGC ACCCAGCTGG GGGAGCAGTG CTGGACCGCG CGCATCCGCG 180
 35 CAGTTGCGCT CCTGACCGTC ATCAGCAAAG GCTGCAGCTT GAACCTGGCTG GATGACTCAC 240
 AGGACTACTA CGTGGGCAAG AAGAACATCA CGTGTGTGA CACCGACTTG TGCAACGCCA 300
 GCGGGGCCCA TGCCCTGCAG CCGGCTGCCG CCATCCTTGC GCTGCTCCCT GCATCGGCC 360
 TGCTGCTCTG GGGACCCGCG CAGCTATAGG CTCTGGGGGG CCCCCTGCA GCCCACACTG 420
 GGTGTGCTGC CCCAGGCCTT TGTGCCACTC CTCACAGAAC CTGGCCCACT GGGAGCCTGT 480
 CCTGGTTCCCT GAGGCACATC CTAACGCAAG TTTGACCATG TATGTTTGA CCCCTTTTCC 540
 40 CCNAACCCCTG ACCTTCCCAT GGGCCTTTTC CAGGATTCCN ACCNGGCAGA TCAGTTTATG 600
 TGANACANAT CCGNTGCAG ATGGCCCTTC CAACNTTIN TGTGNTGTT TCCATGGCCC 660
 AGCATTTTCC ACCCTTAACC GCCAGGTTTG GTCCGTGGTG TCCCCCGCAC CCAGCAGGGG 780
 CCACCCCAT TATGAATTGA GCCAGGTTTG GTCCGTGGTG TCCCCCGCAC CCAGCAGGGG 840
 45 ACAGGCATC AGGAGGGCCC AGTAAAGGCT GAGATGAAGT GGACTGAGTA GAACTGGAGG 900
 ACAAGAGTTG ACGTGAAGTT CTGGGAGTTT CCAGAGATGG GGCCTGGAGG CCTGGAGGAA 960
 GGGGCCAGGC CTCACATTTG TGGGGNTCCC GAATGGCAGC CTGAGCACAG CGTAGGCCCT

Seq ID NO: 169 Protein Sequence
Protein Accession #: NP_005663.1

50 1 11 21 31 41 51
 | | | | |
 MKAVLLALLM AGLALQPSTA LLCYSCKAQV SNEDCLQVEN CTQLGBCQWT ARIRAVGLLT 60
 55 VISKGCSLNC VDDSDQYYVG KKNITCCDTD LCNASGAHAL QPAAAILALL PALGLLLWGP 120
 GQL

Seq ID NO: 170 DNA Sequence
Nucleic Acid Accession #: NM_006952.1
Coding sequence: 11..793

60 1 11 21 31 41 51
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 AATCCCGACA ATGGCGAAG ACAACTCAAC TGTGCTTGC TTCCAGGGCC TGCTGATTTT 60
 65 TGGAAATGTG ATTATTGGTT GTTGCGGCAT TGCCCTGACT GCGGAGTGCA TCTTCTTTGT 120
 ATCTGACCAA CACAGCCTCT ACCCACTGCT TGAAGCCACC GACAACGATG ACATCTATGG 180
 GGCTGCTGGG ATCGGCATAT TTGTGGGCAT CTGCCTCTTC TGCTGTCTG TTCTAGGCAT 240
 TGTAGGCATC ATGAAGTCCA GCAGGAAAT TCTTCTGGCG TATTTTCATC TGATGTTTAT 300
 70 AGTATATGCC TTTGAAGTGG CATCTGTAT CACAGCAGCA ACACAACGAG ACTTTTTCAC 360
 ACCCAACCTC TTCCTGAAGC AGATGCTAGA GAGGTACCAA AACACAGCC CTCCAAACAA 420
 TGATGACCCG TGGAAAAACA ATGGAGTCAC CAAACCTGG GACAGGCTCA TGCTCCAGGA 480
 CAATTGCTGT GGCCTAAATG GTCCATCAGA CTGGCAAAA TACACATCTG CTTCCGGAC 540
 TGAGAATAAT GATGCTGAAT ATCCCTGGCC TCGTCAATGC TGTGTTATGA ACAATCTTAA 600
 75 AGAACCTCTC AACCTGGAGG CTGTGTAAT AGGCGTGCTT GGTTTTATC ACAATCAGGG 660
 CTGCTATGAA TTGATCTCTG GTCCAATGAA CCGACACGCC TGGGGGGTGT CTTGTTTGG 720
 ATTTGCCATT CTCTGCTGGA CTTTTTGGGT TCTCTGGGT ACCATGTTCT ACTGGAGCAG 780
 AATTGAATAT TAAGAA

Seq ID NO: 171 Protein Sequence
Protein Accession #: NP_008883.1

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5      1      11      21      31      41      51
      |      |      |      |      |      |
      MAKDNSTVRC FQGLLIFGNV IIGCCGIALT AECIFFVSDQ HSLYPLLEAT DNDDIYGAAN 60
      IGIFVGLICLF CLSVLGIIVI MKSSRKILLA YFILMFIVYA FEVASCITAA TQRDPFPTNL 120
      PLKQMLERYQ NNSPPNNDDQ WKNNGVTKTW DRLMLQDNCC GVNGPSDWQK YTSAPRTENN 180
      DADYPWPQRQC CVMNNLKEPL NLEACKLGVP GFYHNQGCYE LISGPMNRHA WGVAVWGPPI 240
10     LCWTFWVLLG TMFYNSRIEY

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Seq ID NO: 172 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..672

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15     1      11      21      31      41      51
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      ATGAGGCTCC AAAGACCCCG ACAGGCCCGG GCGGGTGCGG GGCGCGCGCC CCGGGGCGGG 60
      CGGGGCTCCC CCTACCCGCC AGACCCGGGG AGAGGCGCGC GGAGGCTGCG AAGGTTCCAG 120
20     AAGGGCGGGG AGGGGGCGCG GCGCGCTGAC CTTCCCTGGG CACCGCTGGG GACGATGGCG 180
      CTGCTCGCCT TGCTGCTGGT CGTGGCCCTA CCGCGGGTGT GGACAGACGC CAACCTGACT 240
      GCGAGACAAC GAGATCCAGA GGAATCCAGC CGAACGGACG AGGGTGACAA TAGAGTGTGG 300
      TGTGATGTTT GTGAGAGAGA AAACACTTTC GAGTGCCAGA ACCCAAGGAG GTGCAAATGG 360
      ACAGAGCCAT ACTGCGTTAT AGCGGCCGTG AAAATATTTT CACGTTTTTT CATGGTTGCG 420
25     AAGCAGTGCT CCGCTGGTTG TGCAGCGATG GAGAGACCCA AGCCAGAGGA GAAGCGGTTT 480
      CTCCTGGAAG AGCCCATGCC CTTCTTTTAC CTCAGGTGTT GTAAAATTGG CTACTGCAAT 540
      TTAGAGGGGC CACCTATCAA CTCATCAGTG TTCAAAGAAT ATGCTGGGAG CATGGGTGAG 600
      AGCTGTGGTG GGCTGTGGCT GGCCATCCTC CTGCTGCTGG CCTCCATTGC AGCCGGCCTC 660
30     AGCCTGTCTT GA

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Seq ID NO: 173 Protein Sequence
Protein Accession #: Eos sequence

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35     1      11      21      31      41      51
      |      |      |      |      |      |
      MRLQRPRQAP AGRRRAPRGG RGSFYRPDPG RGARRLRFRQ KGGEGAPRAD PPWAPLGTMA 60
      LLALLLVVAL PRVWTDANLT ARQRDPEDSQ RTDEGDNRVW CHVCERENTF ECQNPRRCWK 120
      TEPYCVIAAV KIPPRPFMVA KQCSAGCAAM BRPKPEBKRP LLEPMPPFFY LKCKKIRYCN 180
40     LGGPPINSSV FKEYAGSMGB SCGGLWLAIL LLLASIAAGL SLS

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Seq ID NO: 174 DNA Sequence
Nucleic Acid Accession #: XM_057014
Coding sequence: 143..874

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45     1      11      21      31      41      51
      |      |      |      |      |      |
      GGGAGGGAGA GAGGCGCGCG GGTGAAAGGC GCATTGATGC AGCCTGCGGC GGCCTCGGAG 60
      CGCGGCGGAG CCAGACGCTG ACCACGTTCC TCTCTCGGT CTCTCCGCC TCCAGCTCGG 120
50     CGCTGCCCGG CAGCCGCGGAG CCATGCGACC CCAGGGCCCC GCGCGCTCCC CGCAGCGGCT 180
      CGCGGCGCTC CTGCTGCTCC TGCTGCTGCA GCTGCCCGCG CCGTCCGAGCG CCTCTGAGAT 240
      CCCCAGGGGG AAGCAAAAGG CGCAGCTCCG GCAGAGGGAG GTGGTGACC TGTATAATGG 300
      AATGTGCTTA CAAGGGCCAG CAGGAGTGCC TGGTCGAGAC GGGAGCCCTG GGGCCAATGG 360
      CATTCCGGGT ACACCTGGGA TCCAGGTCG GGATGGATTC AAAGGAGAAA AGGGGGAATG 420
55     TCTGAGGAA AGCTTTGAGG AGTCTGGAC ACCCAACTAC AAGCAGTGT CATGGAGTTC 480
      ATTGAATTAT GGCATAGATC TTGGGAAAAT TGCGGAGTGT ACATTTACAA AGATGCGTTC 540
      AAATAGTGCT CTAAGAGTTT TGTTCAGTGG CTCACCTCGG CTAAATGCA GAAATGCATG 600
      CTGTCAGCGT TGGTATTTC CATTCAATGG AGCTGAATGT TCAGGACCTC TTCCCATTTGA 660
      AGCTATAATT TATTGGACC AAGGAAGCCC TGAAATGAAT TCAACAATTA ATATTCATCG 720
60     CACTTCTTCT GTGGAAGGAC TTTGTGAAGG AATTGGTGCT GGATTAGTGG ATGTTGCTAT 780
      CTGGGTTGGC ACTTGTTCAG ATTACCCAAA AGGAGATGCT TCTACTGGAT GGAATTCAGT 840
      TTCTCGCATC ATTATTGAAG AACTACCAAA ATAAATGCTT TAATTTTCAT TTGCTACCTC 900
      TTTTTTTATT ATGCTTGGG ATGCTTCACT TAAATGACAT TTTAATAAAG TTTATGTATA 960
      CATCTGAATG AAAAGCAAG CTAAATATGT TTACAGACCA AAGTGTGATT TCACACTGTT 1020
65     TTTAAATCTA GCATTATTCA TTTGCTTCA ATCAAAAGTG GTTCAATAT TTTTTTTAGT 1080
      TGGTTAGAAT ACTTCTTCCA TAGTCACATT CTCTCAACCT ATAATTGGA ATATTGTTGT 1140
      GGTCTTTTGT TTTTGTCTT AGTATAGCAT TTTTAAAAA ATATAAAGC TACCAATCTT 1200
      TGTACAATTT GTAAATGTTA AGAATTTTTT TTATATCTGT TAAATAAAAA TTATTTCCAA 1260
70     CAACCTTAAA AAAAAAAAAA AAAA

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Seq ID NO: 175 Protein Sequence
Protein Accession #: XP_057014

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75     1      11      21      31      41      51
      |      |      |      |      |      |
      MRPGQPAASP QRLRGLLLLL LLQLPAPSSA SEIPKQKQKA QLRQREVVDL YNGMCLQGPA 60
      GVPRGRGSPG ANGIPGTGPI PGRDGFKEGK GECLRESFEE SWTPNYKQCS WSSLNNGIDL 120
      GKIAECTFTK MRSNSALRVL FSGSLRLKCR NACCQRWYFT FNGAECSSGL PLEAIIYLDQ 180

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GSPEMNSTIN IHRSSSVDEGL CBGIGAGLVD VAIWVGTCSD YPKGDASTGN NSVSRIIEE 240
LPK

Seq ID NO: 176 DNA Sequence
Nucleic Acid Accession #: XM_084007
Coding sequence: 1..2268

1 11 21 31 41 51
10 ATGGCGAGGA AGTTATCTGT AATCTTGATC CTGACCTTGG CCTCTCTGT CACAAATCCC 60
CTTCATGAAC TAAAGCAGC TGCTTCCCC CAGACCACTG AGAAATTTAG TCCGAATTGG 120
GAATCTGGCA TTAATGTTGA CTGGCAATT TCCACACGGC AATATCATCT ACAACAGCTT 180
TTCTACCGCT ATGGAGAAAA TAATCTTTG TCAGTTGAAG GGTTCAGAAA ATTACTTCAA 240
AATATAGGCA TAGATAAGAT TAAAGAATC CATATACACC ATGACCACGA CCATCACTCA 300
15 GACCACGAGC ATCACTCAGA CCATGAGCGT CACTCAGACC ATGAGCATCA CTCAGACCAC 360
GAGCATCACT CTGACCATGA TCATCACTCC CACCATAATC ATGCTGCTTC TGGTAAAAAT 420
AAGCGAAAAA CTCTTTGCCC AGACCATGAC TCAGATAGTT CAGGTAAAGA TCCTAGAAAC 480
AGCCAGGGGA AAGAGCTCA CCGACCAGAA CATGCCAGTG GTAGAAGGAA TGTCAAGGAC 540
AGTGTAGTG CTAGTGAAGT GACCTCAACT GTGTACAACA CTGTCTCTGA AGGAACTCAC 600
20 TTTCTAGAGA CAATAGAGAC TCCAAGACCT GGAATACTCT TCCCAAAGA TGTAAAGCAGC 660
TCCACTCCAC CCAAGTGCAC ATCAAAGAGC CGGGTGAGCC GGCTGGCTGG TAGGAAAAAC 720
AATGAATCTG TGAGTGAGCC CCGAAAAGGC TTTATGTATT CCAGAAACAC AAATGAAAT 780
CCTCAGGAGT GTTTCATGTC ATCAAAGCTA CTGACATCTC ATGGCATGGG CATCCAGGTT 840
CGCTGAATG CAACAGAGTT CAATATCTC TGTCCAGCCA TCATCAACCA AATTGATGCT 900
25 AGATCTTGTC TGATTCATAC AAGTGAAAAG AAGGCTGAAA TCCCTCCAAA GACCTATTCA 960
TTACAAATAG CCTGGGTGGG TGGTTTTATA GCCATTTCCA TCATCAGTTT CCGTCTCTCG 1020
CTGGGGTTTA TCTTAGTGCC TCTCATGAAT CGGGTGTGTT TCAAAATTTCT CCTGAGTTTC 1080
CTGTGGCAC TGGCGGTGG GACTTTGAGT GGTGATGCTT TTTTACACCT TCTTCCACAT 1140
TCTCATGCA GTACACCACT TAGTCATAGC CATGAAGAAC CAGCAATGGA AATGAAAAGA 1200
30 GGACCACTTT TCAGTCATCT GTCTTCTCAA AACATAGAAG AAAGTGCCTA TTTGATTCC 1260
ACGTGAAGG GTCTAACAGC TCTAGGAGGC CTGTATTCCA TGTTCCTGT TGAACATGTC 1320
CTCACATTGA TCAACCAATT TAAAGATAAG AAGAAAAAGA ATCAGAAGAA ACCTGAAAT 1380
GATGATGATG TGGAGATTAA GAAGCAGTTG TCCAAGTATG AATCTCAACT TTCAACAAAT 1440
GAGGAGAAAG TAGATACAGA TGATCGAACT GAAGGCTATT TAGAGCAGA CTCACAAGAG 1500
35 CCCTCCCACT TTGATTCTCA GCAGCCTGCA GTCTTGGAAG AAGAAGAGGT CATGATAGCT 1560
CATGCTCATC CACAGGAAGT CTACAATGAA TATGTACCCA GAGGGTGCAA GAATAAATGC 1620
CATTCACTTA TCCACGATAC ACTCGGCCAG TCAGACGATC TCATTCACCA CCATCATGAC 1680
TACCATCATA TTCTCCATCA TCACCACCAC CAAACCACCC ATCCTCACAG TCACAGCCAG 1740
CGCTACTCTA GGGAGGAGCT GAAAGATGCC GCGCTGCCA CTTTGGCCTG GATGGTGATA 1800
40 ATGGGTGATG GCCTGCACAA TTTCAGCGAT GCCTTAGCAA TTGGTGCTGC TTTTACTGAA 1860
GGCTTATCAA GTGGTTTAAG TACTTCTGTT GCTGTGTCT GTCATGAGTT GCCTCATGAA 1920
TTAGGTGACT TTGCTTCTCT ACTAAAGGCT GGCATGACCG TTAAGCAGCG TGTCCTTTAT 1980
AATGCATTGT CAGCCATGCT GCGTATCTT GGAATGGCAA CAGGAATTTT CATTTGGTCAT 2040
TATGCTCTAT ATGTTTCTAT GTGGATATTT GCACITACTG CTGGCTTATT CATGTATGTT 2100
45 GCTCTGGTTG ATATGGTACC TGAATGCTG CACAATGATG CTAGTGACCA TGGATGTAGC 2160
CGCTGGGGGT ATTTCTTTT ACAGAATGCT GGGATGCTTT TGGGTTTTGG AATTATGTTA 2220
CTTATTTCCA TATTGAACA TAAATCGTG TTTCTGATAA ATTTCTAG

Seq ID NO: 177 Protein Sequence
Protein Accession #: XP_084007

1 11 21 31 41 51
55 MARKLSVILI LTFALSVNTP LHELKAAAPP QTTEKISPNW ESGINVDLAI STROYHLQOL 60
FYRYGENNSL SVEGFRKLLQ NIGIDKIKRI HIHHDHHS DHEHSDHER HSDHEHSDH 120
EHSDHDSHHS HRNHAASGKN KRKALCPDHD SDSSGKDPN SQKGARPE HASGRRNVKD 180
SVSASEVTST VYNTVSEGT FLETIETPRP GLFPKDVSS STPPSVTSKS RVSRLAGRKT 240
NESVSEPRKG FMYSRNTNEN PQECFNASKL LSHGNGIQV PLNATEFNYL CPAINQIDA 300
60 RSLIHTSEK KAEIPPKTYS LQIANVGGFI AISIISFLSL LGVILVPLMN RVFFKFLSF 360
LVALAVGTLS GDAFLHLLPH SHASHHSHS HEEPAMEMKR GPLPSHLSSQ NIESAYFDS 420
TWKGLTALGG LYFMTLVEHV LTLIKQPKDK KKNQKPKEN DDDVEIKKQL SKYESQLSTN 480
BEKVDTDRT EGYLRADSQE PSHFDSQPPA VLEEEVMIHA HAPQEVYNE YVPRGCKNKC 540
HSHFDTLQ SDDLHSHHSH YHHILHHSHS QNHHPHSHSQ RYSREELKDA GVATLAWMVI 600
65 MGDGLHNSFD GLAIGAAETE GLSSGLSTSV AVFCHLPHE LGDFAVLKKA GMTVKQAVLY 660
NALSANLAYL GMATGIPIGH YAEVSMWIF ALTAGLFMYV ALVDMVPEML HNDASDHGCS 720
RMGYFFLQNA GMLLFGGIML LISIFEHKIV FRINF

Seq ID NO: 178 DNA Sequence
Nucleic Acid Accession #: BC010423
Coding sequence: 248..1780

1 11 21 31 41 51
75 CACAGCGTGG GAAGCAGCTC TGGGGGAGCT CGGAGCTCCC GATCAGGCT TCTTGGGGGT 60
AGCTACGGCT GGGTGTGTAG AACGGGCGCG GGGCTGGGCG TGGGTCCCCT AGTGAGAGCC 120
CAAGTGGGAG AGGCAGAAAC TCTGCAGCTT CCTGCCTTCT GGTTCAGTTC CTTATTCAAG 180
TCTGCAGCCG GCTCCAGGG AGATCTCGGT GGAACCTCAG AAACGCTGGG CAGTCTGCCT 240
TTCACCATG CCCCTGTCCC TGGGAGCCGA GATGTGGGG CCTGAGGCTT GGCTGCTGCT 300

5 GCTGCTACTG CTGGCATCAT TTACAGGCCG GTGCCCCGGG GGTGAGCTGG AGACCTCAGA 360
 CGTGGTAACT GTGGTGCTGG GCCAGGACGC AAAACTGCCC TGCTTCTACC GAGGGGACTC 420
 CGGCGAGCAA GTGGGGCAAG TGGCATGGGC TCGGGTGGAC GGGGGCGAAG GGGCCAGGA 480
 ACTAGCGCTA CTGCACTCCA AATACGGGCT TCATGTGAGC COGGCTTACG AGGGCCGCGT 540
 GGAGCAGCCG CCGCCCCCAC GCAACCCCTT GGACGGCTCA GTGCTCCTGC GCAACGCAGT 600
 GCAGGCGGAT GAGGGCGAGT ACGAGTGCCG GGTGAGCACC TTCCCGCCCG GCAGCTTCCA 660
 GGCGGGAGT CGGCTCGAG TGCTGGTGCC TCCCTGCCC TCACTGAATC CTGGTCCAGC 720
 ACTAGAAGAG GGGCAGGGCC TGACCTGGC AGCTCCTGCG ACAGCTGAGG GCAGCCAGC 780
 10 CCCCAGCGTG ACCTGGGACA CGGAGGTCAA AGGCACAAAG TCCAGCCGTT CCTTCAAGCA 840
 CTCGCGCTCT GCTGCCCTCA CCTCAGAGTT CCACTTGGTG CCTAGCCGCA GCATGAATGG 900
 GCAGCCACTG ACTTGTGTGG TGTCCCATCC TGGCCTGCTC CAGGACCAAA GGATCACCCA 960
 CATCCTCCAG GTGCTCTTCC TTGCTGAGGC CTCTGTGAGG GGCCTTGAAG ACCAAAATCT 1020
 GTGGCACAAT GGCAGAGAAG GAGCTATGCT CAAGTGCCTG AGTGAAGGGC AGCCCCCTCC 1080
 CTCATACAA C TGGACACGGC TGGATGGGCC TCTGCCAGT GGGGTACGAG TGGATGGGGA 1140
 15 CACTTTGGGC TTTCCCCAC TGACCACTGA GCACAGCGGC ATCTACGTCT GCCATGTCAG 1200
 CAATGAGTTG TCCTCAAGGG ATTCTCAGGT CACTGTGGAT GTTCTTGACC CCCAGGAAGA 1260
 CTCTGGGAAG CAGGTGGAGG TAGTGTGAGC CTCGGTGGTG GTGGTGGGTG TGATCGCCGC 1320
 ACTCTGTTC TGCCTTCTGG TGGTGGTGGT GGTGCTCATG TCCCGATACC ATCGCGCAA 1380
 20 GGGCCAGCAG ATGACCCAGA AATATGAGGA GGAGCTGACC CTGACCGGG AGAACTCCAT 1440
 CCGGAGCGTG CATTCCCATC ACACGGACCC CAGGAGCCAG CCGGAGGAGA GTGTAGGGCT 1500
 GAGAGCCGAG GGGCACCCTG ATAGTCTCAA GGACAAAGT AGCTGCTCTG TGATGAGTGA 1560
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 TGAAGTCTG TCTCCAGGCT CTGGGCGGGC CGAGGAGGAG GAAGATCAGG ATGAAGGCAT 1680
 CAAACAGGCC ATGAACCAAT TTGTTCAAGGA GAATGGGACC CTACGGGCCA AGCCACGGG 1740
 25 CAATGGCATC TACATCAATG GCGGGGACA CCTGGTCTGA CCCAGGCGTG CCTCCCTTCC 1800
 CTAGGCTCTG CTCTCTCTGT TGACATGGGA GATTTTAGCT CATCTTGGGG GCGCTCTTAA 1860
 ACACCCGAG TTCTTGCGGA AGATGCTCCC CATCCACTG ACTGCTTGAC CTTTACCTCC 1920
 AACCTTCTG TTTCTCGGA GGGCTCCACC AATTGAGTCT CTCCACCAT GCATGCAGGT 1980
 30 CACTGTGTGT GTGCTGTGT GCCTGTGTGA GTGTGTGACT ACTGTGTGTG TGTGGAGGGG 2040
 TGACTGTCCG TGGAGGGGTG ACTGTGTCCG TGGTGTGTAT TATGCTGTCA TATCAGAGTC 2100
 AAGTGAAGTG TGGTGTATGT GCCACGGGAT TTGAGTGGTT GCGTGGGCAA CACTGTGAGG 2160
 GTTGGCGGTG TGTGTGTGT GGTGTGTGT GACCTCTGCC TGAAAAAGCA GGTATTTTCT 2220
 CAGACCCAG AGCAGTATTA ATGATGCAGA GGTTCAGGA GAGAGGTGGA GACTGTGGCT 2280
 35 CAGACCCAGG TGTGCGGACA TAGCTGGAGC TGGAACTGCG CTCGGTGTG AGGGAACCTG 2340
 TCTCTTACCA CTTGCGAGCC ATGGGGGCAA GTGTGAAGCA GCCAGTCCCT GGGTCAGCCA 2400
 GAGGCTTGAA CTGTACAGA AGCCCTCTGC CCTCTGGTGG CCTCTGGGCC TGCTGCATGT 2460
 ACATATTTTC TGTAAATATA CATGCGCCGG GAGCTTCTG CAGGAATACT GCTCGAATC 2520
 ACTTTTAATT TTTTCTTTT TTTTCTTTG CCCTTTCCAT TAGTTGTATT TTTTATTAT 2580
 40 TTTTATTTT ATTTTCTTT AGAGTTTGAG TCCAGCCTGG ACGATATAGC CAGACCTGT 2640
 CTGTAAAAA ACCAAAAACC AAAAAAAAAA AAAAAAAAAA

Seq ID NO: 179 Protein Sequence
Protein Accession #: AAH10423

45 1 11 21 31 41 51
 MPLSLGAEMW GPEAWLLLLL LLASFTGRCP AGELETSDDV TVVLGQDAKL PCFYRGDSGE 60
 QVQVAVARV DAGEGAQELA LLHSKYGLHV SPAYEGRVEQ PPPRNPLDG SVLLRNAVQA 120
 50 DBGEYECRV TFPAGSPQAR LRLRVLPPL FSLNPGPALE EQQLTLAAS CTAEGSPAPS 180
 VTMDTEVKGT TSSRSFKHSR SAAVTSEPHL VPSRSMGQPL LTCVSHPLG LQDQRITHL 240
 HVSFLAEASV RGLDQNLWH IGRGAMLK LSEGGPPPSY NWTRLDGFLP SGVRVDGDTL 300
 GFPLPTTEHS GIYVCHVSNE FSSRDSQVTV DVLDPEQDSG KQVDLVASV VVVGIAALL 360
 FCLLVVVVVL MSRYHRRKAQ QMTQKYEEL TLTRENSIRR LSHHTDPRS QPEESVGLRA 420
 55 BGHPDSLKDN SSCSVMSEEP EGRSYSTLT VREIETQTEL LSPGSGRAEE EEDQDEGIQ 480
 AMNHVQENG TLRAPKTNG IYINGRGHLV

Seq ID NO: 180 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 482..3007

60 1 11 21 31 41 51
 AACTGAGCTA ACAAGAAATA CTAGAAAAGG AGGAAGGAGA ACATTGCTGC AGCTTGGATC 60
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 65 TGCAATCAGC AGCTTGCAAA TGGTTAACTA TATGCAAAAA AGTCAGCATA GCTGTGAAGT 180
 ATGCGGTGAA TTTTAAATGA GGGAAAAAGG GACAAATGCT TCAGGATGCT CTAGTATGCA 240
 CTCTGCTTGA AATATTTTCA ATGAAATGCT CAGTATTCTA TCTTTGACCA GAGGTTTAA 300
 CTTTATGAAG CTATGGGACT TGACAAAAAG TGATATTGA GAAGAAAGTA CGCAGTGGTT 360
 70 GGTGTTTCT TTTTCTTAAT AAAGGAATG AATTACTTTG AACACCTCT CCAGCTGTGC 420
 ATTACAGATA ACGTCAGGAA GAGTCTCTGC TTTACAGAA CCGATTTCAT CACATGACAA 480
 CATGAAGCTG TGGATTATC TCTTTTATTC ATCTCTCCTT GCCTGTATAT CTTTACACTC 540
 CCAACTCCA GTGCTCTCAT CCAGAGGCTC TTGTGATTCT CTTTGAATTT GTGAGGAAAA 600
 AGATGGCACA ATGCTAATAA ATTGTGAAGC AAAAGGTATC AAGATGGTAT CTGAAATAAG 660
 75 TGTGCCACCA TCAGACCTT TCCAATAAG CTTATTAAAT AACGGCTTGA CGATGCTTCA 720
 CACAAATGAC TTTTCTGGGC TTACCAATGC TATTTCAATA CACCTTGGAT TTAACAATAT 780
 TGCAGATATT GAGATAGGTG CATTAAATGG CCTTGGCCCT CTGAAACAAC TTCAATACAA 840
 TCACAAATCT TTAGAAATTC TTAAGAGGGA TACTTTCCAT GGACTGGAAA ACCTGGAAAT 900
 CCTGCAAGCA GATAACAATT TTATCACAGT GATTGAACCA AGTGCCTTTA GCAAGCTCAA 960

CAGACTCAAA GTGTTAATTT TAAATGACAA TGCTATTGAG AGTCTTCTC CAAACATCTT 1020
 CCGATTGTGT CCTTTAACCC ATCTAGATCT TCGTGGAAAT CAATTACAAA CATTGCCTTA 1080
 TGTGTGTTTT CTCGAACACA TTGGCCGAAT ATTGGATCTT CAGTTGGAGG ACAACAAATG 1140
 5 GGCTGCAAT TGTGACTTAT TGCAGTTAAA AACTTGGTTG GAGAACATGC CTCCACAGTC 1200
 TATAATTTGGT GATGTTGTCT GCAACAGCCC TCCATTTTTT AAAGGAAGTA TACTCAGTAG 1260
 ACTAAAGAAG GAATCTATTT GCCCTACTCC ACCAGTGTAT GAAGAACATG AGGATCCTTC 1320
 AGGATCATT CATCTGGCAG CAACATCTTC AATAAATGAT AGTCGCATGT CAACTAAGAC 1380
 CACGTCCATT CTAATACTAC CCACCAAGC ACCAGGTTTG ATACCTTATA TTACAAAGCC 1440
 10 ATCCACTCAA CTTCCAGGAC CTTACTGCCC TATTCTTGT AACTGCAAAG TCCTATCCCC 1500
 ATCAGGACTT CTAATACATT GTCAGGAGCG CAACATTGAA AGCTTATCAG ATCTGAGACC 1560
 TCCTCCGCAA AATCCTAGAA AGCTCATTCT AGCGGGAAT ATTATTACA GTTTAATGAA 1620
 GTCTGATCTA GTGGAATATT TCACCTTGGG AATGCTTAC TTGGGAAACA ATCGTATTGA 1680
 AGTCTTGAA GAAGGATCGT TTATGAACCT AACGAGATTA CAAAACTCT ATCTAAATGG 1740
 TAACCACCTG ACCAAATTA GTAAAGGCAT GTTCTTGGT CTCATAATC TTGAATACTT 1800
 15 ATATCTTGA ATACATGCCA TTAAGGAAAT ACTGCCAGGA ACCTTTAATC CAATGCCTAA 1860
 ACTTAAAGT CTGTATTAA ATAACAACCT CCTCCAAGTT TTACCACCAC ATATTTTTTC 1920
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 20 CTGCTCCTGT GACCTGGTTG GACTGCAGCA ATGGATACAA AAGTTAAGCA AGAACACAGT 2100
 GACAGATGAC ATCTCTTGCA CTTCCCGCG GCATCTCGAC AAAAAGGAAT TGAAGCCCT 2160
 AAATAGTGAA ATCTCTGTCT CAGGTTTGTG AAATAACCCA TCCATGCCAA CACAGACTAG 2220
 TTACTTTATG GTACCACTC CTGCAACAAC AACAAATACG GCTGATACTA TTTTACGATC 2280
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 25 TATTGTTTTT TGTGCTGCGG GGATAGTGGT TCTTGTCTT CACCGCAGGA GAAGATACAA 2400
 AAAGAAACAA GTAGATGAGC AAATGAGAGA CAACAGTCTT GTGCATCTT AGTACAGCAT 2460
 GTATGGCCAT AAAACCACTC ATCACACTAC TGAAGAGCCC TCTGCCTCAC TCTATGAACA 2520
 GCACATGGTG AGCCCAATGG TTTCTGTCTA TAGAAGTCCA TCTTTGGTC CAAAGCATCT 2580
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 30 TCTTTTGGAA CAGGAAATC ATTCACCACT CACAGGGTCA AATATGAAAT ACAAACACAC 2700
 GAACCAATCA ACAGAAATTT TATCCTTCCA AGATGCCAGT TCATTGTACA GAAACATTTT 2760
 AGAAAAAGAA AGGGAATCTC AGCAACTGGG AATCACAGAA TACCTAAGGA AAAACATTGC 2820
 TCAGCTCGAG CCGTATATGG AGGCACATTA TCCTGGAGCC CACGAAGAGC TGAAGTTAAT 2880
 GGAACATTA ATGTACTCAC GTCCAAGGAA GGTATTAGTG GAACAGACAA AAAATGAGTA 2940
 35 TTTTGAACCT AAAGCTAATT TACATGCTGA ACCTGACTAT TTAGAAGTCC TGGAGCAGCA 3000
 AACATAGATG GAGAGTTTGA GGGCTTTCGC AGAAATGCTG TGATTCTGTT TTAAGTCCAT 3060
 ACCTTGTAAT TAAAGTGCTT ACGTGAGTGT GTCATCAATC AGAACCTAAG CACAGCAGTA 3120
 AACTATGGG AAAAAAAG AAGAGAAAAA GAAACTCAGG GATCACTGGG AGAAGCCATG 3180
 GCATTATCTT CAGGCAATTT AGTCTGTCCC AAATAAAATC AATCTTGCA TGTAATC 3238

Seq ID NO: 181 Protein Sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 MKLWIHLFYS SLLACISLHS QTPVLSSRGS CDSLNCCEER DGTMLINCEA KGIKRVSEIS 60
 VPPSRPFQLS LLNNGLTMLH TNDPSSGLTNA ISIHLPNNI ADIEIGAFNG LGLLKQLHIN 120
 HNSLEILKED TFHGLENLFP LQADNNFITV IEPSAFSKLN RLKVLILNDN AIESLPPNIF 180
 RFVPLTHLDL RGNQLQTLFY VGFLEHIGRI LDLQLEDNKN ACNCDLQLK TWLENNPPQS 240
 50 IIGDVVCSNP PFFKGSILSR LKESICTPT PVYEHEDPS GSHLAATSS INDSRMSTKT 300
 TSILKLPTKA PGLIPYITKP STQLPGPYCP IPCNCKVLS SGLLIHQER NIESLSDLRP 360
 PPQNPRLIL AGNIHSLMK SDLVEYPTLE MLHLGNRIE VLEBGSFNNL TRLQLKYLNG 420
 NHLTKLSKGM FLGLHNLEYL VLEYNAIKEI LPGTFFNMPK LKVLVNNNL LQVLPPHIFS 480
 GVPLTKVNLK TNQPTHLPVS NILDDLDTLL QIDLEDNPDW CSCDLVGLQQ WIKLSKNTV 540
 55 TDDILCTSPG HLDKELKAL NSEILCPGLV NNPSMPTQTS YLMVTTTATT TNDADTILRS 600
 LTDAVPLSVL ILGLLIMPIT IVPCAAGIVV LVLHRRRRYK KKQVDEQMRD NSPVHLQYSM 660
 YGHKTHHTT ERPSASLYEQ HMVSPMVHVY RSPSPGPKHL EEEEEERNEKE GSDAKHLQRS 720
 LLEQENHSPL TGSNMKYKTT NQSTEFLSFQ DASSLYRNIL EKERELQQLG ITEYLRKNIA 780
 60 QLQPDMEAHY POAHEELKLM ETLMYSRPRK VLVEQTKNEY FELKANLHAE PDYLEVLEBQQ 840
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Seq ID NO: 182 DNA Sequence
 Nucleic Acid Accession #: XM_035292.2
 Coding sequence: 1..1524

1 11 21 31 41 51
 ATGGCGGGTG CGGCGCCGAA GCGCGCGCGG CTAGCGGCGC CGGCGGCGGA GGAGAAGGAA 60
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 70 GCGAGGGGCG TGACCTTGCA GCGGAACATC ACGCTGCTCA ACGCGGTGGC CATCATCGTG 180
 GGGACCATTA TCGGCTCGGG CATCTTCTGT ACGCCACGCG GGTGCTCAA GGAGGACAGC 240
 TCGCGGGGCG TGGCGCTGGT GGTGTGGGCC GCGTGGCGCG TCTTCTCCAT CGTGGGCGCG 300
 CTCTGCTACG CGGAGCTCGG CACCACCATC TCCAAATCGG GCGGCGACTA CGCTACATG 360
 75 CTGGAGGTCT ACGGCTCGCT GCCCGCCTTC CTCAAGCTCT GGATCGAGCT GCTCATCATC 420
 CGGCCTTCAT CGCAGTACAT CGTGGCCCTG GTCTTCGCCA CCTACCTGCT CAAGCGCTC 480
 TTTCCCACTC GCCCGGTGCC CGAGGAGGCA GCCAAGCTCG TGGCCTGCCT CTGCGTGTG 540
 CTGCTCACGG CCGTGAACGT CTACAGCGTG AAGGCCGCCA CCGGGTCCA GGATGCCTTT 600
 GCCCGGCCCA AGCTCCTGGC CTTGGCCCTG ATCATCTGCG TGGCTTCTGT CCAGATCGGA 660

5 AAGGGTGATG TGTCCAATCT AGATCCCAAC TTCTCATTG AAGGCACCAA ACTGGATGTG 720
 GGAACACTTG TGCTGGCATT ATACAGCGGC CTCTTTGCCT ATGGAGGATG GAATTACTTG 780
 AATTTCTGCA CAGAGGAAAT GATCAACCCC TACAGAAACC TGCCCTGGC CATCATCATC 840
 TCCCTGCCCA TCGTGACGCT GGTGTACGTG CTGACCAACC TGGCTACTT CACCACCTG 900
 TCCACCGAGC AGATGCTGTC GTCCGAGGCC GTGGCCGTGG ACTTCGGGAA CTATCACCTG 960
 GCGTCATGT CTGTGATCAT CCGGCTCTTC GTGGGCTGT CTGTCTCGG CTCGTCAAT 1020
 GGGTCCCTGT TCACATCTCT CAGGCTCTTC TTCTGGGGT CCGGGGAAG CCACCTGCC 1080
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 10 AGCTTCTTCA ACTGGCTCTG CGTGGCCCTG GCCATCATCG GCATGATCTG GCTGCGCCAC 1260
 AGAAAGCCTG AGCTTGAGCG GCCATCAAG GTGAACCTGG CCTGCTGT GTTCTTCATC 1320
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 15 AAGCCCAAGT GGCTCTCCA GGGCATCTTC TCCACGACCG TCCTGTGTCA GAAGCTCATG 1500
 CAGGTGGTCC CCGAGGAGAC ATAG

Seq ID NO: 183 Protein Sequence
 Protein Accession #: XP_035292.2

20 1 11 21 31 41 51
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 MAGAGPKRRA LAAPAAEKE EAREKMLAAK SADGSAPAGE GEGVTLQRNI TLLNGVAIIV 60
 GTIIGSGIFV TPTGVLEKAG SPGLALVVWA ACCVPSIVGA LCVABLTITI SKSGGDYAYM 120
 25 LEVYGSIPAF LKLWIELLII RPSSQYIVAL VFATYLLKPL FPTCPVPEEA AKLVACLCLVL 180
 LLTAVNCYSV KAATRVQDAF AAKLLALAL IILLGFVQIG KGDVSNLDPN FSPFGTKLDV 240
 GNIVLALYSY LFAYGGWNYL NFVTEEMINP YRNLPALIII SLPFIVTLVYV LTNLAYFTTL 300
 STEQMLSSSE VAVDFGNVHL GVMSWIIIPV VGLSCFSGVN GSLFTSSRLP FVGSREGHLP 360
 SILSMIHPQL LTPVPSLVFT CVMTLIYAFS KDIFSVINFP SFENMLCVAL AIIGMIWLRH 420
 30 RKPELERPIK VNLALPVFFI LACLFLIAVS FWKTPVECGI GFTIILSGLP VYFVGWVWKN 480
 KPKMLLQGI SFTVLQCKLM QVVPQET

Seq ID NO: 184 DNA Sequence
 Nucleic Acid Accession #: NM_005268.1
 Coding sequence: 1..822

35 1 11 21 31 41 51
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 GGGCGCATCT GGCTGTCTCT GGTCTTCATC TTCGGCGTGC TGGTGTACCT GGTGACGGCC 120
 40 GAGCGTGTGT GGAGTGATGA CCACAAGGAC TTCGACTGCA ATACTCGCCA GCCCGGCTGC 180
 TCCAACGTCT GCTTTGATGA GTTCTTCCCT GTGTCCCATG TGCGCCTCTG GGCCTGCGAG 240
 CTTATCCTGG TGACATGCC CTCACTGCTC GTGTCATGC ACGTGGCCTA CCGGAGGTT 300
 CAGGAGAAGA GGCACCGAGA AGCCCATGGG GAGAACAGTG GCGCCTCTA CCTGAACCCC 360
 GGCAAGAAGC GGGGTGGGCT CTGGTGGACA TATGTCTGCA GCCTAGTGT CAAGGCGAGC 420
 45 GTGGACATCG CCTTCTCTA TGTGTTCCAC TCATTCTACC CCAATATAT CCTCCCTCTC 480
 GTGGTCAAGT GCCACGCGA TCCATGTCCC AATATAGTGG ACTGCTTCAT CTCGAAGCCC 540
 TCAGAGAAGA ACATTTTAC CCTCTCATG GTGGCCACAG CTGCCATCTG CATCTGCTC 600
 AACCTCGTGG AGCTCATCTA CCTGGTGAGC AAGAGATGCC ACGAGTGCCT GGCAGCAGG 660
 50 AAAGCTCAAG CCATGTGCAC AGGTCTATCACC CCCACGGTA CCACCTCTTC CTGCAACCAA 720
 GACGACCTCC TTTGGGGTGA CCTCATCTTT CTGGGCTCAG ACAGTATACC TCCTCTCTTA 780
 CCAGACGCC CCCAGAGCA TGTGAAGAAA ACCATCTTGT GA

Seq ID NO: 185 Protein Sequence
 Protein Accession #: NP_005259.1

55 1 11 21 31 41 51
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 60 SNVCPDEFPP VSHVRLWALQ LILVTCPSLL VVMHVAYREV QEKHREAHG ENSGRLYLNP 120
 GKIRGGLWMT YVCSLVFKAS VDIAFLYVFH SFYPKYILPP VVKCHADPCP NIVDCFISKP 180
 SEKNIFTLPM VATAAICILL NLVELIYLVS KRCHCELAAR KAQAMCTGHH PHGTTSSCKQ 240
 DLLSGDLIF LGSDSHPLLL PDRPRDHVKK TIL

Seq ID NO: 186 DNA Sequence
 Nucleic Acid Accession #: NM_002391.1
 Coding sequence: 25..457

70 1 11 21 31 41 51
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 CCGGGGAGC GAGTGGCTG AGTGGGCTG GGGGCCCTGC ACCCCAGCA GCAAGGATTG 180
 CGCGTGGGT TTCCCGAGG GCACCTGCGG GCGCCAGACC CAGCGCATCC GGTGACGGGT 240
 GCCTGCAAC TGAAGAAGG AGTTTGAGC GCACTGCAAG TACAAGTTTG AGAACTGGGG 300
 75 TGGTGTGAT GGGGGCACAG GCACCAAGT CCGCCAAGC ACCCTGAAGA AGGCGGCTA 360
 CAATGCTCAG TGCCAGGAGA CCATCGCGT CACCAAGCCC TGCAACCCCA AGACCAAGC 420
 AAAGGCCAAA GCCAAGAAG GGAAGGGAAA GGAAGGAGC CCAAGCCTGG ATGCCAAGGA 480
 GCGCTGCTG TCACATGGGG CCTGGCCACG CCCTCCCTCT CCCAGGCCCG AGATGTGACC 540

5 CACCAGTGCC TTCTGTCTGC TCGTAGCTT TAATCAATCA TGCCCTGCCT TGTCCCTCTC 600
 ACTCCCCAGC CCACCCCTTA AGTGCCCAAA GTGGGAGGG ACAAGGGATT CTGGGAAGCT 660
 TGAGCCTCCC CCAAGCAAT GTGAGTCCCA GAGCCCCGTT TTGTTCTTCC CCACAATTCC 720
 ATTACTAAGA AACACATCAA ATAAACTGAC TTTTCCCCC CAATAAAAGC TCTTCTTTT 780
 TAATAT

Seq ID NO: 187 Protein Sequence
 Protein Accession #: NP_002382.1

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 CGAQTQIRIC RVPKNWKEF GADCKYKFEN WGACDGGTGT KVRQGTLLKA RYNAQCQETI 120
 RVTKPCTPKT KAKAKAKGK GKD

15 Seq ID NO: 188 DNA Sequence
 Nucleic Acid Accession #: NM_015507
 Coding sequence: 241-1902

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 CGAGTGGAGC GGAGGACCCG AGCGGCTGAG GAGAGAGGAG GCGGCGGCTT AGCTGCTACG 180
 25 GGTCCCGGCC GCGCCCTCC CGAGGGGGGC TCAGGAGGAG GAAGGAGGAC CCGTGCAGAG 240
 ATGCTCTGCG CCTGGAGCCTT TCGCTCCCG CTGCTGCTCT CTGGGTGGC AGGTGGTTTC 300
 GGGAAAGCGG CCAGTGCAGG GCATCACGGG TTGTTAGCAT CGGCACGTCA GCCTGGGGTC 360
 TGTCACTATG GAACTAACT GGCCTGCTGC TACGGCTGGA GAAGAAACAG CAAGGGAGTC 420
 TGTGAAGCTA CATGCGAAC TGGATGTAAG TTTGGTGAAT GCGTGGGACC AAACAAATGC 480
 30 AGATGCTTTC CAGGATACAC CGGAAAACC TGCAGTCAAG ATGTGAATGA GTGTGGAATG 540
 AAACCCCGGC CATGCCAACA CAGATGTGTG AATACACACG GAAGCTACAA GTGCTTTTGC 600
 CTCACTGGCC ACATGCTCAT GCCAGATGCT ACGTGTGTGA ACTCTAGGAC ATGTGCCATG 660
 ATAACTGTCT AGTACAGCTG TGAAGACACA GAAGAAAGGC CACAGTGCCT GTGTCCATCC 720
 TCAGGACTCC GCTCGGCCCC AAATGGAAGA GACTGTCTAG ATATTGATGA ATGTGCCTCT 780
 35 GGTAAAGTCA TCTGTCCCTA CAATCGAAGA TGTGTGAACA CATTTGGAAG CTACTACTGC 840
 AAATGTCACA TTGGTTTCGA ACTGCAATAT ATCAGTGGAC GATATGACTG TATAGATATA 900
 AATGAATGTA CTATGGATAG CCATACGTGC AGCCACCATG CCAATTGCTT CAATACCCAA 960
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 40 ATCCCTGAAA ATTCTGTGAA GGAAGTCCTC AGAGCACCTG GTACCATCAA AGACAGAATC 1080
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 ATAGTTTCCA GAGGCGGGAA CTCTCATGGA GGTAAAAAAG GGAATGAAGA GAAATGAAA 1260
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 45 AGCCTGCGAG GAGATGTGTT TTTCCCTAAG GTGAATGAAG CAGGTGAATT CGGCTGATT 1380
 CTGGTCCAAA GGAAGCGCTT AACTTCCAAA CTGGAACATA AAGATTTAAA TATCTCGGTT 1440
 GACTGTCAGT TCAATCATGG GATCTGTGAC TGGAAACAGG ATAGAGAAGA TGATTTTGAC 1500
 TGGAAATCCTG CTGATCGAGA TAATGCTATT GGCTTCTATA TGGCAGTTCC GCGCTTGCCA 1560
 GGTCAACAAG AAGACATTGG CCGATTGAAA CTCTCTCTAC CTGACCTGCA ACCCCAAAGC 1620
 50 AACTCTGTTT TGCTCTTTGA TTACCGGCTG GCGGAGACA AAGTCGGGAA ACTTCGAGTG 1680
 TTTGTGAAAA ACAGTAACAA TGCCCTGGCA TGGGAGAAGA CCACGAGTGA GGATGAAAAG 1740
 TGGAGACAGG GGAATAATCA GTTGATATCA GGAACCTGAT CTACCAAAG CATCATTTTT 1800
 GAAGCAGAAC GTGGCAAGGG CAAAACCGGC GAAATCGCAG TGGATGGCGT CTGCTTGTT 1860
 TCAGGCTTAT GTCCAGATAG CCTTTTATCT GTGGATGACT GAATGTTACT ATCTTTATAT 1920
 55 TTGACTTTGT ATGTGAGTTC CCGGTTTTT TTGATATTGC ATCATAGGAC CTCTGGCATT 1980
 TTAGAATTAC TAGCTGAAAA ATTGTAATGT ACCAACAGAA ATATTATTGT AAGATGCCTT 2040
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 TTTCTGAATT TTTCCACATT ATATTATAAA ATATGGAAT GTCACTTTAT CTCCCCTCCT 2160
 CAGTATATCT GATTGTGATA AGTAAGTTGA TGAGCTTCTC TCTACAACAT TTCTAGAAAA 2220
 TAGAAAAAAA AGCACAGAGA AATGTTTAA TGTPTGACTC TTATGATACT TCTTGGAAAC 2280
 60 TATGACATCA AAGATAGACT TTTGCCTAAG TGGCTTAGCT GGGCTTTTCA TAGCCAAACT 2340
 TGTATATTTA AATTCTTTGT AATAATAATA TCCAAATCAT CAAAAAATAA AAAAAAAA

Seq ID NO: 189 Protein Sequence
 Protein Accession #: NP_056322.2

65 1 11 21 31 41 51
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 70 LSGHMLMPDA TCVNSRTCAM INCQYSCEDT EGGPQCLCPG SGLRLAPNGR DCLDIDECAS 180
 GKVICPYNRR CVNTFGSYCY KCHIGFELQY ISGRYDCIDI NECTMDSHTC SHHANCFTNTQ 240
 GSPKCKCKQG YKGNGLRCSA IPENSVKEVL RAPGTIKDRI KKLALHKNMS KKKAKIKNVT 300
 PEPTRTPTFK VNLQPFNYEE IVSRGGNSHG GKKGNEEMKM EGLEDEKREE KALKNDIEER 360
 SLRGDVPFPK VNEAGEFGLI LVQRKALTSK LEHKDLNISV DCSFNHGI CD WKQDREDDFD 420
 75 WNPADRDNAI GFYMAVPALA GHKKDIGRLK LLLPDLPQPS NPLLLFDYRL AGDKVGKLRV 480
 FVKNSNNALA WEKTTSEDEK WKTGKIQLYQ GTDATKSIIF BAERGKGTG EIAVDGVLLV 540
 SGLCPDLSLLS VDD

Seq ID NO: 190 DNA Sequence
Nucleic Acid Accession #: NM_006475
Coding sequence: 12..2522

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ACCCATATAA GCCTCAACAAT CATTATGACA AGATCTTGGC TCATAGTCGT ATCAGGGGTC 120
GGGACCAAGG CCCAAATGTC TGTGCCCTTC AACAGATTTT GGGCACCAAA AAGAAATACT 180
TCAGCACTTG TAAGAACTGG TATAAAAAGT CCATCTGTGG ACAGAAAAACG ACTGTTTAT 240
ATGAATGTTG CCCTGGTTAT ATGAGAAATGG AAGGAATGAA AGGCTGCCCA GCAGTTTTCG 300
CCATTGACCA TGTATTATGGC ACTCTGGGCA TCGTGGGAGC CACCACAACG CAGCGCTATT 360
CTGACGCTTC AAAACTGAGG GAGGAGATCG AGGGAAGGGG ATCCTTCACT TACTTTGCAC 420
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TGAATGTTGA ATTACTGAAT GCTTTACATA GTCACATGAT TAATAAGAGA ATGTTGACCA 540
AGGACTTAAA AAATGGCATG ATTATTCCTT CAATGTATAA CAATTGGGGG CTTTTCATTA 600
ACCATATACC TAATGGGTTT GTCACGTGTA ATTGTGCTCG AATCATCCAT GGGAAACCAGA 660
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TTCAAGACTT CATTGAAGCA GAAGATGACC TTTTCATCTT TAGAGCAGCT GCCATCACAT 780
CGGACATATT CGAGGCCCTT GGAAGAGACG GTCACCTTCA ACTCTTTGCT CCCACCAATG 840
AGGCTTTTGA GAAACTTCCA CGAGGTGTCC TAGAAAGGTT CATGGGAGAC AAAGTGGCTT 900
CCGAAGATCT TATGAAGTAA CACATCTTAA ATACTCTCCA GTGTCTGAG TCTATTATGG 960
GAGGAGCAGT CTTTGAGACG CTGGAAGGAA ATACAATTGA GATAGGATGT GACGGTGACA 1020
GTATAACAGT AAATGGAAAT AAAATGGTGA ACAAAAAGGA TATTGTGACA AATAATGGTG 1080
TGATCCATTG GATTGATCAG GTCCTAATTC CTGATCTGCG CAACAAGATT ATTGAGCTGG 1140
CTGGAAACCA GCAAACCAAC TTCAACGATC TTTGGGCCCA ATTAGGCTTG GCATCTGCTC 1200
TGAGGCCAGA TGGAGAATCA ACTTTGCTGG CACCTGTGAA TAATGCATT TCTGATGATA 1260
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AAGTTGGCCT TAATGAGCTT TACAACGGGC AAATACTGGA AACCATCGGA GGCAAAACAGC 1380
TCAGAGTCTT CGTATATCGT ACAGCTGTCT GCATTGAAAA TTCATGCATG GAGAAAGGGA 1440
GTAAGCAAGG GAGAAACGGT GCGATTACCA TATTCGCGGA GATCATCAAG CCAGCAGAGA 1500
AATCCCTCCA TGAAGAAGTA AAACAAGATA AGCGCTTAG CACCTTCCTC AGCCTACTTG 1560
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CCAATGATGC TTTTAAAGGA ATGACTAGTG AAGAAAAAGA AATTCTGATA CGGGACAAAA 1680
ATGCTCTTCA AAACATCATT CTTTATCACC TGACACCAGG AGTTTTCATT GGAAAGGAT 1740
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CAATGGTGT AATTCATGTT GTAGATAAAC TCCTCTATCC AGCAGACACA CTTGTGGGAA 1920
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CTCAGAAATG TTGTCATATG CTTCTTGCAA TGCAATATTT TTAATCTCAA ACCTTTCAAT 3120
AAAACCATTT TTCAGATATA AAGAGAATTA CTTCAAAATG AGTAATTCAG AAAAAGCTCAA 3180
GATTTAAGTT AAAAAAGTGG TTGGACTTGG GAA

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Seq ID NO: 191 Protein Sequence
Protein Accession #: BAA02836.1

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KLREEIEGKG SFTYFAPNSN AMDNLDSDIR RGLSESNVVE LLNALHSHMI NKRMLTKDLK 180
NGMIIPSMYN NIGLFINHPY NGVVTVNCAR I IHGNQIATN GVHVHIDRVL TQIGTSIQDF 240
IEAEDDLSSP RAAATTSIIL EALGRDGHFT LFAPTNEAFE KLPRGVLERF MGDKVASEAL 300
MKYHILNTLQ CSESIMGGAV FETLEGNTIE IGCDDGSITV NGIKMWNKKD IVTNNGVIHL 360
IQQVLIPOSA KQVIELAGKQ QTFTDLVAQ LGLASALRPD GEYTLAPVN NAFSDDTLSM 420
VQRLKLILQ NHILKVKVGL NELYNGQILE TIGGKQLRVF VYRTAVCIEN SCMEKGSKQG 480
RNGATHIFRE I IKPAEKSLH EKLKQDKRFS TFLSLLEAAD LKELLTPQGD WTLFVPTNDA 540
FKGMTSEEKE ILIRDKNALQ NIILYHLTPG VFIGKGFEPG VTNLKTTQK SKIPLKEVND 600
TLVLNELKSK ESDIMTTNGV IHVVDKLLYP ADTPVGNLQ LLEILNKLKY IQIKFVRGST 660

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PKEIPVTVYT TKIITKVVEP KIKVIEGSLQ PIIKTBGPTL TKVKIEGEPE FRLIKEGETI 720
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QBEVTKVTKF IEGGDGHLFE DEEIKRLLQG DTPVRKLQAN KKVQGSRRRL REGRSQ

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Seq ID NO: 192 DNA Sequence
Nucleic Acid Accession #: NM_006670
Coding sequence: 85..1347

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TCTCCCACTT CCTCGGCATC CTCCTTCTCC TCCTCGGCGC CGTTCCTGGC TTCGCGCGTG 240
15 TCCGCCAGC CGCCGCTGCC GGACCAAGTC CCGCGCTGT GCGAGTGCTC CGAGGCAGCG 300
CGCACAGTCA AGTGCCTTAA CCGCAATCTG ACGAGGTGC CCACGGACCT GCCCGCTAC 360
GTGCGCAACC TCTTCTTAC CGGCAACCAG CTGGCGGTGC TCCCTGCGGG CGCCTTCGCC 420
CGCGGGCGCG CGCTGGCGGA GCTGGCGCGC CTCAACCTCA GCGGCGCGG CCTGGACGAG 480
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20 CCACTGGCCG ACCTCAGTCC CTTCGCTTTC TCGGGCAGCA ATGCCAGCGT CTGCGCCCCC 600
AGTCCCTCTG TGGAACTGAT CTTGAACCAAC ATCGTCCCCC CTGAAGATGA GCGGCGAAG 660
CGGAGCTTCG AGGGCATGGT GGTGGCGGCC CTGCTGGCGG GCCGTGCAT GCAGGGGCTC 720
CGCGCTTCGG AGCTGGCCAG CAACCACTTC CTTTACCTGC CGCGGATGT GCTGGCCCAA 780
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30 CAAACCTCTT ATGCTTCTCT GGTATTGTT TTAGCCCTGA TAGGCGCTAT TTTCTCCTG 1200
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AACCTCAGTT CTAACCTCGA TGTCTGAGAA ATATTAGAGG ACAGACCAAG GACAACTCTG 1380
CATGAGATGT AGACTTAAAG TTTATCCCTA CTAGGCTTGC TCCACTTTCA TCCTCCACTA 1440
35 TAGATACAA CGACTTTGAC TAAAAGCAGT GAAGGGGATT TGCTTCCTTG TTATGTAAAG 1500
TTTCTCGGTG TGTCTGTGTA ATGTAAAGAG ATGAACAGTT GTGTATAGTG TTTTACCTTC 1560
TCTTTTTCTT TGGAACTCTT CAACAGTAT GGAGGGATT TTCAGTTTC AGCATGAACA 1620
TGGGCTTCTT GCTGTCTGTC TCTCTCTCAG TACAGTTCAA GGTGTAGCAA GTGTACCCAC 1680
ACAGATAGCA TTCAACAAAA GCTGCCTCAA CTTTTTCGAG AAAATACTT TATTATAAAA 1740
40 TATCAGTTTT ATTCTCATGT ACCTAAGTGT TGGAGAAAAA AATTGCATCC TATAAAGTGC 1800
CTGCAGAGCT TAGCAGGCTC TTCAAAATAA CTCATGGTGC CACAGGAGCA CCTGCATCCA 1860
AGAGCATGCT TACATTTTAT TGTCTGCAT ATTACAAAAA ATAACCTGCA ACTTCATAAC 1920
TTCTTTGACA AAGTAAATTA CTTTTTGTAT TGCAAGTTAT ATGAAAATGT ACTGATTTTT 1980
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ATTCTAAAAA GAA

Seq ID NO: 193 Protein Sequence
Protein Accession #: CAA82324.1

50 1 11 21 31 41 51
| | | | | |
MPOGCSRGA AGDGRRLRL LALVLLGWVS SSSPTSSASS FSSAPFLAS AVSAQPLPLD 60
QCPALCECE AARTVKCVNR NLTEVPTDLP AYVRNLFLTQ NQLAVLPAGA FARRPPLAEL 120
55 AALNLGSRRL DEVRAFAEH LPSLRQLDLS HNPLADLSPP AFGSGNASVS APSPLVELIL 180
NHIVPPEDER QNRSFEGMVV AALLAGRALQ GLRRLLEASN HPLYLPRDVL AQLPSLRHLD 240
LSNNSLVSLT YVSFRNLTHL ESHLEDNAL KVLHNGTLAE LQGLPHIRVP LDNNPWVDC 300
HMADMTWLK ETEVVQGKDR LTCAYPEKMR NRVLLELNSA DLDCDPILEP SLQTSYVFLG 360
IVLALIGAIF LVLVLYLNRK IKKWMHNIRD ACRDHMEGYH YRYEINADPR LTNLSSNSDV

60

Seq ID NO: 194 DNA Sequence
Nucleic Acid Accession #: NM_014400
Coding sequence: 86..1126

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70 GATCTGGACT CGAGGCTGGC TGCTGCTGCT GCTGCTTCGC GGAGGAGCGC AGGCCCTGGA 180
GTGCTACAGC TCGGTGCAGA AAGCAGATGA CGATGCTCC CGGAACAAGA TGAAGACAGT 240
GAAGTGCCTG CCGGCGGTGG ACGTCTGCAC CGAGGCGGTG GGGGCGGTGG AGACCATCCA 300
CGGACAATTG TCGCTGGCAG TCGSGGTTG CGGTTGCGGA CTCCCGGCGA AGAATGACCG 360
CGGCTCGAT CTTCACGGGC TTCTGGCGTT CATCCAGCTG CAGCAATGCG CTCAGGATCG 420
75 CTGCAACGCC AAGCTCAACC TCACCTCGCG GCGCTCGAG CCGGCAGGTA ATGAGAGTGC 480
ATACCCGCCC AACGCGGTG AGTGCTACAG CTGTGTGGCG CTGAGCCGGG AGGCGTGCCA 540
GGGTACATCG CCGCGGTGCG TGAGCTGCTA CAACGCCAGC GATCATGTCT ACAAGGGCTG 600
CTTGACCGGC AACGTCACTT TGACGCGAGC TAATGTGACT GTGTCTTGC CTGTCCGGGG 660
CTGTGTCCAG GATGAATTCT GCACTCGGGA TGGAGTAACA GGCCAGGGT TCACGCTCAG 720

5 TGGCTCTGTG TGCCAGGGGT CCGCTGTAA CTCTGACCTC CGCAACAAGA CCTACTTCTC 780
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 GGAGCCGAGG TTGACTGGAG GCGCGCTGG CCACCAGGAC CGCAGCAATT CAGGGCAGTA 1020
 TCCTGCAAAA GGGGGGCCCC AGCAGCCCCA TAATAAAGGC TGTGTGGCTC CCACAGCTGG 1080
 ATTGGCAGCC CTCTGTGTGG CCGTGGCTGC TGGTGTCTTA CTGTGAGCTT CTCACCTGG 1140
 AAATTTCTCT CTCACTACT TCTCTGGCCC TGGGTACCCC TCTTCTCATC ACTTCTCTGT 1200
 10 CCCACCACTG GACTGGGCTG GCCCAGCCCC TGTTTTTCCA ACATTCCCCA GTATCCCCAG 1260
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 TCCTCTGTG ATGTTAGGAC AGAGTGAGAG AAGTCAGCTG TCACGGGGAA GGTGAGAGAG 1440
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 15 GGTGGGACAA TGGCTCCCA CTCTAAGCAC TGCTTCCCTC ACTCCCCGCA TCTTTGGGGA 1560
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Seq ID NO: 195 Protein Sequence
Protein Accession #: NP_055215

20 1 11 21 31 41 51
 25 MDPAKAGAG AMIWTAGWLL LLLLRRGAQA LECYSCVQKA DDGCSNPKMK TVKCAPGV DV 60
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 SRALDPAGNE SAYPPNGVEY YSCVLSREA CQGTSPFVVS CYNASDHVYK GCFDGNVLT 180
 AANVTVSLPV RGCVDDEFCT RDGVTGPFT LSGSCQGSR CNSDLRNKTY FSPRIPLVR 240
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 30 AHQDRNSNG QYPARKGGPQ PHNKGCVAPT AGLAALLLAV AAGVLL

Seq ID NO: 196 DNA Sequence
Nucleic Acid Accession #: NM_006536
Coding sequence: 109..2940

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 GAACCTCCAT TCCTGGGAGC TGGAGTACAG CTTCAAGACA ATGGGTATAA TGGATTGCTC 240
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 ATAAAGATTT TAATACCTGC CACATGGAAG GCTAATAATA ACAGCAAAAT AAAACAAGAA 420
 TCATATGAAA AGGCAAAATGT CATAGTGACT GACTGGTATG GGGCACATGG AGATGATCCA 480
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 GAATGGGCCC ACCTCCGTTG GGGTGTGTTT GATGAGTATA ACAATGACAA ACCTTTCTAC 660
 ATAAATGGGC AAAATCAAA TAAAGTGACA AGGTGTTTAT CTGACATCAC AGGCATTTTT 720
 GTGTGTGAAA AAGGTCCTTG CCCCAGAGAA AACTGTATTA TTAGTAAGCT TTTTAAAGAA 780
 50 GGATGCACCT TTATCTACAA TAGCACCCAA AATGCAACTG CATCAATAAT GTTCATGCAA 840
 AGTTTATCTT CTGTGGTTGA ATTTTGTAA TGAAGTACCC ACAACCAAGA AGCACCAAAC 900
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 GTACAGGCTG GTGACAAAGT GGTCTGTTTA GTGCTGGATG TGTCCAGCAA GATGGCAGAG 1080
 55 GCTGACAGAC TCCTTCAACT ACAACAGCC GCAGAAATTT ATTTGATGCA GATTGTGAA 1140
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 70 TATGCCAATG TGAACAGGG ATTTTATCCC ATTCTTAATG CCACTGTGAC TGCCACAGTT 2040
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 75 CCAGGAGTCT AAGCCTTTGT TGTACCAAGT TACACAGCAA ACGGTAATAT TCAGATGAAT 2280
 GCTCAAGGA AATCAGTAGG CAGAAATGAG GAGGAGCGAA AGTGGGCTT TAGCCGAGTC 2340
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Seq ID NO: 197 Protein Sequence
 Protein Accession #: NP_006527

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 30 GDDPYTLQYR GCGKEGKYIH FTFNLLNDN LTAGYGSRRG VFWHEWAHLR WGVFDEYNND 180
 KPFIYINGNQ IKVTRCSSDI TGIFVCEKGP CPQENCIISK LFKEGCTFIY NSTQNATASI 240
 MFMQSLSSV EFNCNASTHNQ EAPNLQNMCM SLRSANDVIT DSADFHHSPF MNGTELPPPP 300
 TFSLVQAGDK VVCLVLDVSS KMAEADRLQ LQQAEEFYLM QIVEIHTFVG IASFDSKGEI 360
 RAQLHQINSN DDKRLVSVL PTTVSAKTDI SICSLKKGF EVVEKLNGKA YGSVMILVTS 420
 GDDKLLGNCL PTVLSSGSTI HSIALGSSAA PNLELSRLT GGLKFPVFDI SNSNSMIDAF 480
 35 SRISSGTGDI PQQHILEST GENVKPHHL KNTVTVDNTV GNDTFLVTVW QASGPPEIIL 540
 FDPDGRKYT NNFITNLTPR TASLWIPGTA KPGHWYTLN NTHSLQALK VTVTSRASNS 600
 AVPPATVEAF VERDSLHFPF PVMYANVKQ GFYPILNATV TATVEPETGD PVTLLRLDDG 660
 AGADVINKDG IYSRYFFSPA ANGRYSLKVH VNHSFISITP AHSIPGSHAM VVPGYTANGN 720
 IQMNAKRSV GRNEERKMG FSRVSSGGSF SVLGVPAGPH PDVFPCKII DLEAVKVEEE 780
 40 LTLWSWAPGE DFDQGGATSY EIRMSKSLQN IQDDFNAIL VNTSKRNPOQ AGIREIFTFS 840
 PQISTNGPEH QPNGETHESH RIYVAIRAMD RNSLQSAVSN IAQAPLFIPP NSDPVPARDY 900
 LILKGVLTAM GLIGIICLII VVTHHTLSRK KRADKKENG T KLL

45 Seq ID NO: 198 DNA Sequence
 Nucleic Acid Accession #: NM_001944
 Coding sequence: 84..3083

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 55 ATGATGAAGA AGAGATGACT ATGCAACAAG CTAAGAAGAG GCAAAAACGT GAATGGGTGA 240
 AATTTGCCAA ACCCTGCAGA GAAGGAGAAG ATAACTCAAA AAGAAACCCA ATTGCCAAGA 300
 TTACTCTAGA TTACCAAGCA ACCCAGAAAA TCACCTACCG AATCTCTGGA GTGGGAATCG 360
 ATCAGCGCGC TTTTGGAAAT TTTGTTGTTG ACAAAAACAC TGGAGATATT AACATAACAG 420
 CTATAGTCGA CCGGAGGAGAA ACTCCAAGCT TCCTGATCAC ATGTCGGGCT CTAATGCC 480
 60 AAGGACTAGA TGTAGAGAAA CCACCTTATC TAACGGTTAA AATTTTGGAT ATTAATGATA 540
 ATCCTCCAGT ATTTTCACAA CAAATTTTCA TGGGTGAAAT TGAAGAAAAT AGTGCCTCAA 600
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 65 ATCGTCTGGT TGTGAGTGGT GCAGACAAAG ATGGAGAAGG ACTATCAACT CAATGTGAAT 840
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 70 AGGCTCTAGA TTATGAACAA CTACAAAGCG TGAAACTTAG TATTGCTGTC AAAAAACAAAG 1140
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TAAAGTTGCC TGCCGTATGG AGTATCACAA CCCTCAATGC TACCTCGGCC CTCTCAGAG 1740
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Seq ID NO: 199 Protein Sequence
Protein Accession #: NP_001935

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1 11 21 31 41 51
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PSFLITCRAL NAQLDVEKP LILTVKILDI NDNPPVFSQQ IFMGEIBENS ASNSLVMILN 180
ATDADEPNHL NSKIAFKIVS QEPAGTFMFL LSRNTGVEVRT LTNSLDREQA SSYRLVVSQA 240
DKDGEGLSTQ CECNIKVKDV NDNFPMFRDS QYSARIEENI LSSELLRFQV TDLDEEYTDN 300
WLAVVFFTSQ NEGNWFETQT DPRTNBQILK VVKALDYEQL QSVKLSIAVK NKAEFHQSVI 360
SRYRVQSTPV TIQVINVRG IAPRPASKTF TVQKGISSEK LVDYILGTYQ AIDEDTNKAA 420
SNVKYVMGRN DGGYLMIDSK TABIKPVKNM NRDSTFIVNK TITAEVLAI DYTGTSTGT 480
VYVRVPDFND NCPTAVLEKD AVCSSESPSVV VSARTLNNRY TGPYTFALD QPVKLPVWS 540
ITTLNATSAL LRAQEQIPPG VYHISLVLTQ SQNNRCMPR SLTLEVQCQD NRGICGTSYP 600
TTPGTRYGR PHSGRLGPA IGLLLGLLL LLLAPLLLT CDCGAGSTGG VTGGFIPVPD 660
GSEGTIHQNG IEGAHPEDEK ITNICVPPVT ANGADFMESS EVCTNTYARG TAVEGTSGME 720
MTTLGAATE SGGAAFGATG TVSGAASGPG AATGVGICSS QQSQTMRTRH STGGTNKDYA 780
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LSGSQGSAL SASGSVQPAV SIPDPLQHGN YLVETETYSAS GSLVQPSLAG FDPILLQNV 960
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Seq ID NO: 200 DNA Sequence
Nucleic Acid Accession #: NM_020411
Coding sequence: 86..526

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1 11 21 31 41 51
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ACTGGGCGTC TTCCCATCGG CCCCTTCGCC AGTGTGGGGA ACGCGGCGGA GCTGTAGGCC 180
GGCGACTCGG GTCCTGAGG TCTGGATTCT TTCTCCGCTA CTGAGACACG GCGGACACAC 240
ACAAACACAG AACCAACACG CCAGTCCCAG GAGCCAGTA ATGGAGAGCC CCAAAAAGAA 300
GAACACGACG CTGAAAGTCG GGATCCTACA CCTGGGCAGC AGACAGAAGA AGATCAGGAT 360
ACAGCTGAGA TCCCACTGCG CGACATGGAA GGTGATCTGC AAGAGCTGCA TCAGTCAAAC 420
ACCGGGGATA AATCTGGATT TGGGTTCCGG CGTCAAGGTG AAGATAATAC CTAAGAGGGA 480
ACACTGTAAA ATGCTGAGAAG CAGGTGAAGA GCAACCACAA GTTTAAATGA AGACAAGCTG 540
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Seq ID NO: 201 Protein Sequence
Protein Accession #: NP_065144.1

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1 11 21 31 41 51
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PRSPVMESPK KKNQQLKVG I LHLGSRQKKI RIQLRSQCAT WKVICKSCIS QTPGINLDLG 120

SGVKVKIIPK EEHCKMPEAG EEQPQV

Seq ID NO: 202 DNA Sequence

Nucleic Acid Accession #: AA172056

Coding sequence: 121..339

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GATTTCAGA	AATTACAGGA	AAACTTTTCA	AAGTTCATC	TCACAGANN	TTATTTTNCC	240
AAGAATTC	AGATAAGTTT	AGTTTATGG	AAGACTTTA	TGTGGTTTT	ACTCACTCT	300
CATCTCAGAC	ATCAGACAGT	GATTACATCA	CTTATAGTTC	TAGTAAATTT	ATTAATATAA	360
AATCAGAGA	CATTCCAAAT	TCCACATTGC	TTACACCAAT	AGGCATAGAT	TCAGTGTGAG	420
CTATGCAAT	TGAAATGAG	CTGTTTGTG	ATTTAAAGGT	TTAAATTTCT	CTAACCAAC	480
TGCTTGATCC	AGATGCAGGA	CTGCAATGT	TAATATTTGT	TCTGGAAGAA	CAATCAATA	540
AGACTTAAGA	GGAAAGGGAA	TGGCCCAAT	CCACCTGAAA	TTTTTCTTA	AAAAGTGTG	600
AGCCTACTAA	ATCAGAAATGA	AAATAGAAAT	ACAAGATTAT	AAACAAATG	CAATCAAACT	660
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TTCACTCATC	AAAAAATAAA	GTITGTATCA	TTTAGTATTT	TCCCAATAAA	ATTGGTCGTT	900
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ATTATTTCTA	AATACCAAA					

Seq ID NO: 203 DNA Sequence

Nucleic Acid Accession #: NM_005656.1

Coding sequence: 57..1535

30
35
40
45
50
55
60
65
70
75

1	11	21	31	41	51	
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CGGAAAACCC	CTATCCCGCA	CAGCCCACTG	TGGTCCCCAC	TGCTACGAG	GTGCATCCGG	180
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ACCCCGTGGT	CTGCACGAG	CCCAATTCCT	CATCCGGGAC	AGTGTGCACC	TCAAGACTA	300
AGAAAGCACT	GTGCATCACC	TTGACCTGG	GGACCTTCCT	CGTGGGAGCT	CGCGTGGCCG	360
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Seq ID NO: 204 Protein Sequence

Protein Accession #: NP_005647.1

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   GRAACRDMGY KNNFYSSQGI VDDSGSTSPM KLNTSAGNVD IYKKLYHSDA CSSKAVVSLR 240
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10  VKPVCPLNPG MMLQPEQLCW ISGWGATEEK GKTSEVLNAA KVLLETQRC NSRYVYDNLI 420
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Seq ID NO: 205 DNA Sequence
 Nucleic Acid Accession #: XM_044533
 Coding sequence: 238..2751

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CCACCATATC CACCTCGCT CCATCTTTGA ACTCAAACAC GAGGAACTAA CTGCACCCCTG 3600
 GTCCTCTCCC CAGTCCCCAG TTCACCCCTCC ATCCCTCACC TTCCTCCACT CTAAGGGATA 3660
 TCAACACTGC CCAGCACAGG GGCCTGAAT TTATGTGGTT TTTATACATT TTTTAATAAG 3720
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5

Seq ID NO: 206 Protein Sequence
 Protein Accession #: XP_044533.6

10 1 11 21 31 41 51
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 15 VASAYIPESL GSLQDDDDXI YFFPSETGQE FEFFENTIVS RIARICKGDE GGERVLQQRW 300
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 EGFQQLVASV CPEVVEDGVA DQTDGGGSVP VIISTSRVSA PAGGKASWGA DRSYWKFLV 720
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 25 PLDHRGYQSL SDSPPGSRVP TESEKRPLSI QDSFVEVSPV CPRPRVRLGS EIRDSV

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein
5 incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

1. A method of detecting a bladder cancer-associated transcript in a cell from a patient,
5 the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-13.
2. The method of Claim 1, wherein the biological sample comprises isolated nucleic
10 acids.
3. The method of Claim 2:
 - a) wherein the nucleic acids are mRNA; or
 - b) further comprising the step of amplifying nucleic acids before the step of contacting
15 the biological sample with the polynucleotide.
4. The method of Claim 1, wherein the polynucleotide:
 - a) comprises a sequence as shown in Tables 1A-13; or
 - b) is immobilized on a solid surface.
20
5. The method of Claim 1, wherein the patient is:
 - a) undergoing a therapeutic regimen to treat bladder cancer; or
 - b) suspected of having bladder cancer.
- 25 6. An isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1A-13.
7. The nucleic acid molecule of Claim 6, which is labeled.
- 30 8. An expression vector comprising the nucleic acid of Claim 7.

9. A host cell comprising the expression vector of Claim 8.
10. An isolated polypeptide which is encoded by a nucleic acid molecule having
5 polynucleotide sequence as shown in Tables 1A-13.
11. An antibody that specifically binds a polypeptide of Claim 10.
12. The antibody of Claim 11, further conjugated to an effector component.
- 10 13. The antibody of Claim 12, wherein the effector component is a fluorescent label.
14. The antibody of Claim 12, wherein the effector component is a radioisotope or a
cytotoxic chemical.
- 15 15. The antibody of Claim 11, which is
a) an antibody fragment; or
b) a humanized antibody
- 20 16. A method of detecting a bladder cancer cell in a biological sample from a patient, the
method comprising contacting the biological sample with an antibody of Claim 11.
17. The method of Claim 16, wherein the antibody is further conjugated to an effector
component.
- 25 18. The method of Claim 17, wherein the effector component is a fluorescent label.
19. A method for identifying a compound that modulates a bladder cancer-associated
polypeptide, the method comprising the steps of:

- a) contacting the compound with a bladder cancer-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1A-13; and
- b) determining the functional effect of the compound upon the polypeptide.

5

20. A drug screening assay comprising the steps of

- a) administering a test compound to a mammal having bladder cancer or a cell isolated therefrom;
 - b) comparing the level of gene expression of a polynucleotide that selectively hybridizes
- 10 to a sequence at least 80% identical to a sequence as shown in Tables 1A-13 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of bladder cancer.

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
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(51) International Patent Classification⁷: **C12Q 1/68**,
C07H 21/04, C07K 14/00

(21) International Application Number: PCT/US02/21338

(22) International Filing Date: 3 July 2002 (03.07.2002)

(25) Filing Language: English

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60/343,705 8 November 2001 (08.11.2001) US
60/350,666 13 November 2001 (13.11.2001) US
60/372,246 12 April 2002 (12.04.2002) US

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(81) Designated States (*national*): AE, AG, AL, AM, AT, AU,
AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU,
CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,
LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW,
MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG,
SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN,
YU, ZA, ZM, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM,
KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW),
Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM),
European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE,
ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK,
TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ,
GW, ML, MR, NE, SN, TD, TG).

Published:

— with international search report

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6 November 2003

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.



WO 03/003906 A3

(54) Title: **DIAGNOSTIC AND SCREENING METHODS FOR BLADDER CANCER**

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in bladder cancer. Also described are such genes whose expression is further up-regulated or down-regulated in drug-resistant bladder cancer cells. Related methods and compositions that can be used for diagnosis, prognosis, or treatment of bladder cancer are disclosed. Also described herein are methods that can be used to identify modulators of bladder cancer.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/21338

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C12Q 1/68; C07H 21/04; C07K 14/00

US CL : 536/24.3; 435/6; 514/2; 530/350, 300

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/24.3; 435/6; 514/2; 530/350, 300

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Please See Continuation Sheet

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y. E	US 2003/0050470 A1 (AN et al) 13 March 2003 (13.03.03), column page 6, par. 57-62; page page 13, par. 135-141; page 15, par. 158-163; page 30, par. 349-351.	1-20
Y	US 5,866,535 A (GBTZENBERG et al) 02 February 1999 (02.02.1999), column col. 5, lines 43-55; col. 10, lines 31-60; col. 11, lines 30-67.	1-5, 7-20
A	SRINIVAS, P.R. Proteomics in Early Detection of Cancer. Clinical Chemistry. 22 June 2001, Vol. 47, No. 10, pages 1901 -1911, especially pages 1906-1908.	1-20

☐ Further documents are listed in the continuation of Box C.

☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

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"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T"

later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X"

document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y"

document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&"

document member of the same patent family

Date of the actual completion of the international search

07 April 2003 (07.04.2003)

Date of mailing of the international search report

23 MAY 2003

Name and mailing address of the ISA/US

Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

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